Thu May

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May

Run on:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

908470 seqs, 133250620 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Perfect score:

Title:

Sequence:

Scoring table:

Searched:

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B. bronchiseptica
Human ORFX ORF2085
Novel human diagno
Novel human diagno
Human polypeptide
Human polypeptide
                                                                                                                                                                                                                                            Human polypeptide
Human polypeptide
Human polypeptide
Peptide 683 derive
Poptide BBO5 deriv
Drosophila melanog
Sequence of a bloa
Sugar beet chitina
Drosophila melanog
Ser-Pro-Pro-Pro ge
Novel human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thalia
Bioadhesive precur
Ser-Pro-Pro-Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidally activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ser-Pro-Pro gene
Prod. of DNA of p
Complete form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                            AAO04412
AAO02076
AAO020124
AAO02134
AAO02036
AAR11739
AAR11739
AAR28150
AAB1730
AAB77250
AAB77250
AAB77250
AAB77250
AAB9333
AAB9332
AAB9332
AAB105332
AAR063338
                AAE16201
AAE16193
AAE16200
AAE16200
AAE16202
AAE16203
AAE16203
AAE16203
AABG09876
ABG09877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE16198 standard; peptide; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-097639/13.
                                                                                                                                                                                          W0200190143-A2.
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147.5
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143
140.5
138
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137.5
137.5
136.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
 B. bronchiseptica
Bordetella paraper
Bordetella paraper
Pertactin antigen
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
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Bordetella bronchi
                                                                                                                                   (without alignments)
256.453 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_101002:*

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:*
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                                                                                                                                                                                  US-09-855-754B-19
335
1 GARAPPAPRPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
                                                                                                                7, 2003, 16:31:28 ; Search time 30.1363 Seconds
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SUMMARIES

AAR25578
AAR14321
AAR16195
AAR16197
AAR16197
AAR16194
AAR16320
AAR26503

58 922 922 922 60 60 56 52 911 911

100.0 100.0 93.7 90.4 84.8 84.8 84.8

335 335 335 320 314 303 303 284 284 284

42967860

AAE16198

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В

Length

Score

Result Š

% Query Match I

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                                                                                                                                                            Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  present invention relates to Bordetella bronchiseptica pertactin
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/label= P70
260.263
/note= "motif associated with cell-cell adhesion"
266.285
/note= "contains 5 direct *---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "contains 9 direct repeats of Pro-Gln-Pro"
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/note= "motif associated with cell-cell adhesion"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 335; DB 23;
100.0%; Pred. No. 3.9e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR25578 standard; Protein; 922 AA.
Claim 26; Fig 1c; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AA;
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\overset{\mathcal{A}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\mathcal{C}}{\times}\overset{\ma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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when
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            A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digetion of B.parapertussis chromosomal DNA with Sau3A and cloining of 40-50kb fragments into the BamHI site of cosmid pHG79. The cosmids were screened with a 1.8kb clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (*P95*) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella parapertussis pertactin outer membrane protein, p.70.
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                                                                                                                                                                                                                                                                                                   Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                               Score 335; DB 13;
Pred. No. 2.7e-17;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pertactin region I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16185 standard; Protein; 922 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 34; 47pp; English.
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Best Local Similarity 100.0%; Pi
Matches 58; Conservative 0;
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/note= "P
564..621
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                                                                                                                                                                                                                                                             922 AA;
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                                                                                                                                                                                                                                                              Sequence
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used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal ciells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative or grantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                   Gaps
                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                 Length 922;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                     Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                             100.0%; Score 335; DB 23;
100.0%; Pred. No. 2.7e-17;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                AAR14321 standard; Protein; 922 AA
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/label= .
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                                                                                                                                                                                                                                                                                                                266..270
/label= repeat
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/label≖ re
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/label- re
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/label = re
                                                                                                        Local Similarity 100.
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/label- ru
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/label= re
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/label= r
                                                                                                                                                                                                                                                                                      Bordetella parapertussis
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                                                                                                                                                                                                                                                    Pertactin antigen P.70.
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                                                                                922 AA;
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                                                                                                                                                                                                                                   20-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clare JJ,
                                                                                Sequence
                                                                                                                                                                                                                 AAR14321;
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                   pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448 (1989).
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRDPAPQPPAGRELSAA
                                                                                                                                                                                                                                                           The 46 Xs represent amino acids missing in the specification.
                                                                                                                                                                                                                                                                                                                                 Length 922
                                                                                                                                                      microproganisms are transformed for the expression of
                                                                Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                             95.5%; Score 320; DB 12;
96.6%; Pred. No. 3.4e-16;
live 0; Mismatches 2;
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                                                                                                                Disclosure; Fig 1C; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE16195 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR
           WPI; 1991-325214/44.
N-PSDB; AAQ14320.
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                                                                                                                                                                                                                                                                                              922 AA;
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                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                               Query Match
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52 AA.

AAE16194 standard; peptide;

RESULT 7

(first entry)

26-MAR-2002

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    B. bronchiseptica strain II-5 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                 Gaps
                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQP-PQP-PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                              Length 60;
                                                                                                            Score 314; DB 23;
Pred. No. 1.3e-16;
                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                 AAE16197 standard; peptide; 56
                                                                                                          93.7%;
96.7%;
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                                                                                                                                             Conservative
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                                                                                                                           Similarity
                                                                           AA;
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                                                                                                                                            58;
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                                                                         Sequence
                                                                                                       Query Match
Best Local S
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                      pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRGPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.8%; Score 284; DB 23;
89.7%; Pred. No. 1.9e-14;
.lve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR14320 standard; Protein; 911 AA.
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                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Fig 1c; 47pp; English.
                B. bronchiseptica strain II-2
                                                                                                                                                                                                            23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                             25-MAY-2000; 2000US-206969P
                                                                                                      Bordetella bronchiseptica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.7
Matches 52; Conservative
                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 AA;
                                                                                                                                      WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Gaps

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Length 56; Indels

Score 303; DB 23; Pred. No. 8.1e-16;

90.4%; 94.8%;

Mismatches

0;

Conservative

Local Similarity

Query Match

Best Loca Matches

8 8

 us-09-855-754b-19.rag

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Pertactin; PNN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against arrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPA, KPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPPAPPAPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284; DB 13;
Pred. No. 1.4e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
254..299
/note= "Pertactin region I"
                                                                                                                             260..262
/label= RGD_tripeptide
701..703
/label= RGD_tripeptide
                                                                                       /label- Repeat_region
                                                                                                                   Repeat_region
                              Location/Qualifiers
35..632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 28pp; English.
                                                  35..632
/label= P.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.8%;
ilarity 89.7%;
Conservative
                                                                                                                                                                                                                                                                             91GB-0006568
                                                                                                                                                                                                                                                  92WO-GB00561
                                                                                                                                                                                                                                                                                                      (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                 3/0..589
/label= Re
         Bordetalla bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       911 AA;
                                                                                                                                                                                                                                                  27-MAR-1992;
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                                                                                                                                                                                                WO9217587-A
                                                                                                                                                                                                                                                                                                                                Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                  Protein
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Region
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                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%; Score 284; DB 12; Length 911;
89.7%; Pred. No. 1.4e-13;
11ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · 6
                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1B; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                           (WELL ) WELLCOME FOUNDATION LTD
                                                                                                                                                                                                                                87..589
|abel= repeat
                                               166..270
'label - repeat
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        Bordetella bronchiseptica
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/label- re
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/label- re
                                                                         . 275
                                                                                                                             ..576
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                                                                                                                                          /label=
578..580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ14319
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                                            Peptide
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                                                                                                                             Peptide
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(1989).
                                                                                                                                                                               Peptide
                                                                                                                                                                                                          Peptide
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Matches
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RESULT 9 AAR26503

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Length 911; Indels 28

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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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89.7%; Pred. No. 1.4e-13;
ive 0; Mismatches 0; Indels
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28; 47pp; English.
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                                                                                                                                                                                                        Guiso-maclouf N, Boursaux-eude
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-EP06457
                                                                                                        23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.7
Matches 52; Conservative
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                                                                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                    WPI; 2002-097639/13.
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                                              WO200190143-A2
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AAE16196
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.3%; Score 282.5; DB 2.89.7%; Pred. No. 2.4e-14; ive 0; Mismatches 1.
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                                                                                                                                                              Claim 26; Fig 1c; 47pp; English.
                 Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16201 standard; peptide; 54
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                                                  WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 AA;
                 Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when weed in affinity chromatographic columns. Pertectin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, is well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Bordetella infections
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRPQRPQRPAPQPPAGRELSAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 54;
                                                                                                                                                                                                                                                                                                                                                        5; Indels
Pertactin antibody is useful for treating
                                                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                                                                                            Score 265; DB 23;
Pred. No. 4.6e-13;
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84.5%;
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                                                                                                                                                                                                                                                                    54 AA;
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 B. bronchiseptica strain II-1 pertactin outer membrane protein region II. AAE16193 standard; peptide; 49 (first entry) 26-MAR-2002 AAE16193; RESULT 13 **AAE1619**3 g

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. 23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P Bordetella bronchiseptica (INSP) INST PASTEUR WO200190143-A2

WPI; 2002-097639/13.

Guiso-maclouf N, Boursaux-eude C;

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica The present invention relates to Bordetella bronchiseptica pertactin pertactin outer membrane protein region il.

49 AA; Sequence

AAE16200 standard; peptide; 52

RESULT 15

AAE16200 ID AAE1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques an imal tissue and human or other animal cells, as well as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiques can be used for qualifative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                           B. bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                       r membrane protein; vaccine; Bordetella infection; antibacterial; region II.
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of
                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to Bordetella bronchiseptica
                Length
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                                           Indels
               DB 23;
      Score 263.5; DB 23;
Pred. No. 5.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guiso-maclouf N, Boursaux-eude
                                                                                                                                                                         AAE16199 standard; peptide; 48
             78.78;
84.58;
                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                          Conservative
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therapy; antibiotic; a
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Best Local Similarity
Labes 49; Conserve
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B. bronchiseptica strain II-8 pertactin outer membrane protein region II.
                                                     26-MAR-2002 (first entry)
AAE16200;
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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. Bordetella bronchiseptica, WO200190143-A2 29-NOV-2001.

(INSP) INST PASTEUR.

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as veccine. Pertactin artibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

52 AA; Sequence

Gaps ; 9 Score 256; DB 23; Length 52; Pred. No. 2e-12; 0; Mismatches 3; Indels 3; Indels Query Match 76.4%; Best Local Similarity 84.5%; Matches 49; Conservative C

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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRDPAPPQPPAGRELSAA

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Search completed: May 7, 2003, 16:47:08 Job time : 31.1363 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2003, 16:53:34 ; Search time 16.7905 Seconds

(without alignments)
306.927 Million cell updates/sec

Title: US-09-855-754B-18
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Published Applications_AA:* 1: /cgn2_6/ptodata/2/pubpaa/US0B_NEW_PUB.pep:* 2: /cgn2_6/ptodata/2/pubpaa/US0B_NEW_PUB.pep:* 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:* 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:* 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:* 7: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:* 8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:* 13: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:* 13: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:* 14: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
Post-processing	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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IES		-75	-75	-75	-75	-75	-75	-75	-75	-75	-75	-75	-75	-75	-75	-74	3-5	3-5	-74	3-5
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	12 US-10-023-523-47	9 US-10-171-384-3	10 US-09-823-240-2	12 US-10-042-417-32	9 US-10-020-215-2	9 US-09-959-987-2	9 US-09-925-299-1002	10 US-09-925-299-1002	10 US-09-904-987-7	10 US-09-850-887-4	10 US-09-765-272-160	9 US-10-171-384-1	10 US-09-791-171-70	10 US-09-864-761-34988	10 US-09-864-761-36844	10 US-09-764-864-967	9 US-09-298-523B-62	9 US-09-298-523B-2	9 US-10-067-457-5	9 US-10-077-584-4	9 US-09-298-523B-61	9 US-09-298-523B-1	9 US-09-298-523B-60	9 US-09-824-574-4	9 US-10-077-584-9	9 US-09-820-843A-17	
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4 4 7 1	132.5	128.5	127	122.5	122.5	121.5	121.5	121.5	121.5	121	120.5	120.5	119	118	118	118	117.5	117.5	116.5	116	115.5	115.5	115.5	115	114.5	114.5	
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: ROLLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUGSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FITLE OF INVENTION: INMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR ELLING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUISO-MACLOUF, NICOLE TITLE OF INVENTION: POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYMEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BONDETELA PARAPERTUSSIS, AND BORDETELA TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
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FILE REPERENCE: 0395-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 2.4e-14;
0; Mismatches 1;
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Pred. No. 2.3e-13;
0; Mismatches 1
                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUNSAUX: EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bordetella parapertussis US-09-855-754-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09855754 publication No. US20020192237A1 GENERAL INFORMATION:
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94.8%;
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1 Similarity 94.8%;
55; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Best Local Similarity
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Matches 55; Conserv
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LENGTH: 922
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFECTION IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNCERIC (COMPOSITIONS)
FILE REFERENCE: 03495-0206-00000
CORRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 66/206,969
PRIOR APPLICATION NUMBER: 66/206,969
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE DE INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2010-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                             Score 294.5; DB 9;
Pred. No. 8.9e-14;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Bordetella bronchiseptica US-09-855-754-15
                                                                                                                                                                                                                           ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09855754 Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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1 Similarity 91.7%;
55; Conservative
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Matches 52; Conservative
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Gaps

7;

Length 49;

J US-09-855-754-14

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYBEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTUCSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION UNMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SSOFTWARE: PALENTIN Ver. 2.1
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Publication No. US2020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISSO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                          1 GAKAPPAPKPA------PQPGPQPPQPPQPPQPPQPPQRQPEAPAPGPPGRELSAA 48
                                                                                                                                                                 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQRQPEAPAPQPPAGRELSAA
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                                                            Score 264.5; DB 9;
Pred. No. 7.4e-12;
0; Mismatches 0;
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Best Local Similarity 86.0%; Pred. No. 2.4e-11;
Matches 49; Conservative 0; Mismatches 2;
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Pred. No. 2e-11;
0; Mismatches
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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US-09-855-754-20
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US-09-855-754-21
                                                                                                                                                                                                                                                                                                                  US-09-855-754-20
Sequence: 20, Application US/09855754
Publication No. US20020192237A1
PUBLICATION INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                            82.18;
ilarity 87.58;
Conservative
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idarity 85.7%;
Conservative
                                                         Query Match
Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 48; Conserv
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US-09-855-754-21
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LENGTH: 48
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CARCLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PREPACTION IN BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US,09/9855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOY: 2.1
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                                                                                                                                                                                                                                                                                                                  559 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQPPQPPQPPQPPAPAPPAPPAFFESAA 610
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                                                                                                                                                                                       Length 911;
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                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                  Score 285; DB 9;
Pred. No. 3.5e-12;
0; Mismatches 0,
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Pred. No. 5.4e-13;
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                                                                            ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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PRIOR FILIRO DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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ilarity 92.9%;
Conservative
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1 Similarity 91.1%;
51; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 4
LENGTH: 911
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Best Local Similarity
Matches 52; Conserva
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Best Local Similarity
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LENGTH: 52
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RESULT 13
US-09-855-754-5
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LENGIH: 910
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIOUS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                        APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA
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Pred. No. 2.9e-11;
0; Mismatches 5; Indels
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Pred. No. 2.6e-08;
0; Mismatches 1
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                                                                                                                                                                Sequence 22, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
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1 Similarity 73.2%;
41; Conservative
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Best Local Similarity 87.5%;
Matches 49; Conservative
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Matches 41; Conserv
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; ORGANISM: BO:
US-09-855-754-23
                                                                                                                                            US-09-855-754-22
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LENGTH: 54
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                                                                                                                      APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQPPQREAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THERR USE IN DIAGNOSTICS, AN
TITLE OF INVENTION: INMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.2%; Score 210; DB 9; I Best Local Similarity 73.2%; Pred. No. 3.2e-07; Matches 41; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.9%; Score 189.5; DB 9
Best Local Similarity 67.9%; Pred. No. 5.7e-07;
Matches 38; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 39
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                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
Sequence 5, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                   2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Bordetella pertussis
US-09-855-754-5
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| GENERAL INFORMATION:
| APPLICANT: Lees, Ann M. |
| APPLICANT: Lees, Robert S. |
| APPLICANT: Lees, Simon W. |
| TITLE OF INVENTION: POYEEL LOW DENSITY LIPOPROTEIN BINDING |
| TITLE OF INVENTION: ATHEROSCLEROSIS |
| FRIOR PELICATION NUMBER: US/09/9616,289 |
| PRIOR PELICATION NUMBER: US (08/979,608 |
| PRIOR PELING DATE: 1997-06-03 |
| PRIOR FILING DATE: 1997-11-26 |
| PRIOR FILING DATE: 1997-11-27 |
| PRIOR FILING DATE: 1997-11-27 |
| PRIOR FILING DATE: 1997-06-03 |
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Search completed: May 7, 2003, 17:30:52 Job time : 16.7905 secs

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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein

7, 2003, 16:41:02 ; Search time 10.494 Seconds (without alignments) 513.008 Million cell updates/sec Мау Run on:

US-09-855-754B-18

Title: Perfect score:

322 1 GAKAPPAPKPAPQPGPQPGP.......QRQPEAPAPQPPAGRELSAA 56 Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	pertactin - Bordet	me	outer membrane pro	hypothetical 47,8K	pherophorin-S - Vo	proline-rich prote	UL36 protein - hum	hypothetical proli	sulfated surface g	proline-rich prote	T20H2.9 protein -	hypothetical prote	nuclear protein EB	cysteine-rich exte	chitinase (EC 3.2.	cysteine-rich exte	hypothetical prote		protein-tyrosine-p	hypothetical prote		proline-rich prote		hypothetical prote	_		hypothetical prote	S	hydroxyproline-ric
CHTWWWOC	ID	S15204	A47675	A32560	JC2301	T10798	S16748	ММВЕН6	A34043	A33647	S21961	A86335	T48814	S42442	A48232	S51939	B48232	н83619	S47538	T14355	AE2295	T17547	T17531	S22697	T10340	T31611	T17737	T24470	JQ1696	T07907
	Length DB	922 2		910 2					141 2		•	•	1952 2	487 2	209 2	439 2		270 2						•		1585 2			426 2	446 2
ф	Query Match L	94.1	88.5	65.2	51.1	46.3	45.8		45.3	45.3	44.7	44.3	٠	43.9	43.5	43.5	٠	43.0	43.0	٠	41.9	٠	41.6	41.6	41.5	41.5	41.3	41.1	41.1	41.1
	Score	303	285	210	164.5	149	147.5	٠	-	146	-		142.5	141.5	140	140	139.5	138.5	138.5	138.5	135	134.5	134	134		133.5	133		132.5	132.5
	Result No.	 	7	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

proline/lysine-ric hypothetical prote	proline-rich prote extensin-like prot proline-rich prote Ammediate-early pr	extensin-like prot procyclin homolog lysine/proline-ric extensin homolog T pistil extensin-li	hypothetical prote ORF2 protein - sai procyclic acidic r proline-rich prote
T17908 B96534 T17815	T17636 JQ1686 T17525 EDBEIF	T10741 T17557 T17887 T06291 PQ0476	S75138 B34770 A26036 B24264
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496 494 225	339 151 549 1460	461 309 456 760 154	1749 102 129 240
41.1	40.5 40.4 40.4 40.1	39 39 39 39 39 4	39.4 39.3 39.3
132.5 132 131	130.5 130 130 129	128 127.5 127.5 127.5	127 126.5 126.5 126.5
30 31 32	8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	37. 38 40 41	4 4 4 4 2 4 4 4 5 4 3 2

ALIGNMENTS

RESULT 1 -815204
pertactin ⊨ Bordétella parapertussis N;Alternate names: outer membrane protein P70
C;Species: Bordețella parapertussis
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999 C:Accession: S15204: S14659
Rill, L.J.; Dougan, G.; Novotny, P.; Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
A,Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A: Neterence number: S15204; MUID:91251771; PMID:2041476
A: MOLECULE TYPE: DNA
A; Residues: 1-922 <lil></lil>
A;Cross-reference's: EMBL:X54547; NID:g39761; PIDN:CAA38419.1; PID:g39762
C;Genetics:
A;Gene: prn C;Keywords: membrane protein
Query Match 94.1%; Score 303; DB 2; Length 922;
 Pred. No. 4.7e-13; O. Mismatches 1. Indole
Oy 1 GAKAPPAPAPAPOPGPQPGPQPPQPPQPPQPPQRQPBAPAPQPPAGRELSAA 56
Db 564 GAKAPPARPAPGPGPGPGPGPPQPPQPPQPPQPPQPPQPPQPPQROPEAPAPQPGRELSAA 621

C; Accession: A47675 R; Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J. Gen. Mcroblol. 138, 1697-1705, 1992 A; Title: Cloning, nucleotide sequence and heterologous expression of the protective o A; Contents; CN7531 68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica C;Species: Bordetella bronchiseptica C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 RESULT 2

4. Query Match 88.5%; Score 285; DB 2; Length 911; Best Local Similarity 92.9%; Pred. No. 6.6e-12; Matches 52; Conservative 0; Mismatches 0; Indels

1;

Gaps

A;Status: preliminary
A;Status: preliminary
A;Molecule type: nucleic
A;Residues: 1-911.clll>
A;Residues: 1-911.clll>
A;Cross-references: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397
A;Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

A; Accession:

GAKAPPAÅKPAPOPGPQPGPQPPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 56

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Gaps

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proline-rich protein - rape (fragment)

C;Species: Brassica napus (rape)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997

C;Accession: S16748

R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991

A;Description: Cloning and characterization of a proline-rich gene expressed specific A;Recession: S16748

A;Accession: S16748

A;Recession: S16748

A;Residues: 1-449 <ROBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: 130085
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
                A;Cross-references: EMBL:Y07752; NID:91655698; PIDN:CAA69032.1; PID:91655699
A;Experimental source: strain HK.10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: 130085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KPQPKPPPRPQPKPQPKPQPKPPPRPPRPSPCPPQPPKPQPKPPPPPPFP 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 147.5; DB 2; Length 449;
Pred. No. 0.0026;
3; Mismatches 16; Indels 17
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A;Wolecule type: DNA
A;Residues: 1-3164 <MCG>
                                                                                                                                                                                Length 599;
                                                                                                                                                                                                                                              19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                             Score 149; DB 2;
Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146.5; DB Pred. No. 0.014;
                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UL36 protein - human herpesvirus 1 (strain 17)
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Best Local Similarity 67.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.6%;
Matches 29; Conservative
                                                                                                                                                                                Query Match 46.3%;
Best Local Similarity 54.5%;
Matches 24; Conservative
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Best Local Similarity
A; Residues: 1-599 <GOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 QPPAG 50
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C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
R;Accession: J02301
R;Mada, M; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Titles. MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis.
A;Reference number: J02299; MUID:96051989; PMID:8535973
A;Accession: J02301
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A;Title: Molecular cloning and characterization of protective outer membrane protein P.6 A;Reference number: A32560; MUID:89264462; PMID:2542937
A;Accession: A32560
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C; Species: Volvox carteri
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T10798
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
A; Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin A; Reference number: 217154; MUID:97162277; PMID:9009264
A; Reference number: 217154; MUID:97162277; PMID:9009264
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-430 <WAD>
A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                             C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Cross references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A; Cross references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator.
C; Keywords: membrane protein
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAKAPPAPKPA----PQPGPQPGPQPPQPPQPPQPQPQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQ--RQPEA-----
                                                                                                                                                         outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 2;
Pred. No. 4.4e-07;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 47.8K protein - Pneumocystis carinii
N;Alternate names: ORF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.2%; ; imilarity 73.2%; ; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pherophorin-S - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 41; Conserv
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PEPQPP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 PAPQPP 48
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Length 3164;

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Ritheologis, A.; Scker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maith, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Tille: Sequence and analysis of chromosme 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48814
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
Stbmitted to the protein Sequence Database, April 2000
A;Reference numbe;: 224541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1137 <STO>
A;Cross-references: GB:AE005172; NID:g8778985; PIDN:AAF79900.1; GSPDB:GN00141
                                                                                                                                                                                                                      T20H2.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
                                                              A, Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220 A; Experimental source: cosmid contig 15E6; strain 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 15E6.220 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 142.5; DB 2;
Pred. No. 0.011;
4; Mismatches 13;
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C;Species: human herpesvirus 4, Epstein-Barr virus
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Pred. No. 0.017;
3; Mismatches
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ilarity 54.5%;
Conservative
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Best Local Similarity 59.23
Matches 29; Conservative
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A; Molecule type: DNA
A; Residues: 1-1952 <SCH>
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nes 24; Conserv
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                                                                                                                                                                                                                                                                                                     C; Accession: A86335
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A; Introns: 281/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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7. Cell Biol. 109, 3403-3501, 1989
A:Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A:Reference number: A33647; MUID:90094551; PMID:2689458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S21961
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
A;Description: Clouding and characterization of a proline-rich gene expressed specificall
A;Reference number: S16748
                                                                            C; Accession: A34043; B34043
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
A; Title: Presence in invertebrate genomes of sequences characterized by the repetition A; Reference number: A90159; MUID:90147742; PMID:2105723
hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment) C; Species: Owenia fusiformis C; Date: 07-Jun-1990 #text_change 01-Dec-2000
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Residues: 1-485 <ERT>
A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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Pred. No. 0.0013;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 146; DB 2; Length 485;
Pred. No. 0.0035;
3; Mismatches 18; Indels
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Best Local Similarity 54.9%; Pred. No. 0.0051;
Matches 28; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQPEAPAPQPPAGR 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sulfated surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 256/1; 299/3; 387/3; 470/1
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1 Similarity 52.3%;
23; Conservative
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ilarity 53.2%;
Conservative
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A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M32217
A;Accession: B34043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
Matches 23; Conserv
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A; Residues: 1-534 <ROB>
                                                                                                                                                                                                                                                                      A; Residues: 1-141 <BAK>
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Indels

Length 1137;

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Length 1952;

DB 2;

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chifinase (EC 3.2.1.14) precursor - beet
Cispecies: Beta vulgaris (beet)
C;Date: 28-Oct-1996 #sequence_rovision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: S51939; S72315; S4505
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A
Plant Mol. Biol. 27, 211-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X79301; NID:9488730; PID:9488731
A;Note: the authors translated the codon TGC for residue 416 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 РРАРКРАРОРСРОРСРОРСРОРОРОР----РОРРОРОВОРЕАРАРОРАСКЕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%; Score 140; DB 2;
46.2%; Pred. No. 0.0079;
ive 5; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introdes: 248/1; 300/2
C; Superfamily: plant chitinase homology
C; Keywords: glycosidase; hydrolase
F; 1-25/Domain: signal sequence #status predicted <S
F; 26-439/Product: chitinase #status predicted <WAT>
F; 183-423/Domain: plant chitinase homology <PCH>
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A; Residues: 191-397 <BER2>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 24; Conserv
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A; Molecule type: DNA
A; Residues: 1-439 <BER>
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ne : 11.494 secs
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-487 cFRR>
A; Residues: 1-487 cFRR>
A; Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
R; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
B; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
A; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
A; Title: Uz region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2.
A; Reference number: S42447; MUID:85063846; PMID:6209719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6823-5833, 1995
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Developmental expression of tobacco pistil-specific genes encoding novel extens
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000 C;Accession: $42442; $32988; $42447 R;Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E. Proc. Natl. Acad. $61, U.S.A. 83, $605-5100, 1986 A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a A;Reference number: $42440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 39-209 <GGL>
A; Cross-references: EMBL:14020; NID:g19918; PID:g19919
A; Cross-references: EMBL:14020; NID:g19918; PID:g19919
C; Superfamily: glutelin
C; Superfamily: glutelin
C; Reywords: cell wall; extracellular matrix; fertilization; glycoprotein
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-209/Product: cysteline-rich extensin-like protein 1 #status experimental <MAT>
F; 146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48232; PQ0475; S24617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-88,'PPP',89-487 <DAM>
A; Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cysteine-rich extensin-like protein 1 precursor - common tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.5%; Score 140; DB 2; Length 209; Best Local Similarity 53.3%; Pred. No. 0.0044; Matches 24; Conservative 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQPEAPAPQPPAGRE 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141.5; DB 2;
Pred. No. 0.0068;
1; Mismatches 19;
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-487 <SAM>
R; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Reference number: S32973
A; Accession: S32988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:L13439; NID:g310922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.9%;
nilarity 52.1%;
Conservative
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-209 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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Gaps

Length 439;

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:49 ; Search time 5.43782 Seconds (without alignments) 427.133 Million cell updates/sec Мау Run on:

Title: Perfect score: Sequence:

US-09-855-754B-18 322 1 GARAPPAPRPAPGPGPQPGP......QRQPEAPAPQPPAGRELSAA

56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	8	a	Description
1	303	94.1	922	-	PERT_BORPA	P24328 bordetella
7	285	8	911	П	PERT_BORBR	Q03035 bordetella
m	210		910	÷	PERT_BORPE	P14283 bordetella
∢	147.5	S	449	٦	APG_BRANA	P40603 brassica na
S	146.5	45.5	3164	-	TEGU_HSV11	_
ø	146	٠	141	+	YPRO_OWEFU	_
7	146	•	485	-	SSGP_VOLCA	P21997 volvox cart
6 0	142.5	44.3	534	-	APG_ARATH	arabido
a	141.5	٠	487	-	EBN2_EBV	-
10	140	٠	2004	-	MOZ_HUMAN	
11	138.5	43.0	431	7	ACRO_RABIT	_
12	136	ď	555	Н	GP1_CHLRE	
13	133.5		875	7	Y066_NPVOP	_
14	132.5	41.1	426	П	EXLP_TOBAC	
15	131.5	_	105	П	COLL_HSVS7	P25050 herpesvirus
		40.5	265	Н	MOT8_MOUSE	O70324 mus musculu
17	126.5	39.3	102	-	COLL_HSVSC	_
18	126.5	39.3	129	ч	PARB_TRYBB	P09791 trypanosoma
19	126.5	39.3	261	ч	PRP2_MOUSE	_
50	126.5	39.3	296	7	PRP3_MOUSE	P05143 mus musculu
21	126.5	6	1059	٦	CAPU_DROME	_
22	126	φ.	440	-	G3PT_MOUSE	Q64467 mus musculu
23	125.5	σ.	1206	ч	FM14_MOUSE	Q05859 mus musculu
24	125.5	39.0	1468	7	FWN1_MOUSE	Q05860 mus musculu
22	124.5	38.7	143	٦	PAR1_TRYBB	P08469 trypanosoma
56	124.5	38.7	145	П	PARC_TRYBB	•
27	124	38.5	1790	-	SEPA_EMENI	_
28	123.5	38.4	339	7	CSP_PLABE	
53	123.5	38.4	347	П	CSP_PLABA	P23093 plasmodium
30	123.5	38.4	3110	П	HD_RAT	P51111 rattus norv
31	123	38.2	296	-	GDA6_WHEAT	P04726 triticum ae
32	122	37.9	520	-	WASP_MOUSE	P70315 mus musculu
33	122	•	979	П	RFX1_HUMAN	P22670 homo sapien

			P14918 zea mays (m P10164 rattus norv	
CSP_PLAYO	HD_HUMAN ACRO_PIG	SRA4_RAT BRD4_HUMAN	EXTN_MAIZE PRP2_RAT MB11 ARATH	KPC1_TRIRE PRP3_RAT
				144
367	3144 415	1048	267 172 642	1139
37.7	37.7	37.4	37.0 36.8 36.8	36.8
121.5	121.5	120.5	119 118.5 118.5	118.5
34 35	35	39	4 4 4 3 7 3 6 1	44 5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       J. Gen. Microbiol. 138:1697-1705(1992).

-!- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCES MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
-!- SUBCELLOLAR LOCATION: Outer membrane.
-!- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-!- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
--- CONCENTRATIONS.
                                                                                                                                                          (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        56
                           LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella bronchiseptica.";
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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PERTACTIN (P.68).
POTEMPIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                ; DB 1;
6.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane; Signal; Virulence; Repeat. SIGNAL 1
                                                                                                                                                                                                                                                                  Score 303;
                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A47675; A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           · PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                              95178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54815; CAA38584.1; -. EMBL; A19180; CAA01453.1; -.
                                                                                                                                                                                                                                                                ch 94.1%;
1 Similarity 94.8%;
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                              280
285
603
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(Rel. 26, I
(Rel. 41, I
                                                                                                                                                                                                              922 AA;
                                                    266
266
271
271
281
575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CN7531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERT_BORBR
Q03035;
                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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SITE
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REPEAT
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REPEAT
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PERT_BORBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-SAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=96196517; PubMed=8609998;
BENSIGY P., Charles I.G., Fairweather N.F., Isaacs N.W.;
Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
-!- FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADMESION, AND THUS FLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.; "Molecular coloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis."; Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Outer membrane.
-i- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                ELL ATTACHMENT SITE (POTENTIAL).
X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                              Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                             4
                                                                                                                                                                         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRIOR OMPG9A.
                                                                                                                                                                                                           0; Indels
                                                                                                   (APPROXIMATE).

X 3 AA REPEATS OF P-Q-P.

3078DF6EC2D987A1 CRC64;
                                                                                                                                                                       Score 285; DB 1;
Pred. No. 7.2e-11;
0; Mismatches 0;
                                CELL ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                 910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bronchiseptica.";
J. Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89264462; PubMed-2542937;
                                                                                                                                       93995 MW;
                                                                                                                                                                         88.5%;
92.9%;
                                                                                                                                                                                                           52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 264 AND 332
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                703
275
270
275
280
601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella pertussis.
                                                                                                                                       911 AA;
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                            PERT_BORPE
P14283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella.
                                                                                                                                       SEQUENCE
                                                                  REPEAT
                                                                                      REPEAT
                                                                                                      REPEAT
                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                   PERT_BORPE
                                                                                                                                                                                                           Matches
SEEEEEES
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                               46 OPPAG 50
                                                                                                                                                                                                      SPKPG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPRO_OWEFU
ID YPRO_OWEFU
                                                                                                                                                                                                                                                                 TEGU_HSV11
                         NON_TER
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                  Query Match
                                                                                                                                                                                                                                         RESULT 5
TEGU_HSV11
                                                                                                          fatches
                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draper J., Scott R.;

"Gametophytic and sporophytic expression of an anther-specific arabidopsis thallana gene.";

-I-TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-I-DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT, HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus (Rape).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-94004980; Pubmed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                  LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                          CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                 1; Indels 14;
                                                                                                                                                                                                                                     5 (APPROXIMATE).
5 X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                      Length 910;
                                                                                                                                                                                                                                                                                      Score 210; DB 1;
Pred. No. 1.9e-06;
0; Mismatches 1;
                                                                                                                  PERTACTIN (P.69).
                                                                                                                                                                                                                              4 (APPROXIMATE).
                                                                                  Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                 POTENTIAL,
          InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam. PF03212; Pertactin; 1.
PRINYS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                93452 MW;
                                                                                                                                                                                                                                                                                        65.2%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                       910
711
910
262
PIR; A32560; A32560.
                                                                                                                                                                                                                276
281
286
579
910 AA;
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APG OR CEX
                                                                                                                                                                                                                                                                                                                                                                                                                        APG_BRANA
P40603;
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                  CHAIN
PROPEP
SITE
                                                                                                                                                                            DOMAIN
REPEAT
REPEAT
                                                                                            SIGNAL
                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                              REPEAT
                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                             268
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
APG_BRANA
                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88274327; PubMed-2839594; MEGEOCH D.3., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McGeoch D.3., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McGeoch D.3., Scott J.E., Taylor P.; The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1."; The complete DNA sequence of the long unique region in the genome of J. Gen. Virol. 69:1531-1574(1988).

1- FUNCTION: TEGINENT PROTEIN.

1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                             3 KAPPAPKPAPQPGPQPGPQPPQPPQPPQ------PPQPPQRQPE---APAP 45
                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
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                                                                                                                    Match 45.8%; Score 147.5; DB 1; Length 449; Local Similarity 44.6%; Pred. No. 0.0053; No. 29; Conservative 3; Mismatches 16; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQP-PQRQPEAPAPQPPAG 50
132 132 BY SIMILARITY.
428 428 POTENTIAL.
449 AA; 48779 MW; 9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 146.5; DB Pred. No. 0.025; Aismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 3164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; 130085; WMBEH6.
InterPro; IP3005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
ilarity 67.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10299;
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Ź 141

PRT;

ö

Gaps

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Length 485; 18; Indels

45.3%; Score 146; DB 1; 52.3%; Pred. No. 0.0069; iive 3; Mismatches 18

Similarity

A52216400A031421 CRC64;

50436 MW;

485 AA;

PRO-RICH POLY - PRO

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Glycoprotein; Sulfation; Hydroxylation
                                                                                                                         23; Conservative
                                                                                       Query Match
Best Local S:
Matches 23
                                    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                      RESULT 8
APG_ARATH
 SFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INIVIDIAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
ATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE-90147742; PubMed-2105723;
MEDILINE-10147742; PubMed-2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bressnce in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Biochem. Biophys. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-f. wagarlensis / HK10;
MEDILE-90094551; PubMed-2689458;
Ertl H., Wengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri; molecular structure of
                                                                                                        Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 1; Length 141;
Pred. No. 0.0028;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 РРАРКРАРОРСРОРСРОРСРОРРОРРОРРОРРОРРОРРОРРАСЯ 51
                                                                                                                                                                                                                                                                                                                                                                                                                      15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
H-T-H MOTIF (POTENTIAL).
             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
pypothetical proline-rich protein (Fragment).
Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                         Hypothetical protein; DNA-binding.
NON_TER 1 1 1 DOMAIN 9 58 POLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
01-OCT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.2%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA;
                                                                                                                                            MCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSGP_VOLCA
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SEQUENCE FROM N.A.

STRATN=C.** Columbia;

A Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Con L., Conway A.B., Conway A.R., Ergigl J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nerman W.C., Osborne B.I.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Ru D., Yu G., Fraser C.M., Voysotskala V.S., Walker M.,

"Sageuence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
APG OR ATIG20130 OR T20H2.9.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CY. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (Salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
--- TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
--- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATURATION.
SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Draper J., Scott R.; "Gametophytic expression of an anther-specific addaptions that and specific Arabidopsis thaliana gene."; Plant J. 3:111-120(1993).
                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eurosids II; Brassicales; Brassicaceae; Arabidopsis.
5 РРАРКРАРОРСРОРСРОРСРОРРОРРОРРОРОВРОВАРАРОРР
                                                                                                                                                                                                                            P40602; 093214; 09LNT8;
01-FBB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                    534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-94004980; Pubmed-8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 408:816-820(2000).
                                                                                                                                                                                                    STANDARD;
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MIM; 601408;
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                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIDDRY REPAYED DESCRIPTION OF THE PROPERTY OF 
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-84270667; PubMed-6087149;
Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glason T.J., Haffull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. VITOL. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                              ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE-90266473; PubMed-2161150;
Pettl L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen J.I., Wang F., Kieff E.; "Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142.5; DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 КАРРАРКРАРОРСРОРСРОРСРОРРОРРОРРОРОЯ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
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4; Mismatches
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01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 AA
                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AY058847; AAL24235.1;
                                                                                                                                                                                                                                                                                     PIR; $21961; $21961.
InterPro; IPR001087; Lipase_GDSL.
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                                                                                                                                                                                                                              EMBL; X60377; CAA42925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 59.2
Matches 29; Conservative
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ACT_SITE
CONFLICT
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P12978;
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                                                                                                                                                                                                                                                                                                                                                                             Signal.
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MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968; PubMed-8782817;
MEDLINE-96376968;
MEDLINE-96376968;
MEDLINE-96376968;
MEDLINE-96376968;
MEDLINE-96376968;
MEDLINE-96376969;
MEDLIN
SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
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Transcription regulation; Activator; Nuclear protein; DNA-binding;
Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF2ZO OR MOĢ.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X 2 AA TANDEM REPEATS OF R-G.
DEF40D7F8ED61D1A CRC64;
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InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Inf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V01555; CAA24877.1; ALT_INIT.
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Genew; HGNC:13013; ZNF220.
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                                                        -1- PTM: PHOSPHORYLATED.
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Matches 25; Conserv
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glycoprotein 1).
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                                                       MEROPS; S01.223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBÇNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE-Testis;
STRAIN=New Zealand white; TISSUE-Testis;
Richardson R.T., O'Rand M.G.;
Blochim Biophys. Acta 1219:215-218(1994).
I-TOWINGTON: ACROSIN IS THE MAJOR PROTERSE OF MAMMALIAN SPERMATOZOA.
IT IS A SERINE PROTESES OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID=9986;
                                                                                                                                                                                                                                                                                                                            BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                      translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                            Score 140; DB 1; Length 2004;
Pred. No. 0.043;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                     9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPAPKPAPQPGPQPGPQPPQP-PQPPQPPQRQPEAPAPQPP 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA
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MET-RICH.
                                                                                                               PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
C2HC-TYPE.
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GLU-RICH.
GLU-RICH.
POLY-GLU.
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POLY-GLU.
POLY-ARG.
POLY-GLU.
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 Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00226; H15; 1.
SMART; SM00249; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_2; 2.
Proto-oncogene; Chromosomal ti
                                                                                                                                                                                                                                                                                                                                                                                 43.5%;
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Best Local Similarity 60.00
Best Local Similarity 50.00
Conservative
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1242
1302
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                                                                                                        Nuclear protein
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P48038;
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PARTIAL PRELIMINARY SEQUENCE FROM N.A. MEDLINE=91017504; PubMed=1699225; Adair W.S., Apt K.E.; "cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-.i.F. FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosylated polyproline II rods-with-kinks as a structural motif in
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                MENORS: 2011.12.7.

INTERPROFILE TRYOURS TO THE TRYOURS THE TRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACROSIN LIGHT CHAIN (BY SIMILARITY)
ACROSIN HEAVY CHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09FPQ6; 003927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.017;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant hydroxyproline-rich glycoproteins.";
Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.0%; Score 138.5;
or send an email to license@lsb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21159092; PubMed=11258910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.38;
                                                                                                 EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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223
264
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Conservative
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                                                                                                                                                                                           Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLLINATION.
                                                                                                                                                                                                                                                                                                     TOBAC
                                                                                                                                                                                    Query Match
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REPEAT
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                                                                                                                                                                                                                                                                                           EXLP_TOBAC
                                                                                                                                                                                                                                                                               RESULT 14
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJUE-97343549; Pubmed-1618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3,
gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyla
                                                                                                                                                                                                                VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                                                                                  POLY-PRO.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                           ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-97271300; PubMed-9126251; Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.; Annual Annual Moltmann G.F.;
                                                                                                                                                                                                                                                                                                   DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                        4 APPAPK-PAPQPGPQPGPQPGPQPPQP---PQPPQPPQRQPEAPAPQPP 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VICOLOGY 210:372-382(1995).
                                                                                                                                                                                                                                                                                                                       17; Indels
                                                                                                                                                                                                                                                                                                   Score 136; DB 1,
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                          083949; 065364; 010323; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) Hypothetical 98.6 kDa protein (ORF71).
                                                                                                                                                                                                                                                                                                                                                                                                                      875 A.A.
 SUBUNIT: Associates with GP2 and GP3. PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                      POTENTIAL
                                                                                                                         EMBL; M58496; AAA69706.1; ALT_SEQ. GlycoSulteDB: Q9FPQ6; ...
InterPro: IPRO02965; P. Tich_extensn. InterPro: IPRO03882; PIStIl_extensin. PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; Pubmed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     udosugata.";
Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                               54219 MW;
                                                                                                                 EMBL; AF309494; AAG45420.1; -
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                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                  ch 42.2%;
l Similarity 53.1%;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                               555
339
279
399
455
                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                  259
399
455
455
555 AA;
                                                                                                                                                                                        Glycoprotein;
SIGNAL
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                                                                                                                                                                                                              CHAIN
DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco).

Wikaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermitophyta; Agnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                          F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PPAPKPAPQPGPQPGPQPP-QPPQPPQPPQRQPEAPAPQP
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Pfam; PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.5%; Score 133.5; DB 1;
56.8%; Pred. No. 0.057;
ive 2; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 AA.
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MEDLINE-93005740; PubMed-1392607;
                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
DOMAIN 86 91 P
SEQUENCE 875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                       EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; IFOS.
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or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-90279084; PubMed-2161952;
Geck P., Whitaker S.A., Medveczky M.M., Medveczky P.G.;
"Expression of collagenlike sequences by a tumor virus, herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92046383; PubMed-1658399;
Geck P., Whitaker S.A., Medveczky M.M., Medveczky P.G.;
"Expression of collagenlike sequences by a tumor virus, herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQ--PGPQ--PGPQ--PGPQPPQPPQPPQPPQRQPEAPAPGPPAG 50
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N-LINKED (GLCNAC. . .) (POTENTIAL).
; 51A495CC94017812 CRC64;
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                                                                                                                                                              41.1%; Score 132.5; DB 1; Length 426; 50.0%; Pred. No. 0.039; 1ve 3; Mismatches 18; Indels 5.
                                                                                                                                            48
                                                                                                                                        2 AKAPPAPKPAPQPGPQPGP----QPGPQPPQPPQPPQPPQRQPE-APAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss institute of Bioinformatics and the the European Bioinformatics institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
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EF3DF0FE0FB446F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Herpešvirus saimīrī (strain 484-77).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Sammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.8%; Score 131.5; DB 1; Best Local Similarity 53.6%; Pred. No. 0.016; Matches 30; Conservative 2; Mismatches 17;
                                                                                                                                                                                                                                                                                          (Rel. 34, Last sequence update)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                              105 AA
                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 1.
Collagen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 70 C
105 AA; 10260 MW;
                                     426 AA; 44278 MW;
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                                                                   Query Match
Best Local Similarity 50.09
Matches 26; Conservative
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                              Collagen-like protein.
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                                                                                                                                                                                                                                                        COLL_HSVS7
P25050;
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01-0CT-1996
REPEAT
CARBOHYD
SEQUENCE
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COLL_HSVS7
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Title:

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Database

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Q9jle9 rattus norv
Q9cx9 streptomyce
O13305 pneumocysti
Q69023 human herpe
P9797 volvox cart
Q88777 oryza sativ
Q96v11 pneumocysti
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Boursaux-Eude C., Guiso N.;

Fortaussis, Bordetella bronchiseptica.";

Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250087; CAB764411;

EMBL; AJ250087; CAB764411;

InterPro; IPR004899; Pertact_gup.

InterPro; IPR002965; P_rich_extensn.

PRINTE; PR01217; PRICHEXTENSN.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella
NCBI_TaxID-518;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.168) (Fragment).
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100.0%; Pred. No. 3.2e-20;
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                    GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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09K5H2
09K1P9
09ALP9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 97
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                     Pertactin (Fragment).
sordetella bronchissptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Infect. Immun. 69:1917-1921(2001).

InterPro; IPR001992; pertactin.

InterPro; IPR004899; Pertactin.

InterPro; IPR002965; P_rich_extensn.
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1; -.
InterPro: IPR004899; Pertact_sup.
InterPro: IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXIENSN.
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26107 MW; 368C142508D77057 CRC64;
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122 AA; 12395 MW; BED00966A40FF994 CRC64;
                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%; Score 322; DB 2; Local Similarity 100.0%; Pred. No. 3.5e-20; les 56; Conservative 0; Mismatches 0;
                        122 AA
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MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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                        PRELIMINARY;
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252 AA;
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                                                                                                                                                                                                                                                                                                                                             STRAIN-16039;
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SEQUENCE
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Best Local 5
                      Q9KJX9
Q9KJX9;
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09KJX9
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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL; AJ250089; CAB76443.1; -.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR004899; Pertact.sup.
PinterPro; IPR002965; P_rich_extensn.
Pen; PF03212; Pertactin; IPR004899; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQRQPPARPAPQPPAGRELSAA 56
                               1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 115 115
SEQUENCE 115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                      115 AA
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MEDLINE-20359389; Pubmed-10899896;
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RESULT 6 Q9K5H1

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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1; ...
Interpro: IPR004899; Pertact.sup.
Interpro: IPR002965; Prich_extensn.
PF03212; Pertactin; I
                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GAKAPPAŖKPA----PQPGPQPGPQPPQPPQPPQPPQRPPGRPAPAPQPPAGRELSAA 72
                                                                                                                                                  DB 2; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        boruecella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.5%; Score 285; DB 2; Length 107; 92.9%; Pred. No. 3.6e-17; 1ve 0; Mismatches 0; Indels
                                                                                     215 215
215 AA; 22327 MW; 5C21D45CF784B4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AA; 11036 MW; 1AC13209D0238107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
                                                                                                                                                Score 291.5; DB 2;
Pred. No. 1.8e-17;
0; Mismatches 0;
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MEDLINE-20359389; Pubmed-10899896;
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STRAIN-KM22;
MEDLINE-21117018; Pubmed-11179374;
  Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                  90.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin (P.68) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 92.9
Matches 52; Conservative
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                Query Match
Best Local Simi
Matches 53;
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Q9ALP9
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Q9K5H5
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MEDLINE_2039389; PubMed-10899896;
BOUTSAUX-EDGE C., Guiso N.;
POLYMOTPHISM of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250085; CAB76439.1;
InterPro; IPR004899; Pertact_sup.
PRO3212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                          26
                                                                                                                                                22 GAKAPPAPKPAPQPGPQPGPQPGP---PQPPQPPQPPQPPGRPAPAPAPRELSAA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 109;
                                             Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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EMEL, ANOTOZ63; AAG38439.1; -. InterPro; IPR0013992; Pertactin.
InterPro; IPR0013992; Pertact.Sup.
InterPro; IPR002965; P_rich_extensn.
                                       Query Match 94.1%; Score 303; DB 2; Length 11
Best Local Similarity 94.8%; Pred. No. 1.2e-18;
Matches 55; Conservative 0; Mismatches 1; Indels
9B67012D3B9AEECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
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                                                                                                                                                                                                                                                                          109 AA
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
  11453 MW;
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  111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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Query Match

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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250079; CAB76433.1; InterPro; IPR004099; Pertact_sup. Pf03212; Pertact_sup.
                                                                                                                                                   pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250077; CAB76431.1; -.
InterPro; IPR004899; Pertact_sup.
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                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQRQPEAPAPQPPAGRELSAA 56
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                                                                                                                Boursaux-Eude C., Guiso N.; "Polymorphism of Repeated Regions of Pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
                                                                                                                                                                                                                                                                                             104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cr-2000 (TrEMBLrel. 15, Created)
1-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-UCr-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%; Score 264.5; DB 2;
ilarity 87.5%; Pred. No. 1.7e-15;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                Query Match 82.1%; Score 264.5; DB 2; Best Local Similarity 87.5%; Pred. No. 1.7e-15; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LAPR;
MEDLINE-20359389; PubMed-10899896;
                                                                                            MEDLINE=20359389; PubMed=10899896;
                                                                                                                                                                                                                                   Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boursaux-Eude C., Guiso N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                          104
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Les 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=518;
                  NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
Bordetella
                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KJY1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9K5H7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9K5H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09K5H7
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ245927; CAB82515.1; InterPro: IPR003992; pertactin.

InterPro: IPR003992; pertactin.

InterPro: IPR003991; pertactin.

InterPro: IPR003991; pertactin.

PROMIS: PR01482; PERTACTIN.

PRINTS; PR01482; PERTACTIN.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King A., Berbers G., Hoogerhout P., Olrschot van H.F., Knipping K., Mool F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 GAKAPPAPKPA----PQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceaė;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 911;
                                                                                                                                                                                                                                                                        Score 285; DB 2; Length 200;
Pred. No. 5.9e-17;
0; Mismatches 0; Indels
Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94093 MW; DF531A9EB4383A32 CRC64;
                                                                                                                                                                                                                   200
20826 MW; 9F3AC6E4128942E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 88.5%; Score 285; DB 2; Similarity 92.9%; Pred. No. 2e-16; 52; Conservative 0; Mismatches
                                Infect. Immun. 69:1917-1921(2001).
EMBL, AX007271; AAG38447.1; -.
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_ich_extensn.
Pfam; PF03212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                     PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 1000
SEQUENCE 200 A0; 20826 MW;
                                                                                                                                                                                                                                                                          / Match 88.5%;
Local Similarity 92.9%;
nes 52; Conservative
                    bronchiseptica Pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella,
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Best Local
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                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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Q9L4E2
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09K5H9
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Search completed: May 7, 2003, 16:53:14
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                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                    STRAIN-MBORDE 31
                                                                                                NCBI_TaxID-518;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                    Rell D.J., Fenwick B.;
*Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-B;
Kerll D.J., Fenwick B.;
*Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and POP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPGPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF156771; AAF82395.1; -... InterPro: IPR004899; Pertact_sup. InterPro: IPR002965; P_riol_extensn. PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA; 11693 MW; FA3A76596F7097EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E1ABD4D347D20652 CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-07N-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 1.9e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 264.5; DB 2;
Pred. No. 1.9e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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115 AA; 11705 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01217; PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.1%;
ilarity 87.5%;
Conservative
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1 Similarity 87.5%;
49; Conservative
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                                                                                                                                                                                                                                                           amino acid repeats.
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                                                                                             SEQUENCE FROM N.A.
Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WCBI_TaxID-518;
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NON_TER
SEQUENCE
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SEQUENCE
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Q9AHP0
ID Q9AHP
AC Q9AHP
DT 01-JU
DT 01-JU
DT 01-JU
DE PERTA
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OC OX OX SERVICE SERVI
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
82.1%; Score 264.5; DB 2; Length 198;
Best Local Similarity 87.5%; Pred. No. 2.9e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 7
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 AA; 20575 MW; AC940EC331A725AF CRC64;
                                                                                                                                                                                                                                                                                                                                        Infect. Immut. 69:1917-1921(2001).

ZMBL; Ar298590; AAK16691.1; -
Interpro; IPR003992; pertactin.

Interpro; IPR004899; Pertact_sup.

Interpro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                    MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	B. bronchiseptica	B. bronchiseptica	Pertactin antiqen	prn proteins. Bor	Bordetella bronchi	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Pertactin antiqen	Bordetella paraper	
SUMMARIES			ខ	AAE16193	AAE16194	AAR14320	AAR26503	AAE16183	AAE16196	AAE16197	AAE16198	AAR14321	AAR25578	
			DB	23	.23	12	13	23	23	23	23	13	13	
			Match Length DB	49	25	911	911	911	53	56	28	922	922	
	ф	Query	Match	100.0	95.9	95.9	95.9	95.9	95.7	95.1	94.8	94.8	94.8	
			Score	278	266.5	266.5	266.5	266.5	266	264.5	263.5	263.5	263.5	
		Result	Q	П	71	m	4	'n	o	7	80	6	10	

Bordetella paraper	B. bronchiseptica		B. bronchiseptica		B. bronchiseptica	Bordetella pertuss		ະທ	Peptide 683 derive	Peptide BBO5 deriv	Synthetic Bordetel	Human ORFX ORF2085	Novel human diagno	human	phila m	Novel human diagno	o-Pro-		Human polypeptide	Human polypeptide	Human polypeptide	Human polypeptide		human		Herbicidally activ	Human low density	Rabbit low density	Sugar beet chitina	Np70 protein carbo	Human Npw38BP1 tra	Np70 protein seque	Human RNA metaboli	NpwBP. Homo sapie
AAE1618	AAE16195	AAE1619	AAE16200	AAE16201	AAE16202		AAE17146			AAR11739	AAR87649		ABG09876	ABG0987		ABG27250	ABB78537	AAO02036	-	AA00441	_		-		-	-	-	-	AAR2815	•	AAY8232	AAY6746	-	AAB47514
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AAE16193	Æ	¥	26	В.
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ALIGNMENTS

mbrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2. 29-NOV-2001.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P. (INSP) INST PASTEUR. Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AA;
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Gaps
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       Length 49;
                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                    Indels
100.0%; Score 278; DB 23;
100.0%; Pred. No. 3.5e-15;
tve 0; Mismatches 0;
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AAE16194 standard; peptide; 52 AA. 26-MAR-2002 (first entry) AAE16194; AAE16194 RESULT

B. bronchiseptica strain II-2 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

forPolypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as veccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquent to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Pichia microorganisms are transformed for the expression of pertectin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.59 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                         Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\tt II.}
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                                                     Length
                                                                                     1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                   Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                           Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                      0; Mismatches
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                         AAR14320 standard; Protein; 911 AA
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                                                                                                                                                                                                                   Pertactin antigen P.68.
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                                                          Best Local Similarity
                              52 AA;
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                                                                   49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                    B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                                                        Length 911;
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                                                                                                                                           1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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NO. 2.3e-13;
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/label- P.68
266.279
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/label- RGD_tripeptide
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/label- RGD_tripeptide
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/label- Repeat_region
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                                                                    Query Match 95.9%;
Best Local Similarity 94.2%;
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                                                                                                                                                                                                                                                                                                                                           12-MAR-1993 (first entry)
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                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypertides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
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254. 299
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559. Gld
/note= "Pertactin region II"
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                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 94.2
es 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-097539/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD26440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
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Boursaux-eude C;

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                      23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                              25-MAY-2000; 2000US-206969P
                Bordetella bronchiseptica.
                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                  WPI; 2002-097639/13,
                                                                                                                                                                                                                                                              Guiso-maclouf N,
                                                      WO200190143-A2.
                                                                                                29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as veccine. Pertactin antibody is useful for treating Bordetella infections and used to detect bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                 B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                         Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 266; DB 23; Length 53;
Pred. No. 3.1e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16196 standard; peptide; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16197 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%;
Llarity 92.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000; 2000US-206969P
                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                    Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA;
                                                                                                                                                                                                                                                                                                        WO200190143-A2.
                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                    AAE16196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                       AAE16196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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    RESULT
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----POPPOPPOROPEAPAPOPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                Score 264.5; DB 23;
Pred. No. 4.2e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16198 standard; peptide; 58 AA.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                95.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                  56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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us-09-855-754b-14.rag

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W09115571-A
                                                                                                             17-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR25578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Protein
                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tells, as well as bloodsical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                          pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPRPAPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptides containing polymorphisms of the repeated regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.8%; Score 263.5; DB 23;
84.5%; Pred. No. 5.2e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR14321 standard; Protein; 922 AA
Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266..270 /label repeat 271..275 /label repeat
                                                                                                                                            Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575..577
/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583..585
/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92..594
label - repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= repeat
598..600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586..588
/label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281..285
/label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     579..581
/label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin antigen P.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3ordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR14321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pept1de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260..262
/note= "motif associated with cell-cell adhesion"
266..285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575.612
//note= "contains 9 direct repeats of Pro-Gln-Pro"
712.714
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      è,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.8%; Score 263.5; DB 12; Length 922; liarity 84.5%; Pred. No. 3.9e-13; Conservative 0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
35..643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR25578 standard; Protein; 922
/label= repeat
610..612
/label= repeat
                                                                                                                                                                                                                                                                                            (WELL ) WELLCOME FOUNDATION LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35..643 //
                                                                                                                                                                                                91WO-GB00487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                             Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AA014320
                                                                                                                                                                                                28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                 02-APR-1990;
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Boursaux-eude C;
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                    WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guiso-maclouf N,
  Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-2001
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        AAE16195;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; p.70.
                                                                                                                                                                          A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of Cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro. gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQPQPEAPPAPAGRELSAA 49
                                                                                                              Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 922;
                                                                                                                                                                                                                                                                                                                                               Score 263.5; DB 13;
Pred. No. 3.9e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
254..304
/note= "Pertactin region I"
764..621
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16185 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                         Claim 1; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                               94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000; 2000US-206969P.
91WO-GB02302
                   90GB-0027901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2001; 2001WO-EP06457
                                       (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                WPI; 1992-250033/30.
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                             922 AA;
                                                                                            N-PSDB; AAQ26509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190143-A2
23-DEC-1991;
                   21-DEC-1990;
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                                                            Charles IG;
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                                                                                                                                                                                                                                                                                                                             Sequence
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Region
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Matches
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.8%; Score 263.5; DB 2
84.5%; Pred. No. 3.9e-13;
ive 0; Mismatches 0
                                                                                                                                                             Disclosure; Page 34; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16195 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2001; 2001WO-EP06457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodsical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      -----PQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 60;
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                             Score 262.5; DB 2.
Pred. No. 6.3e-14;
0; Mismatches 0
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0
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Best Local Similarity 81.7%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPG
                                                                                                                                                                                                                                                                                  60 AA;
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    888888888888888
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 B. bronchiseptica strain II-7 pertactin outer membrane protein region II. AAE16199 standard; peptide; 48 AA (first entry) 26-MAR-2002 AAE16199; RESULT 13 AAE16199 g

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

3ordetella bronchiseptica

40200190143-A2

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Weccine. Wetherlan artibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

48 AA; Sequence

AAE16201 standard; peptide; 54 AA.

RESULT 15
AAE16201
ID AAE16

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    bronchisertica strain II-8 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                     Pertactin; P_{\rm N}^{\rm N}N; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                    Gaps
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   DB 23; Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP----PQRQPEAPAPQPPAGRELSAA
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated pertactin in Bordetella species, useful in immunogenic
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   Score 261.5; DB 23;
Pred. No. 6.4e-14;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 238.5; DB
Pred. No. 4e-12;
0; Mismatches
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                               0;
                                                                                                                                                                        AAE16200 standard; peptide; 52
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ilarity 86.8%;
Conservative
94.1%;
Llarity 98.0%;
Conservative
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                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica.
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Best Local Similarity
Matches 46; Conserv
Query Match
Best Local Similarity
Matches 48; Conserv
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                                                                                                                                          RESULT 14
AAE16200
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to decemine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                           Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                              Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P
                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                  Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                             29-NOV-2001.
                 AAE16201;
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP-----PQRQPEAPAPQPPAGRELSAA 49 7; Score 237.5; DB 23; Length 54; Pred. No. 5e-12; 0; Mismatches 2; Indels 7; 85.4%; Scor. 83.6%; Pred. No. 5e. 0; Mismatches Query Match Best Local Similarity 83.64 Matches 46; Conservative ò g

54 AA;

Sequence

5

Gaps

7, 2003, 16:47:04 Search completed: May Job time: 26.46 secs

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NUMBER OF SEQUENCES: 17
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US-08-460-269C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 2, sequence 2, sequence 11 Sequence 11 Sequence 16 Sequence 16 Sequence 14 Sequence 2, sequence 2, sequence 2, sequence 2, sequence 2, sequence 6, sequence 6, sequence 12, sequen
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
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Patent
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US-08-750-61-11

US-08-750-61-11

US-08-460-269-8

US-08-46-982A-16

US-08-314-268-149

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US-09-227-420-4

US-09-227-420-4

US-09-041-886-28

US-09-041-886-39

US-09-041-886-30

US-09-041-886-30

US-09-041-886-30

US-09-041-886-31

US-09-041-886-30

US-09-041-886-30

US-09-041-886-30

US-09-05-441-886-30

US-09-05-441-886-30

US-09-05-441-886-30

US-09-05-56-419-21

US-08-26-982A-6

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US-08-26-982A-6

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US-08-26-982A-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 200000000
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Match Length
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Maximum DB seq
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263.5
213.5
131.5
128.5
121.5
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Sequence 8
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAME: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LEBNGTH: 11 and no acids
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ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
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Best Local Similarity 94.2%; Pred. No. 1.6e-16;
Matches 49; Conservative 0; Mismatches 0;
US-09-056-556-230
US-09-072-596-225
US-09-072-596-225
US-08-471-780C-44
US-08-471-282A-44
US-08-467-282B-44
US-08-46-710C-44
US-08-46-710C-44
US-08-46-710C-44
US-08-46-710C-44
US-08-46-710C-44
US-08-46-710C-87
US-08-46-710C-87
US-08-46-710C-87
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US-08-860-635A-21
US-09-281-476-21
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Gaps

Indels

Length 910;

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568 GAKAPPAPKPAPQPG-----PQPPQPPQPQPEAPAPQPPAGRELSAA 609
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STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATE: US/08/237,716 FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 213.5; DB 4
Pred. No. 7.3e-12;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
                                                                                    NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHRRACTERISTICS:
LENGTH: 910 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE FINYENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PULCATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UTN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-UTN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08237716
Patent No. 5589384
GENERAL INFORMATION:
                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.8%;
83.7%;
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SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.8
Best Local Similarity 83.7
Matches 41; Conservative
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STRANDEDNESS: single
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STATE: Virginia
COUNTRY: USA
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ROPANOS, MICHAEL A.
ROPENOS: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                     ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 922;
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263.5; DB 4;
Pred. No. 3e-16;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/460,269C
ATORILING DATE: 02-10n-1995
ATORILING DATE: 02-10n-1995
ATORILING DATE: 02-10n-1995
NAME: Lebovitz, Richard M.
REFERENCE/DOCKET NUMBER: 37,067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 243-6333
                                                  Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243-6410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 243 (100) TELEFAX: (703) TELEFAX: (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VA
                       US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-460-269C-2
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Gaps
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                                                                                     Sequence 8, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Casella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.7%; Score 121.5; DB 4
88.0%; Pred. No. 3.3e-05;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,269C
FILIAG DATE: 02-Un-1955
ATTORNEY, AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11near
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 POPGPOPPOPPOROPEAPAPOP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 POPGPOPPOPPOP---OPEAPAPOP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                       YEAST
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-246-982A-16
                                               RESULT 6
US-08-460-269C-8
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Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: Chong, Pele
APPLICANT: Lein, Michel H
TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                /label- P69 BB05 epitope of Bordetella pertussis sequence
                                                                                                                                                                                                                                                                                                        Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-PEB-1997
                                                                                                                                                                                                                                                                                                    Query Match 47.3%; Score 131.5; DB 1; Best Local Similarity 74.2%; Pred. No. 6e-06; Matches 23; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2e-06;
0;
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

46.2%; Score 128.5;
Best Local Similarity 88.5%; Pred. No. 8.2e
Matches 23; Conservative '0; Mismatches
                                            /label- LTB sequence
                                                                                                                             /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                    10 PAPQPGPQPGPQPPQPPQRQPEAPAPQP 40
                                                                                                                                                                                                                                                                                                                                                                                                             5 PGPEIAPQPGPQPPQPPQP---QPEAPAPEP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                    NAME/KEY: Region
LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: Region LOCATION: 1..2 OTHER INFORMATION:
                                                                                   NAME/KEY: Region
LOCATION: 4.7
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-750-624-11
                                                                                                                                                                                                                                                         US-08-237-716-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: TO
STATE: O
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-750-624-11
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PC-DOS/MS-DOS

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Gaps

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GENERAL INFORMATION:
APPLICANT: DOORDAT, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIROSS
FILE REFERENCE: 3789/80902
CURRENT APPLICATION NUMBER: US/09/314,268
EARLIER APPLICATION NUMBER: 09/314,268
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PALENTING PATE: 1999-05-18
NUMBER OF SEQ ID NOS: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 334;
                                                                               9 KPAPQPGPQPGPQPPQ-PPQRQPEAPAPQPPA-----GRELSA 48
                                 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID ITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       í, indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 APPAP-----KPA-PQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.3%; Score 112; DB 4; Best Local Similarity 48.9%; Pred. No. 0.00064; Matches 23; Conservative 6; Mismatches 16
         Pred. No. 0.012;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.0027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.1%; Score 111.5;
Best Local Similarity 48.9%; Pred. No. 0.0
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human papillomavirus type 49
US-09-314-268-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
                                                                                                                                                                                           Sequence 149, Application US/09314268
Patent No. 6346377
Best Local Similarity 50.0%; Pr
Matches 25; Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09026587
Patent No. 5912128
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Patent No. 5202236
                                                                                                                                                                        US-09-314-268-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 149
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US-09-026-587-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
CORRESPONDENCE: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KPAPQPGPQPGPQPPQPPQ-PPQRQPEAPAPQPPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Score 114;
                                   APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.0%; Score 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/COCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                              TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                   41.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven P
                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 50.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: protein
                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D C
                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                      US-08-246-982A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-453-265-16
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POLYNUCLEOTIDE VACCINE PROTECTIVE
AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR
DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 110; DB 2; Length 380;
Pred. No. 0.0042;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GPPAPPAGGPPPPGPPPPGPPPPGLPPSGVPAAAHGAGGGPPPAPP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAKAPPAPKPAPQPGPQPGPQPPQPP-QPPQRQPEA-----PAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
           FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: Bidg. 1, T-12 8901 Wisconsin Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, Martha
TITLE OF INVENTION: POLYNUCLEOTID
TITLE OF INVENTION: AGAINST MALAR
TITLE OF INVENTION: DELIVERING PO
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical Res. 6
                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION, NOMBER: 09/026,587
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-155-888-2
: Sequence 2, Application US/08155888
: Patent No. 6066623
                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICAȚION: 514
ATTORNEY AGENT INFORMATION:
NAME: SPEVACK, A. DAVId
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.6%;
49.0%;
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ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 49.0
Matches 24; conservative
                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
    SOFTWARE: FASTSEO F.
CURRENT APPLICATION DA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: GenB;
; CLONE: 624964
US-09-227-420-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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Pred. No. 0.0042;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPPQPP-QPPQRQPEA-----PAPQPP 41
APPLICANT: Lal, Preetl
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY BAIL TOTTE DILVE STREET: 3174 Porter Drive STREET: 3174 Porter Drive STATE: STATE: ...
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/026,587 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09227420
Patent No. 5990087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.6%;
49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.04
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: Genbank
CLONE: 624964
                                                                                                                                                                         Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                   94304
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STATE: CA
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TITLE OF INVENTION:
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Job time: 11.188 secs
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9
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                                                                                                                             Score 108; DB 3; Length 478;
Pred. No. 0.0077;
3; Mismatches 14; Indels
                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                       329 GPGAPQGPGAPQGPPQQPPQQPPQQPPQQPPQQPPQQPRPQP 374
                                                                                                                                                                                                        1 GAKAPPAP----KPAPQPGPQPGPQPPQ--PPQPPQRQPEAPAPQP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CLOSSEN, Date E.
TILLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores ILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/09041886
Patent No. 6335872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KPAPQPGPQPGPQPP---QP--PQRQPEAPAPQPPAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
38.7%; Score 107.5; I
Best Local Similarity 45.6%; Pred. No. 0.00;
Matches 26; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09041886
Patent No. 6235872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
LENGTH: 513 antho acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz
                                                                                                                         Query Match 38.8%;
Best Local Similarity 50.0%;
Matches 23; Conservative
: LENGTH: 478 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECCLE TYPE: protein

US-08-155-888-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California : United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UR
                                                                                                                                                                                                                                                                                                                               US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-041-886-29
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7, 2003, 16:57:01

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Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 530;
Polypeptides and Methods of Use
           NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Sulte 700
                                                                                                                                                                                                                  SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KPAPQPGPQPPQPP---QP--PQRQPEAPAPQPPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 107.5; DB Pred. No. 0.0093; 2; Mismatches 1:
                                                                                                                                                                                                                                                                                            FILING CALASSIFICATION:
ATTORNESING CAMPANION:
NAME: CAMPANION:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
"PT.RPHONE: (519) 535-9001
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.7%;
ilarity 45.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 530 amino acids
amino acid
                                                                                     CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                              92122
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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7, 2003, 16:53:34; Search time 14.6917 Seconds (without alignments) 306.927 Million cell updates/sec
    - protein search, using sw model
                                                                                                                   US-09-855-754B-14
OM protein
                                     Run on:
                                                                                                                     Title:
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278 1 GAKAPPAPKPAPQPGPGP.....QRQPEAPAQPPAGRELSAA 49 **BLOSUM62** Perfect score: Scoring table: Sequence:

349150 segs, 92025710 residues Gapop 10.0 , Gapext 0.5 Searched:

349150 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Published_Applications_AA: Database :

/cgn2_6/ptodata/2/pubpaa/PCT_NEW_TUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/U /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.p/ /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB. /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB. /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB. /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	l Query Match Length DB	DB	QI	Description
-	278	100.0	49	6	US-09-855-754-14	Sequence 14, Appl
7	266.5	95.9	52	σ	US-09-855-754-15	
m	266.5	95.9	911	6	US-09-855-754-4	
4	264.5	95.1	26	σ	US-09-855-754-18	2
S	263.5	94.8	58	6	US-09-855-754-19	Sequence 19, Appl
9	263.5	94.8	922	6	US-09-855-754-6	6.4
7	261.5	94.1	48	σ	US-09-855-754-20	20.
60	250.5	90.1	52	6	US-09-855-754-17	17
σ	247	88.8	59	σ	US-09-855-754-16	16,
10	238.5	85.8	52	σ	US-09-855-754-21	21.
11	237.5	85.4	54	σ	US-09-855-754-22	Sequence 22, Appl
12	213.5	76.8	42	6	US-09-855-754-23	23,
13	213.5	76.8	910	6	US-09-855-754-5	2
14	193	69.4	39	σ	US-09-855-754-24	24
12	117	42.1	827	σ	US-10-171-384-3	'n
16	116.5	41.9	538	0	US-09-976-740-43	43
17	116.5	41.9	538	12	US-10-023-529-43	43
18	116.5	41.9	538	12	US-10-023-523-43	Sequence 43, Appl
19	116.5	41.9	550	5	US-09-976-740-47	

Sequence 47, Appl Sequence 2, Appl Sequence 2, Appli Sequence 1002, Ap	0 A D	Sequence 123, Appl Sequence 282, Appl Sequence 2, Appl Connect 2, Appl Sequence 3, Appl Seq	Sequence 3, Appli Sequence 4, Appli Sequence 34988, A Sequence 34988, A	`	Sequence 15, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 138, App
	10 US-09-925-299-1002 9 US-10-171-384-1 10 US-09-823-240-2 1 US-09-823-240-10 0 US-10-072-036-125	10 US-09-850-887-4 9 US-10-043-487-282 9 US-10-0020-215-2	10 US-09-864-761-36844 10 US-09-864-761-34988 10 US-09-864-761-34988	9 US-09-298-523B-62 9 US-09-298-523B-2 9 US-10-067-457-5 9 US-10-067-457-1 10 US-10-770-6898-5	9 US-09-548-933-15 10 US-09-910-087-21 9 US-09-922-199A-14 10 US-09-800-729-138
550 641 647	647 824 380 380	274 416 1274	171 171 171	701 707 863 889	875 509 66 172
0.0.4.4. 0.0.4.4.	4 4 4 6 6 4 0 0 0 0 4 0 6 0 0	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	37.00	37.1 37.1 37.1 1.7 9	3 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
116.5 116.5 115	112.5	108 107.5 107.5	104.5 103.5 103.5	100 100 100 100 100 100	102.5 101.5 101
20 22 23	4500 4500 4500 4500	31 31 31		37 38 39 40	

ALIGNMENTS

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: HANDOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALCHILIN VET. 2.1
SED ID NO 14
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPPQPPQPPQRPQREAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 278; DB 9;
100.0%; Pred. No. 2e-13;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
Sequence 14, Aprilication US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09855754; Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-855-754-15
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RESULT 5
US-09-855-754-19
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 18
LENGIH: 56
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LAWENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
LAWENTION: BORDCHIELELA PARAPERTUSSIS, AND BORDSTELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOUTHWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 52
TYPE: PRT
USAGANT
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TITLE OF INVENTION: POLYEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA,
TITLE OF INVENTION: BONDEFERLA, PARAPERTUGSSIS, AND BONDEFELLA,
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2001-09-05
SOFTWARE: PATENTING UNIVER: 21.
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
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BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 1.3e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0; Mismatches
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Pred. No. 1.46
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US-09-855-754-4
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; Sequence 18, Application US/09853754
; Publication No. US2002019237A1
; GENERAL INFORMATION:
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ilarity 94.2%;
Conservative
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Best Local Similarity 94.2%;
Matches 49; Conservative (
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TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA, THEIR OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                    7;
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Pred. No. 1.9e-12;
0; Mismatches 0
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Pred. No. 2.2e-12;
0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                      TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT CORGANISM: Bordetella bronchiseptica US-09-855-754-19
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Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Publication No. US20020192237A1
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Best Local Similarity 87.5%;
Matches 49; Conservative
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84.5%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
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PRIOR FILING DATE: 2000-05
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Matches 49; Conserv
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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US-09-855-7,54-16
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US-09-855-754-21
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Sequence 16, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION
APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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                                                   Query Match
Best Local Similarity 90.6%;
Matches 48; Conservative
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80.0%;
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Best Local Similarity 80.0
Matches 48; Conservative
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Matches 46; Conservative
       US-09-855-754-17
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LENGTH: 59
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Sequence 20, Application US/0985554

Publication No. US20020192237A1

Sequence 20, Application US/0985554

Sequence 20, Application No. US20020192237A1

SEQUENCE 20, APPLICANT SEQUENCE CAROLINE

APPLICANT: BOURSAUX EUDE, CAROLINE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BRONDFILLA PARAPERTUSSIS, AND BORDETELLA

TITLE OF INVENTION: BRONDFILLA PARAPERTUSSIS, AND BORDETELLA

TITLE OF INVENTION: BRONDFILLA PARAPERTUSSIS, AND IN

TITLE OF INVENTION: HAWUNGENIC COMPOSITIONS

TITLE OF INVENTION: HAWUNGENIC COMPOSITIONS

TITLE OF INVENTION: HAWUNGENIC COMPOSITIONS

TITLE OF INVENTION: LAWONDER: US/09/855,754

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SECTUMANE PATOLICATION VOT: 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERRUSSIS, AND BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 01495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
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                                                                                                                                                                  Length 922;
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Pred. No. 2.3e-
0; Mismatches
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
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                                                                                             ; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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Publication No. US20020192237A1
GENERAL INFORMATION:
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1 Similarity 98.0%;
48; Conservative
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ilarity 84.5%;
Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 17
LENGTH: 52
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Best Local Similarity
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Matches 49; Conserv
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                                                                       TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS
GURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALCHLIN VAT. 2.1
                                                                   Gaps
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APPLICANT: GUISO-MACLOUP, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE REFERENCE; GASS-C206-0000
CURRENT APPLICATION NUMBER: US/O9/9655,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                     1 GAKAPPAPKPA----POPGPOPGPOPPOPPOROPEAPAPOPPAGRELSAA 49
                                                                                                                                                      DB 9; Length 52;
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Score 250.5; DB 9;
Pred. No. 1.6e-11;
0; Mismatches 0;
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86.8%; Pred. No. 1.1e-10;
tive 0; Mismatches 2;
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Pred. No. 3.1e-11;
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Sequence 5, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver.
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US-09-855-754-24
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LENGTH: 910
                                          US-09-855-754-5
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US-10-171-384-3
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA

TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS

FILE REPERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: 2001-09-10

PRICA APPLICATION NUMBER: 60/206,969

PRICA PLOATION NUMBER: 60/206,969

PRICA PLOATION DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUCON: DAPPOSITIONS BRONCHISEPTICA, THEIR USE INVENTION: BRONCHISEPTICA, THE CONTOUT COMPOSITIONS
FILLE OF INVENTION: INMERICAL CONTOUT CO
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                                      DB 9; Length 42;
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1.3e-10;
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; Pred. No. 4.7e-
0; Mismatches
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Pred. No. 1.36
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US-09-855-754-23
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1 GAKAPPAPKPAPQPGPQPGPQPPQP-
                                                                                                                                                                                                                                                   Sequence 22, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX:EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-855-754-23; Sequence 23, Application US/09855754; Publication No. US20020192237A1
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APPLICANT: BOURSAUX-BUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.4%;
Best Local Similarity 83.6%;
Matches 46; Conservative
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Best Local Similarity 83.7%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 42
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LENGIH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISBEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISBEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03469-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                               TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITILE OF INVENTION: IMMUNOSENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPPQPPQRPQREAPAPQPPAGRELSAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213.5; DB 9
Pred. No. 6.2e-08;
0; Mismatches 1
                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10171384 Publication No. US20030031680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella pertussis
US-09-855-754-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.7%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 39
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Search completed: May 7, 2003, 17:30:50 Job time: 15.6917 secs

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OM protein - protein search, using sw model

Мау Run on:

7, 2003, 16:41:02 ; Search time 9.18228 Seconds (without alignments) 513.008 Million cell updates/sec

US-09-855-754B-14
278
1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 49 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	68K outer membrane		ā	proline-rich prote	hypothetical 47.8K	pherophorin-S - Vo	nuclear protein EB	hypothetical prote		sulfated surface q				hypothetical prote	UL36 protein - hum	hypothetical prote	hydroxyproline-ric	proline-rich prote	T20H2.9 protein -	glyceraldehyde-3-p	protein-tyrosine-p	hypothetical prote			pistil extensin-li	chitinase (EC 3.2.	hypothetical prote	cysteine-rich exte	acrosin (EC 3.4.21
SUMMARIES	. QI	A47675	S15204	A32560	S16748	JC2301	T10798	S42442	C96623	T02632	A33647	A34043	T17547	A48232	T48814	ММВЕН6	H83619	T07907	S21961	A86335	149681	T14355	AE2295	T10340	T17531	JQ1696	S51939	T24470	B48232	A34170
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	Query Match Length	911	922	910	449	430	599	487	929	1684	485	141	544	209	1952	3164	270	446	534	1137	440	1494	383	875	412	426	439	165	196	415
dР	Query	95.9	94.8	76.8	47.5	47.1	46.0	45.0	44.8	44.8	44.6	43.9	43.9	43.7	43.7	43.5	43.3	43.2	43.0	42.4	42.3	42.3	42.1	42.1	41.9		41.5	41.4	41.4	41.4
	Score	266.5	263.5	213.5	132	131	128	125	124.5	124.5	124	122	122	121.5	121.5	121	120.5	120	119.5	118	117.5	117.5	117	117	116.5	116	115.5	115	115	115
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S22697	T31611	B96534	T17908	PQ0476	T17737	T17815	A96650	S47538	T06291	OZZOMB	T17636	OZZOBK	D87682	S61918	S14970
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464	1585	464	496	154	288	225	70	431	760	332	339	348	449	1139	132
41.4	11.4	40.6	10.6	40.5	10.5	40.3	10.1	10.1	40.1	39.9	39.9	39.9	39.9	39.9	39.7
115	115	113	113	112.5	112.5	112	111.5	111.5	111.5	111	111	111	111	111	110.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Perfactin - Bordetella parapertussis

NaAlternate names: outer membrane protein P70

Cispecies: Bordetella parapertussis

Cispecies: Bordetella parapertussis

Cispecies: Bordetella parapertussis

CiDate: 07-Apr-1954 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999

CiAccession: S15264; S14659

CiDate: 07-Apr-1954 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999

CiAccession: S15264; S14659

No. Int. L.J.; Dougan, G.; Novotny, P.; Charles, I.G.

No. Int. L.J.; Dougan, G.; Novotny, P.; Charles, I.G.

A; Molecule Type: DiA

A; Cross references: EMBL: X54547; NID: 939761; PIDN: CAA38419.1; PID: 939762

C; Genetics:

A; Gene: prn

C; Keywords: membrane protein

6 Score 263.5; DB 2; Length 922; Pred. No. 2.2e-11; 0; Mismatches 0; Indels 9 Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative C

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Gaps

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Cispecies human herpesvirus 4
Cispecies human herpesvirus 4
Cispecies; human herpesvirus 4, Epstein-Barr virus
Cispecies; Human herpesvirus 4, Epstein-Barr virus nuclear proteins; Risample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Risample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Risample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
A; Reference number: $42440; MUID:86259739; PMID:3460083
A; Residues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Reference number: $32973
A; Residues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Reference number: $32973
A; Residues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM>K; Farrell, P.J.
Submitted to the EMBL Data Library, March 1988
A; Resedues: 1-487 <SAM
A; 
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C;Species: Volvox carteri
C;Species: Volvox carteri
C;Dete: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 10.798
R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophori
A;Reference number: Z17154, WUID:97162277; PMID:9009264
A;Reference number: Z17154, WUID:97162277; PMID:9009264
A;Residues: T10798
A;Residues: 1-599 <GOD>
A;Residues: 1-599 <GOD>
A;Residues: 1-599 <GOD
A;Residues: 1-599 <GOD
A;Reperlmental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Reywords: extracellular matrix; glycoprotein; pheromone
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R;Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen
A;Reference number: S42447; MUID:85063846; PMID:6209719
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A; Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                                          Gaps
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Pred. No. 0.034;
1; Mismatches 1
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1; Mismatches
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3; Mismatches
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1 Similarity 51.2%;
21; Conservative 1
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28; Conservative
                                                                  2 AKAPPAPKPAPQPGPQP-
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313 PEPQPP 318
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Best Local S
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C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Accession: A32560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.6
A; Reference number: A32560; MUID:89264462; PMID:2542937
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R. Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
Submitted to the EMBL Data Library, August 1991
A; Reference number: S16748
A; Accession: S16748
A; Molecule type: mRNA
A; Residues: 1-449 < ROB>
A; Cross-references: EMBL:X60376; NID:g22596; PID:g22597
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DNA Res. 1, 163-168, 1994

A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
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C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
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A; Residues: 1-910 <CHA>
A; Residues: 1-910 <CHA>
A; Cross-references: GB: 304560; NID: 9144053; PIDN: AAA22980.1; PID: 9144054
A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
C; Keywords: membrane protein
F; 1-34/Domain: signal sequence #status predicted <SIG>
F; 35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
564 САКАРРАРКРАРОРОРОРОРРОРРОРРОРРОРРОРРОРОРОВЕЛЕННЯЯ 621
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Pred. No. 0.011;
3; Mismatches 14; Indels
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                                                                                                                                                                            precursor - Bordetella pertussis
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Pred. No. 5.4e-08;
0; Mismatches 1;
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Pred. No. 0.012;
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83.7%;
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Best Local Similarity 55.3%;
Matches 21; Conservative
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                                                                                                                                                                                outer membrane protein P.69
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A; Molecule type: DNA
A; Residues: 1-430 <WAD>
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Best Local Similarity
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Matches 41; Conser
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hypothetical prolline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C; Species: Owenia fusiformis
C; Species: Owenia fusiformis
C; Stecession: A34043; B34043
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A; Title: Presence in invertebrate genomes of sequences characterized by the repetitio A; Thile: Presence number: A90159; MUID:90147742; PMID:2103723
A; Accession: A34043
A; Molecule rype: DNA
A; Residues: 1-141 - CBAK>
A; Cross-references: GB:M32217
                                                                                                                structure of the cellu
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000 C;Accession: A33647
R;Ertl, H; Mengele, F; Wenzl, S; Engel, J.; Sumper, M.
J. Cell Biol. 1097, 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of A;Reference number; A33647; MUD: 90094551; PMID: 2689458
A;Status: preliminary
A;Molecule type: MRNA
A;Residues: 1-485 cERT>
A;Coss-references: GB:X51616; NID: 921999; PIDN: CAA35953.1; PID: 91405821
C;Keywords: 91ycoprotein
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 0.059;
4; Mismatches 10; Indels
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A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: A57R
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A;Molecule type: DNA
A;Residues: 1-544 <GRA>
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Pred. No. 0.039;
1; Mismatches
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Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: T17547
R, Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A, Reference number: Z18806
A, Accession: T17547
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.1%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%;
1)arity 59.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%;
ilarity 52.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A,Residues: 59-136 <BA2>
A,Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 23; conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B34043
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                                                                                                                                                                                                                                                                     Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.X.; Luros, J.S.; Maiti, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title; Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-929 <STO>
A; Cross-references: GB:AE005173; NID:g5080823; PIDN:AAD39332.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Sate: 05-Mar-1999 $sequence_revision 05-Mar-1999 $text_change 05-Nov-1999
C; Accession: 105632
R; Bemis, G; Rohlfing, T.; Morris, M.
Submitted to the EMBL Data Library, July 1998
A; Description: The sequence of Homo sapiens PAC clone DJ1186C01.
A; Reference number: 214682
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1684 < DBM>
                                                                                                                                                                  hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AKAPPAPK-PAPQPGPQPGPQP----PQPPQPPQRQPEAPAPQPPAGRE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: intron positions not resolved (incomplete sequence)
A;Note: WUGSC:H_DJ1186C01.1
  Score 124.5; DB 2;
Pred. No. 0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 APPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein DJ1186C01.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 124.5; DB Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sulfated surface glycoprotein 185 - Volvox carteri
C;Species: Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 51.0 tes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C96623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: F23H11.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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human herpesvirus 1 (strain 17)
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                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T48814
R; Schulter, U; Adgn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24541
A; Accession: T48814
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1952 <SCH>A; Residues: 1-1952 <SCH>A; Residues: 1-1952 <SCH>A; Cross-references: EMBL: Al353822; GSPDB:GN00112; NCSP:15E6.220
A; Experimental source: cosmid contig 15E6; strain 74
                                                                                                                                                       cysteine-rich extensin-like protein 1 precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequencian 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48323; P00475; S24617
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Developmental expression of tobacco pistil specific genes encoding novel extens
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein F;1-19/Domain: signal sequence #status predicted <SIG> F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT> F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T4884
C;Accession: T4884 V; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923 R;de S GOldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C. Plant Cell 4, 104-1051, 1992 A:Title: Developmental expression of tobacco pistil-specific genes encod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: mRNA
A; Residues: 39-209 <GOL>
A; Cross-references: EMBL:214020; NID:g19918; PID:g19919
A; Experimental source: stigma, style; strain Petit Havana SR1
C; Superfamily: glutelin
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DB 2;
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Pred. No. 0.03;
3; Mismatches
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Pred. No. 0.17;
%; Mismatches
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55.38;
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ilarity 56.8%;
Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-209 <WUA>
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Best Local Similarity
Matches 21; Conserv
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A;Map position: 2
A;Introns: 281/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: PQ0475
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RESULT 15

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C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 fsequence_revision 31-Dec-1989 ftext_change 16-Jun-2000
C;Accession: 130085
R;McGeoch, D.J; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: 130085
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-3164 cMCS>
A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2943 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPG 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQRQPEAPAPQPPAG 43
                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: UL36
C,Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
43.5%; Score 121; DB 1;
Best Local Similarity 65.9%; Pred. No. 0.28;
Matches 27; Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7, 2003, 16:55:23
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49; Search time 4.75809 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-14 278 I GAKAPPAPKPAPQPGPQPGP........ORQPEAPAPQPPAGRELSAA 49 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

																													•					
	Description	5 bord	P24328 bordetella	P14283 bordetella		P12978 epstein-bar	•	P21260 owenia fusi	Q92794 homo sapien		P40602 arabidopsis	Q64467 mus musculu	Q83949 orgyia pseu			Q9fpq6 chlamydomon			-		P23093 plasmodium	O70324 mus musculu	Q99014 trichoderma	P78621 emericella	P50552 homo sapien	P51111 rattus norv	_	P06914 plasmodium	P41467 autographa	.,	Q95107 bos taurus	O00401 homo sapien	2858 homo	P93329 medicago tr
SUMMARIES	ID		PERT_BORPA	PERT_BORPE	APG_BRANA	EBN2_EBV	SSGP_VOLCA	YPRO_OWEFU	MOZ_HUMAN	TEGU_HSV11	APG_ARATH	G3PT_MOUSE	X066_NPVOP	EXLP_TOBAC	HXA3_MOUSE	GP1_CHLRE	ACRO_PIG	BRD4_HUMAN	ACRO_RABIT	CSP_PLABE	CSP_PLABA	MOT8_MOUSE	KPC1_TRIRE	SEPA_EMENI	VASP_HUMAN	HD_RAT	CIKF_HUMAN	CSP_PLAYO	Y066_NPVAC	WASL_RAT	WASL_BOVIN	WASL_HOMAN	HD_HUMAN	NO20_MEDIR
	DB	-	П	-	-	П	-	П	-	Н	-	-	-	Н	П	-	-	-	_	-	Н	-	-	-	-	-	-	Н	Н	Н	-	П	Н	Н
	Query Match Length	911	922	910	449	487	485	141	2004	3164	534	440	875	426	443	555	415	1362	431	339	347	265	1139	1790	380	3110	757	367	808	501	505	202	3144	268
df	Query Match	95.9	94.8	76.8	47.5	45.0	44.6	43.9	43.5	43.5	42.4	42.3	42.1	41.7	41.7	41.7	41.4	40.5	40.1	•	٠.	39.9	39.9	39.9	39.6	39.6	39.4	38.8	38.8	38.7	38.7	38.7	38.7	38.5
	Score	266.5	263.5	213.5	132	125	124	122	121	121	118	117.5	117	116	116	116	115	112.5	111.5	111	111	111	111	111	110	110	109.5	108	108	107.5	107.5	107.5	107.5	107
	Result No.	1	7	e	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

	Q9umn6 homo sapien P58840 homo sapien P05142 mus musculu			
EXTN_MAIZE MEFD_MOUSE	TRX2_HUMAN ACRL_HUMAN PRP2_MOUSE	PRP3_MOUSE MB11_ARATH	FFAL_HUMAN FM14_MOUSE FMN1_MOUSE	HD_MOUSE VGLD_PRVRI
267	2715 232 261	296 642	1206 1468	3119
8.8 8.0 6.0	8.8.8 6.4.4	8 8 6 T.T.	3 8 6	38.1
106.5	106.5 106 106	106	106 106	105.5
34 35	36 37 38	39	4 4 4	4 4 5

ALIGNMENTS

RESULT 1 PERT_BORBR 1D PERT_ 03030 DT 01-Ju DT 0

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                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li.L.J., Dougan G., Novotny P., Charles I.G.;
P.70 pertactin, an outer-membrane protein from Bordetella
parapertussis: cloning, nucleotide sequence and surface expression in
Escherichia coli.;
Mol. Microbiol. 5:409-417(1991).
-!- FUNCTION: AGGIUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
MEDIATED BY THE R.G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
-!- SUBUNIT: MONOMER.
-!- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-!- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-!- MISCELLANDOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG (2+)
CONCENTRATIONS.
                                                                                                                                              Gaps
CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                              э;
                                                                                                                                                                       DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                                                                                              Indels
                                                        3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                             Score 266.5; DB 1 pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERTACTIN (P.70).
                                                                                                                                 Pred. No. 1.66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S14659; S14659.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR0033931; pertactin_vir.
Pfam; PF03212; Pertactin, 1.
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CN2591;
MEDLINE-91251771; Pubmed-2041476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY
                                                                                        93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                                                Query Match 95.9%;
Best Local Similarity 94.2%;
Matches 49; Conservative C
                                                                                                                                                                                                                                                                                                                                                                              Bordetella parapertussis
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647
922
262
 703
275
270
275
280
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PIR; S14659; S14659.
                                                                                        911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane:
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-519;
                                                                                                                                                                                                                                                                           PERT_BORPA
P24328:
                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella.
                                                                                        SEQUENCE
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PROPEP
                                             REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 381:90-92(1996).
-!- FUNCTION: AGGLOTINOGEN THAT BINDS TO BUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novciny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterizathon of protective outer membrane protein P.69 from Bordetella pertusais.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                3 AA APPROXIMATE REPEATS OF P-Q-P
                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPQPQPAPAPGPPAGRELSAA 49
                                  X 5 AA TANDEM REPEATS OF G-G-A-V-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                           ٠<u>.</u>
                                                                                                                                                                        DB 1; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                       3DF7BC58D4712478 CRC64;
                                                                                                                                                             Score 263.5; DB 1;
Pred. No. 2.4e-10;
                                                                                                 4 (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                   910 AA
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 264 AND 332.
MEDLINE=92407514; PubMed=1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J04560; AAA22980.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96196517; PubMed-8609998
                                                                                                                                         ME.
                                                                                                                                                                          94.88;
                                                                                                                                       95178
                                                                                                                                                                                           Local Similarity 84.5
nes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                 290
275
275
280
285
603
                                                                                                                                       922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRN OR OMP69A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
                                                                                                                                                                                                                                                                                                                                                                   BORPE
                                                                                                                                           SEQUENCE
                                                                                                                                                                          Query Match
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REPEAT
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                                  DOMAIN
                                                 REPEAT
                                                                     REPEAT
                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                   PERT_BORPE
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATURATION.
SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                               X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                    CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                          ;
                                                                                                                                                                        (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                           76.8%; Score 213.5; DB 1; Length 910;
                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                            1; Indels
                                                                                     PERTACTIN (P.69).
                                                                                                                                                                 (APPROXIMATE).
                                                                                                                                                                                                                    Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                          449 AA.
                                                                                                                                                                                                                            0; Mismatches
                                                          Signal; Virulence; Repeat.
                                                                                             POTENTIAL
        InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                        CINES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
                                Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                          93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                     83.78;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Brassica napus (Rape).
PIR; A32560; A32560.
                                                                                                                                                      276
281
286
579
910 AA;
                                                                                                                                                                                                                     Local Similarity
                                                            Outer membrane;
                                                                                                                                                                                                                                                                                                                                                            OR CEX.
                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                        APG_BRANA
P40603;
                                                                                                                                                                                 DOMAIN
SEQUENCE
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                                                                   SIGNAL
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APG_BRANA
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MEDLINES 4127(667; PubMed-6087149;

MEDLINES 4127(667; PubMed-6087149;

Back R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,

Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,

Tuffnell P.S., Barrell B.G.,

"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";

Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coben J. L., Wang F., Kleff E., "Epstein Bar; virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SÜBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE=90266473; PubMed=2161150;
Petti L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
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TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                47.5%; Score 132; DB 1; Length 449; 55.3%; Pred. No. 0.02; tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 2 AA TANDEM REPEATS OF
DEF40D7F8ED61D1A CRC64;
                                                                                                                                POTENTIAL.
9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                          3 KAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQP
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
NON_TER 1 13 BY SIMILA
ACT_SITE 428 POTENTIAL
SEQUENCE 449 AA; 48779 MW; 9EFB6A3
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                          Local Similarity
tes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF LMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBN2_EBV
P12978;
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAINS
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DB 1; Length 487;

45.0%; Score 125;

Query Match

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NCBI_TaxID-9606;
                                                                                                                                                                                                     Local Sin
                                                                                                                                                                                                                                                                                                                              MOZ_HUMAN
Q92794;
                                                                                                                                                     DNA_BIND
NON_TER
SEQUENCE
                                                                                                                               NON_TER
DOMAIN
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                     MOZ_HUMAN
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                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                           the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. SUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC DRECURSOR OF THIS SUBSTITUTE (C3Z STRUCTURE). THE COVALENT CROSS-LIKKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
I. PIM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                        MEDLINE-90094551; PubMed-2689458;
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.,
The extracellular matrix of Volvox carteri: molecular structure of
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124; DB 1; Length 485;
Pred. No. 0.065;
1; Mismatches 16; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 POLY-PRO.
50436 MW; A52216400A031421 CRC64;
                                                              Pred. No. 0.057;
                                          PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRE 45
                                                                                                                    PRT; 485 AA. P21997; 01-MC1991 (Rel. 19, Created) 01-MC1991 (Rel. 19, Last sequence update) 01-CT-1996 (Rel. 34, Last annotation update) Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P11260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOY-1995 (Rel. 32, Last annotation update)
Hypothetical proline-rich protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AA.
                    1; Mismatches
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfation; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-RICH.
        51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sabellida; Owenlidae; Owenia.
NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.6%;
illarity 54.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYPROLINE RESIDUES.
        Similarity 51.2:
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                 STRAIN-f. Nagariensis ,
                                                                                                                                                                                                                   Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPRO_OWEFU
        Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                               SSGP_VOLCA
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                                                                                                   RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chagantl R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.B.; "The translocation 1(8;16)(p11;p13) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).

-!- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
MEDLING-90147742; PubMed-2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.",
Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; B34043; A34043.
Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -: SUBCELLULAR LOCATION: Nuclear.
-: DISEABE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL
TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
-: SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
-: SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Score 122; DB 1; Length 141;
llarity 52.5%; Pred. No. 0.035;
Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601408; -.
Interpro; IPR001386; Histone_H1/H5.
Interpro; IPR002717; MOZ_SAS.
Interpro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=96376968; PubMed=8782817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:13013; ZNF220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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4

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Query Match
                                                                                  RESULT 10
                                                                                             APG_ARATH
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-88374327; Pubmed-2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCGBob D.J., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BREAKPOINT FOR TRANSLOCATION TO FORM
                   translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2911 2980 35 X 2 AA TANDEM REPEATS OF P-O. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                             Score 121; DB 1; Length 2004;
Pred. No. 0.28;
1; Mismatches 15; Indels
                                                                                                                                                                                            9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                            1659 PQPPPPQPQPAPQPPPPQQQPQQPQPQPQPPPPP 1695
                                                                                                                                                                                                                                                 5 PPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPP 41
                                                                                                                                                                                                                                                                                                                                  01-MAR-1889 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                 3164 AA.
                                                                                                                                                         GLN/PRO-RICH
                                    PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
                                                                C2HC-TYPE
                                                                                         POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
POLY-GLU.
                                                                         POLY-GLU.
                                                                                   POLY-GLU
                                                                                                                                                                                   MOZ-CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; 130085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
9; ZF_PHD_1; 1
6; ZF_PHD_2; 2
Chromosomal t
                                                                                                                                                                                                             43.5%;
56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                           2004 AA; 225054
                                                                                                                                                                                                                               21; Conservative
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                               302
                                                                                                                                               597
                                                                                                                                                                                                             Query Match
Best Local Similarity
PS01359;
PS50016;
                          Nuclear protein.
ZN_FING 206
ZN_FING 259
DOMAIN 371
ZN_FING 538
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10299;
PROSITE; PS01359
PROSITE; PS50016
Proto-oncogene;
                                                                                                                                               1593
1643
1897
1546
                                                                                                                                                                                                                                                                                                     TEGU_HSV11
ID TEGU_HSV11
AC P10220;
                                                                                                                                                                                                                                                                                                                                  01-MAR-1989
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat.
DOMAIN
SEQUENCE
                                                                                                                                                                                            SEQUENCE
                                                                                                                             DOMAIN
                                                                        DOMAIN
                                                                                   DOMAIN
                                                                                                   DOMAIN
                                                                                                                     DOMAIN
                                                                                                                                                DOMAIN
                                                                                                                                                         DOMAIN
                                                                                                                                                                 DOMAIN
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X MEDLINE-21016/19; PubMed-11130712;

X MEDLINE-21016/19; PubMed-11130712;

X MEDLINE-21016/19; PubMed-11130712;

X Milte O. Aloinso J. Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

X Milte O., Aloinso J., Chan H., Chen H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Huter, J.L., Jenhins J., Johnson-Hopson C., Khan S., Knaykin E.,

RA Langin-Hooper S., Lee A., Lee J.W., Lan B., Kwan A., Lam B.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltis R., Marziali A.,

RA Millscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,

RA Millscher J., Miranda M., Nguyen M., Nlerman W.C., Osborne B.I.,

RA Sano H., Zalzeng S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallen L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 534 AA.

P40602; 093214; 091NT8;

P40602; 093214; 091NT8;

P40602; 093214; 091NT8;

P501 FEB-1995 (Rel. 31, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

Anter-specific proline-rich protein APG precursor.

ARG OR AT1620;30 OR T201129

ARG OR AT1620;310 OR T201129

ARG OR AT1620;310 OR T201129

BUALYOTA; VHIdiplananae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudioctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-cv. Columbia;
Sincarki K., Davis R.W., Ecker J.R., Theologis A.;
**RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SIREN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP coinsortium (Salk/Stenford/PGEC).";
Submitted (Sip-2001) to the EMBL/GenBank/DDBJ databases.
--- TISSUE SPECIFCITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
--- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar.
Draper J., Scott R.;
Gametophytic; and sporophytic expression of an anther-specific
Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                              4
                                    DB 1; Length 3164;
                                                                                                                     Indels
                                                                                                                                                                                                                                                   2943 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQNG 2982
                                                                                                                                                                                                 6 PAPKPAPQFGPQPGPQP-PQP-PQP-PQRQPEAPAPQPPAG 43
                                                                                                                     .;
8
Score 121; DB 1
                                                                                                                     2; Mismatches
                               43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene model prediction.
                                                                   Best Local Similarity 65.9
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                                                                                                                                  ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POOTENTIAL.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ICR Swiss; TISSUB-Testis; MEDLINE-95254745; PubMed=7736666; MEDLINE-95254745; PubMed=7736666; MEDLINE-95254745; Prown P.R., O'Brien D.A., Eddy E.M.; Genomic organization of a mouse glyceraldehyde 3-phosphate dehydrogenase gene (Gapd-s) expressed in post-meiotic spermatogenic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                        .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-Testis;
MEDLINE-92273722; Pubmed-1375514;
Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.;
"Expression of a glyceraldehyde 3-phosphate dehydrogenase gene specific to mouse spermatogenic cells.";
Biol. Reprod. 46:869-878(1992).
                                                                                                                                                                                                                                                               Score 118; DB 1; Length 534;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                      3 KAPPAPKPAPQPGPQPGPQPPQ----PPQPPQRQPE-APAPQP-PA 42
                                                                                                                                                                                                          S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                           Pred. No. 0.16
4; Mismatches
                                                                 EMBL; X60377; CAA42925.1; -
EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AX058847; AAL24235.1; -
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                        58007 MW;
                                                                                                                                                                                                                                                               42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Genet. 16:179-189(1995).
                                                                                                                                                                                                                                                                     Local Similaricy
hes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                141
325
34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    G3PT_MOUSE
                                                                                                                                                                                ACT_SITE
ACT_SITE
CONFLICT
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CONFLICT
SEQUENCE
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                                                                                                                                                           SIGNAL
                                                                                                                                                 Signal
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                                                                                                                                                                                                                                                                                                                                                                         G3PT_MOUSE
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     24 AND THEN REMAIN CONSTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
(BY SHYLLARITY).
MISSING (IN REF. 2).
L -> V (IN REF. 2).
; 05FP0A093D1ABD9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
"The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear
Polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      083949; 065364; 010323;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71),
Creyla pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                    POLY-PRO.
GLYCERALDEHYDE 3-PHOSPHATE (BY
                          SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PPAPK-----BAPQPGPQPGPQPPQPPQRQP----BAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  875 AA.
 GERM CELLS. LEVELS INCREASE UNTIL DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%; Score 117.5;
46.2%; Pred. No. 0.1!
                                                                                                                                                                                                                                                                                                                         CYS/PRO-RICH.
                                                                                                                                                                                                       HSSP; P56649; IDSS.
MGD; MGI:9563; Gapds.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF000044; gpdh, 1.
Pfam; PF02800; gpdh, C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426, PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 806-875 FROM N.A. MEDLINE-95343549; PubMed=7618274;
                                                                                                                                                                                                                                                                                                           Glycolysis; Oxidoreductase; NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                440 AA; 47657 MW;
                                                                                                                                                                                 EMBL; M60978; AAA53033.1; -.
                                                                                                                                                                                                EMBL; U09964; AAA80276.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 46.2
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                            41
73
100
256
                DURING MATURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                    84
256
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CONFLICT
SEQUENCE
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BINDING
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DNA-BINDING
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CARBOHYD
SEQUENCE
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REPEAT
                                                           DOMAIN
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETRAINCY. Petit Havana; TISSUE-Pistil;
MEDLINE-93005740; PubMed-1392607;
Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;
Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;
Goldmental expression of tobacco pistil-specific genes encoding novel extensin-like proteins.";
Plant Cell 4:1041-1055(1992).
-1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
-1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DUBING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE PRESPECTOR POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusaterids I; Solanales; Solanaceae; Nicotiana.
Ahrens C.H., Carlson C., Rohrmann G.F.; "Identification, sequence, and transcriptional analysis of lef-3, gene essential for Orgyia pseudotsugata baculovirus DNA replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 117; DB 1; Length 875;
Pred. No. 0.27;
3; Mismatches 13; Indels
                                                                                          Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                            F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIN, TOTAL TROUGHS, POLIER_OLE_I.
Pfam: PF01190; Poller_OLE_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 РРАРКРАРОРСРОРСРОРРОРРОРОВРОРЕАРАРОР 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                               EMBL; U75930; AAC59070.1; -. ERMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z14019; CAA78397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.69
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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"The homeo domain of a murine protein binds 5' to its own homeo box.";
Proc. Natl. Acad. Sci. U.S.A. 83:9532-9536(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryogenesis.";
Dev. Biol. 134:125-133(1987).
-I- FÜNCTION; SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
                                                                                                                                                                                                Gaps
          PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 185-258 FROM N.A. MEDLINE-85024859; PubMed-6091896; McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.; McGinnis T. cloning and chromosome mapping of a mouse DNA sequence homologous to homeotic genes of Drosophila."; cell 38:675-680(1984).
                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
51A495CC94017812 CRC64;
                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ICR Swiss;
MEDLINE=96323206; PubMed=8710855;
Tan D.; Shao X., Pu L.; Guo V., Nirenberg M.;
"Sequence and expression of the murine Hoxd-3 homeobox gene.";
Proc. Natl. Acad. Sci. U.S.A. 93:8247-8252(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fainsod A., Bogarad L.D., Ruusala T., Lubin M., Crothers D.M., Ruddle F.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruddle F.H., Hart C.P., McGinnis W.;
"Structural and functional aspects of the mammalian homeo-box
sequences.";
                                                                                                                                                                                                                                                         165 АКОРРОРРАКОРЅРРРРРРУКАРЅРЅРАКОРРРРРУКАРЅРБАТОРР 216
                                                                                                                                                                                                                             41
                                                                                                                                                           DB 1; Length 426;
                                                                                                                                                                                                                            2 AKAPPAPKPAPQPGPQPGPQP-----PQPPQPPQRQPE-APAPQPP
                                                                                                                                                                                            14; Indels
                        X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE.
MEDLINE-88030407; PubMed-2444477;
Fainsod A., Awgulewitsch A., Ruddle F.H.;
"Expression of the murine homeo box gene Hox 1.5 during
                                                                                                                                                                                                                                                                                                                                          HXA3_MOUSE STANDARD; PRT; 443 AA. P02831; 061197; 1.7 Created) 01-10UL:1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update). 15-JUB-2002 (Rel. 41, Last annotation update) HOXA3 OR HOXA-3 (HOX-1.5) (MO-10).
                                                                                                                                                           Score 116; DB :
Pred. No. 0.19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87092283; PubMed=2879282;
                                                                                                                          44278 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rends Genet. 1:48-51(1985).
                                                                                                                                                         41.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 54-280 FROM N.A.
                                                                                                                                                                           46.28;
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c;
Hofmann M., Boehm T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
42 AAS
                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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4 APPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPA 42
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SEQUENCE
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                               ï
                      SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: EXPRESSED IN A SPATIALLY RESTRICTED MANNER BABRYOS 8.5 DAYS P.C., EXPRESSION IS LIMITED TO THE CNS WITH AN ANTERIOR BOUNDARY IN THE HINDBRAIN AND EXTENDING POSTERIORLY THROUGH CADDAL REGIONS OF THE SPINAL CORD, THE SAME SPATIAL EXPRESSION IS SEEN IN EMBRYOS 9.5 TO 12.5 DAYS P.C. SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS BINDS 5' TO ITS OWN HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21159092; PubMed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
HOMEObox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S -> G (IN REF. 3 AND 4).
A -> G (IN REF. 3 AND 4).
SA -> P (IN REF. 3 AND 4).
C -> M (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQ-PPQPPQRQPEAPAP----QPP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTP-TYPE HEXAPEPTIDE. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 41.7%; Score 116; DB 1 Similarity 54.3%; Pred. No. 0.19 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                       MGD; MGI:96175; Hoxa3.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00024; HOMEOBOX,
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP1_CHLRE STANDARD; F 09FPQ6; Q03927; 15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0025; ANTENNAPEDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46429 MW;
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                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation
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Matches 25; Conserv
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DNA_BIND
CONFLICT
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GP1_CHLRE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
"Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                    MEDLINE=91017504; Pubmed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-I. FUNCTION: Major component of the outer cell wall W6 (crystalline)
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKED (GLCNAC. .) (P. 6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Associates with GP2 and GP3.
-!- PIM: N-glycosylated and O-glycosylated.
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EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSulteabs, 09FP06; --
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003882; Pistil_extensin.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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Search completed: May 7, 2003, 16:48:06 Job time : 6,75809 secs

09k5g1 bordetella 09alg bordetella 09alg bordetella 09alg bordetella 09s6m bordetella 09s6m bordetella 09s6n bordetella 09s6n bordetella 06139 bordetella 06139 bordetella 06139 bordetella 06139 bordetella 06139 bordetella 06139 bordetella 08140 pordetella 0919 bordetella 0919 bordetella 096v1 pneumocysti 096v1 pneumocysti 096v1 pneumocysti 09p94 pneumocysti 09p94 pneumocysti 09p94 pneumocysti 09p91 pneumocysti 09p11 bordetella 09p11 bordetella

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MEDLINE=20359389; PubMed=10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Brothusphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250077; CAB76431.1;
Interpro; IPR004899; Pertact.
Interpro; IPR004899; Pertact.
NON_IER
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
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Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 49; Conservative 0; Mismatches 0;
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525
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NCBI_TaxID=518;
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09a1p9
0914e2
0915h1
09a1q4
09k5h1
    GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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104 AA

PRT;

ALIGNMENTS

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Q90VD1 Q96VI4 Q8W158 Q93L97 Q9P944 Q9SBM1

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Q9ALP5 Q9AIX8 Q9S6M9

Q9S3M8 Q9S6N0 Q9S6N1

088143 Q93L98 O69257 Q8RSU0 069259

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Gaps

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Length 104;

PRELIMINARY;

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Keil D.J., Fenwick B.;
Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.".
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                                                                                                          Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel Genetic and Phenotypic Heterogeneity in Bordetella Bonochiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AF298590; AAK16691.1; ...
InterPro: IPR003992; pertactin.
InterPro: IPR004899; Pertact.sup.
InterPro: IPR002965; P_ICh_extensn.
                                                                                                                                                                                                                                                                                          Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AR156772; AR82396.1; -. InterPro; IRRO4889; Pertact_sup. Pfam; PF03212; Pertactin; 1. NON_TER 1 1 15 15 SEQUENCE 115 AA; 11705 MW; ElABD4D347D20652 CRC64;
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                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                  115 AA.
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PRINTS; PR01217; PRICHEXTENSN.
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                                  PRELIMINARY;
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Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250079; CAB76433.1; -.

InterPro; IPR004899; Pertact_sup.

Pfam; PF03212; Pertactin; 1.
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                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156771; AAF82395.1;
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                                                                                                                                                                                                                                                                                                                                                                   105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 105 AA
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InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1
 PRT;
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100.0%;
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID-518;
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                                                                                                                                      Bordetella.
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Matches 4
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Matches
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STRAIN-CVGEO;
MEDLINE-20359389; DubMed=10899896;
MEDLINE-20359389; DubMed=10899896;
MEDLINE-20359389; DubMed=1080896;
Poursaux-Eude C., Gulso N., Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250085; CAB76439.1; -.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "MOLE of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (Aug.1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJZ45927; CAB82515.1.

InterPro; IPR003992; pertactin.

InterPro; IPR003999; pertactin.

InterPro; IPR004899; Pertactin.

InterPro; IPR04899; Pertactin.
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Mooi F.R.;
                                                                                   3;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                          1 GAKAPPAFKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                               Length
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PRINTS; PRO1484; PRTACTIVAMLY.
SENDIENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
    200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 266.5; DB 2;
Pred. No. 1.6e-15;
                                          Score 266.5; DB 2;
Pred. No. 4.5e-16;
0; Mismatches 0;
                                                                                                                                                                                                                                                                     911 AA
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                                        Query Match
Best Local Similarity 94.2%;
Matches 49; Conservative
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Best Local Similarity 94.2%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                       FRELIMINARY;
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      SEQUENCE
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09K5H1
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Q9L4E2
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1;
InterPro; IPR004899; Pertact_sup.
InterPro: IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
127 GAKAPPAPRPAPAPPGPQPGPQPPQPPQPPQPPQPQPGPAPAPQPPAGRELSAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AA; 11036 MW; 1AC13209D0238107 CRC64;
                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Last annotation update)
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Pred. No. 2.7e-16;
0; Mismatches 0;
                                                                                                                        107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Infect. Immun. 69:1917-1921(2001).
EMBL; AY007211, AAG3447.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003995; Pertactin.
InterPro; IPR002965; P. Ich_extensn.
Pfam; Pf03212; Pertactin; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
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PRINTS; PR01217; PRICHEXTENSN
NON TER 200 200
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                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                          Bordetella.
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NON_TER
SEQUENCE
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Q9K5H5;
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                                                                               RESULT 6
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817 (2000).
EMBL: AJ250087; CAB76441.!.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_ICh_extensn.
Pfan; PF03212; Pertactin; IPR0ARBN.
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPPGPPQPPQPPQPPQRPPGRPAPAPAPAPGRELSAA 76
                                                                                                                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families amino acid repeats.";
Submitted (JWN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1; -.
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                                                                                                                                                                                                                                                                 Score 264.5; DB 2; Length 111;
Pred. No. 4.1e-16;
0; Mismatches 0; Indels 7;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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122 AA; 12395 MW; BED00966A40FF994 CRC64;
                                                                                                                                                                                                                           11416 MW; 5140669692808F8E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 264.5; DB 2;
Pred. No. 4.4e-16;
0; Mismatches 0;
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InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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87.58;
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Best Local Similarity 87.5%;
Matches 49; Conservative
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Best Local Similarity
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NON_TER 111 1
SEQUENCE 111 AA;
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NON_TER
SEQUENCE
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Q9KJX9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPA----PQPGPQPGPQPPQPPQRPQREAPAPQPPAGRELSAA 49
                                                                                                                                                                                                  1 GAKAPPAPKPA----PQPGPQPGPQPPQPPQRPQREAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                           22 GAKAPPAPKPAPQPGPQPGPQPQPPQPPQPPQRPRAPAPQPPAGRELSAA 74
                                                                                                          ch 95.7%; Score 266; DB 2; Length 109; I Similarity 92.5%; Pred. No. 3e-16; 49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.7%; Score 266; DB 2; Length 215; 92.5%; Pred. No. 5.3e-16; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                             109 109
109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA; 22327 MW; 5C21D45CF784B4AE CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AY007263, AAG38439.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03312; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SO10328;
MEDLINE-21117018; PubMed-11179374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
NON_TER 215 215
SEQUENCE 215 AA; 22327 AW;
  Pertactin (P.68) (Fragment).
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                                                                                                          Query Match
Best Local Similarity
Matches 49; Conserv
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPGPG-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 94.8%; Score 263.5; DB 2; Length 111; Best Local Similarity 84.5%; Pred. No. 5e-16; Matches 49; Conservative 0; Mismatches 0; Indels 9
                                                                                                                                                                                                                                 Match 95.1%; Score 264.5; DB 2; Length 252; Local Similarity 87.5%; Pred. No. 8.1e-16; les 49; Conservative 0; Mismatches 0; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                               "Novel Genetic and Phenotypic Heterogeneity in Bordetella Bornofilsaphica Perfectin.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AX007265; AAG38441.1;
InterPro; IPR003995; pertaction.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                        26107 MW; 368C142508D77057 CRC64;
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Last annotation update)
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01-CCT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last sen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ250089; CAB76443.1; -.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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MEDLINE-20359389; Pubmed-10899896;
                        MEDLINE-21117018; PubMed-11179374;
                                                                                                                                                      PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
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01-CCT-2000 (TTEMBLFEl. 15, 01-CCT-2000 (TTEMBLFEl. 15, 01-JUN-2002 (TTEMBLFEl. 15, 01-JUN-2002 (TTEMBLFEl. 21,
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252 AA;
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NON_TER
SEQUENCE
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09K5H3
1D 09K5H:
AC 09K5H:
DT 01-OC:
DT 01-OC:
DT 01-DC:
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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella perdetusis, Bordetella parapertusis, and Bordetella bronchiseptica."; Infect. Immun, 68:4815-4817(2000).

EMBL; AJ250083; CAB76437.1; -...
EMBL; AJ250083; CAB76437.1; -...
EMBL; AJ250083; CAB76437.1; -...
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; Prich—extensn.
PRINTS; PR01217; PRICHEXTENSN.
NON_TER 11 1 15
NON_TER 115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 115;
                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Pred. No. 6.2e-16;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 7, 2003, 16:53:12
Job time: 27.0426 secs
                                                                                                                                                                                                                               MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.7%;
Matches 49; Conservative
Pertactin (P.68) (Fragment).
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                                                                                                                                                                                   SEQUENCE FROM N.A.
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec Мау Run on:

US-09-855-754B-15

1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA 52 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	B. bronchiseptica	Pertactin antiqen	prn proteins. Bor	Bordetella bronchi	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Pertactin antiqen	Bordetella paraper	Bordetella paraper
		! ! ! ! ! !									
	8	AAE16194	AAR14320	AAR26503	AAE16183	AAE16196	AAE16197	AAE16198	AAR14321	AAR25578	AAE16185
	80	23	12	13	23	23	23	23	12	13	23
	Query Match Length DB ID	52	911	911	911	53	26	28	922	922	922
dР	Query	100.0	100.0	100.0	100.0	96.5	0.96	92.6	92.6	92.6	92.6
	Score	297	297	297	297	286.5	285	284	284	284	284
	Result No.	٦	7	æ	4	S	9	7	80	6	10

B. bronchiseptica Bordetella pertuss	Bloadhesive predur Herbicidally activ Human low density Novel human diagno Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
	9 AAP82971 23 ABB93838 22 AAB82806 22 ABG04360 21 AAG36453 21 AAG36452 21 AAG36451
	334 350 538 356 1222 1257 1257
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11111111111111111111111111111111111111	0 4 4 4 4 4 4 0 0 0 1 0 0 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

AAE16194 standard; peptide; 52 AA. AAE16194; RESULT 1

26-MAR-2002 (first entry)

B. bronchiseptica strain II-2 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Thu May

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Courter membrane protein) or their fragments. Pertactin (pure membrane protein) or their fragments. Pertactin (PNN) is used as and used to detect antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, anch as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                        Length 52;
                     present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                  ch 100.0%; Score 297; DB 23; 1 Similarity 100.0%; Pred. No. 2.8e-16; 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     AAR14320 standard; Protein; 911 AA.
Claim 26; Fig 1c; 47pp; English.
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/label= rer
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'label- repeat
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/label= re
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|abel= re
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'label= re
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/label- re
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                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                              52 AA;
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                                                                                                                                                                                              Sequence
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Pichla microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                         B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                      610
                                                                                                                                                                                       Length 911;
                                                                                                                                                                                                                            Bordetella pertactin antigens for whooping cough vaccines
                                 microorganism transformants - for production of
                                                                                                                                                                                    100.0%; Score 297; DB 12;
100.0%; Pred. No. 2.3e-15;
1ve 0; Mismatches 0;
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/label= RGD_tripeptide
701..703
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/label- RGD_tripeptide
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/label Repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
35..632
/label= P.68
                                                               Disclosure; Fig. 1B; 38pp; English.
                                                                                                                                                                                                                                                                                                       AAR26503 standard; Protein; 911
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WPI; 1991-325214/44.
N-PSDB; AAQ14319.
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Best Local Similarity
...t-rhes 52; Conserve
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N-PSDB; AAQ34566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09217587-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-0CT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charles IG;
                                                                                                                                                               Sequence
                              Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; Bordetella infection;
            The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                              Length 911;
                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQREAPAPQPPAGRELSAA
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                     Query Match 100.0%; Score 297; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254..299
/note= "Pertactin region I"
559..610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; v
therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                AAE16183 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSP ) INST PASTEUR.
                                                                                                                    entire P.94 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                      911 AA;
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                AAE16183;
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Region
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                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; P_{RN}; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to Bordetella bronchiseptica
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                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 286.5; DB 23;
Pred. No. 1.8e-15;
                                                                                Score 297; DB 23;
Pred. No. 2.3e-15;
Mismatches 0;
                                                                              Query Match 100.0%; Score 297; I
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                       AAE16196 standard; peptide; 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                         (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 52; Conserv
                                                  911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200190143-A2.
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                                                                                                                                                                                                                                                                                       AAE16196;
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                                                   Sequence
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Fig 1c; 47pp; English.
                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                          25-MAY-2000; 2000US-206969P
                  Bordetella bronchiseptica.
                                                                                                                                                                                                                (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                         WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fulids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                              B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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Pred. No. 2.4e-15;
); Mismatches 0; Indels
                                            AAE16197 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Fig 1c; 47pp; English.
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92.9%;
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                                                                                                                           (first entry)
                                                                                                                                                                                                                                                           Bordetella bronchiseptica,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097639/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 AA;
                                                                                                                                                                                                    Pertactin; PRN;
                                                                                                                                                                                                                                                                                               WO200190143-A2.
                                                                                                                         26-MAR-2002
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                                                                                     AAE16197;
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Matches
        RESULT 6
                              AAE16197
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                Length 58;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                          Score 284; DB 23
Pred. No. 3e-15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR14321 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281..285
/label- repeat
575..577
/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat
                                                                                                                                                                                                                                                                                        95.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.7
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276..280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                         58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JAN-1992
                                                                                                                                                                                                                                                         Sequence
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B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

(first entry)

26-MAR-2002

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AAE16198;

AAE16198 standard; peptide; 58 AA.

RESULT 7 **AAE16198**

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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

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A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (*P95*) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"contains 5 direct, tandem repeats"
575..612
/note-"contains 9 direct repeats of Pro-Gln-Pro"
712..714
/note-"motif associated with cell-cell adhesion"
                  "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                         Acellular vaccine for immunisation against whooping cough comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GÄKAPPAPRPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella parapertussis pertactin outer membrane protein, p.70
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9
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                              ..285
te= "contains 5 direct, tandem
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Pred. No. 2.2e-14;
0; Mismatches 0;
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254..304
/note= "Pertactin region I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16185 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 20pp; English
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                                                                                                                                                                                                                91WO-GB02302
                                                                                                                                                                                                                                                                             (WELL ) WELLCOME FOUND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.6
Best Local Similarity 89.7
Matches 52; Conservative
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   260..262
                                                                                                                                                                                                                                                                                                                                           WPI; 1992-250033/30.
N-PSDB; AAQ26509.
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   Binding-site
                                                                                                 Binding-site
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                                                                                                                                               W09211292-A.
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                                                                                                                                                                               09-JUL-1992
                                                                                                                                                                                                                                                                                                            Charles IG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16185
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Region
                                   Region
                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                   ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPPGPQP-----PQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 284; DB 12; Length 9 Pred. No. 2.2e-14; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
35..643
/label- P70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR25578 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1C; 38pp; English.
                                                                                                                                            /label= repeat
595.597
/label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                        (WELL ) WELLCOME FOUNDATION LTD
                  repeat
                                               'label- repeat
                                                                                  repeat
                                                                                                                repeat
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                                                                                                                                                                                                                                           /label= repeat
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89.78;
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                                                           ວປ6..588
/label- r
                                                                                                                            . 594
                                                                                                                                                                                             98..600
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                              583.,585
                                                                                             589..591
                                                                                                               'label-
                                                                                                                                                                                                             label-
                                                                                                                                                                                                                                                                                                                                                                                                                                           Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ14320
                                                                                                                                                                                                                                                                                                                                         28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                          02-APR-1990;
                                                                                                                                                                                                                                                                        W09115571-A
                                                                                                                                                                                                                                                                                                         17-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                         Clare JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Protein
Pept1de
                                Pept1de
                                                               Peptide
                                                                                             Peptide
                                                                                                                              Pept1de
                                                                                                                                                             Peptide
                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                            Pept1de
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Boursaux-eude C;

Guiso-maclouf N,

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a materials. Thus the pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPGPG-----PQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 284; DB 23;
Pred. No. 2.2e-14;
); Mismatches 0;
564..621
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                        Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE16195 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.6%;
                                                                                                                                25-MAY-2000; 2000US-206969P
                                                                                                     23-MAY-2001; 2001WO-EP06457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                            (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR.
                                                                                                                                                                                                                      WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 AA;
                                          WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200190143-A2
                                                                      29-NOV-2001
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AAE16195
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin attibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used to affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B, bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPA------PQPGPQPGPQPPQPPQPPQPPQRPGREAPAPQPPAGRELSAA
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 95.3%; Score 283; DB 23;
Best Local Similarity 86.7%; Pred. No. 3.6e-15;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16193 standard; peptide; 49 AA.
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                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2001; 2001WO-EP06457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Gaps

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Thu May

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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQPPQRPPAPAPQPPAGRELSAA 49
                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                Score 266.5; DB 23; Length
Pred. No. 5.6e-14;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16199 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                89.78;
94.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                  Similarity 94.2
49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-097639/13.
                                                                                                                                                                                                                                                         49 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16199;
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                              B. bronchiseptica strain II-8 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relyperlies containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                        4
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                                                                                         Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA
                                                                     1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides containing polymorphisms of the repeated pertactin in Bordetella species, useful in immunogenic
 Score 260; DB 23;
Pred. No. 1.7e-13;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 259; DB 23;
Pred. No. 2.2e-13;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guiso-maclouf N, Boursaux-eude
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                                    ;
                                                                                                                                                                                            AAE16200 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE16201 standard; peptide; 54
87.5%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.2%;
ilarity 92.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica.
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-097639/13.
Ouery Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       40200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001
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                                                                                                                                                                                                                              AAE16200;
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                                                                                                                                                                                                                                                               Gaps
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3

48 AA;

Sequence

AAE16201;

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in buildy corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                      B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                       25-MAY-2000; 2000US-206969P
                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                     Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-097639/13.
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                                                                                                                                                                                                                         WO200190143-A2.
                                                                                                                                                                                                                                                              29-NOV-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Search completed: May 7, 2003, 16:47:05 Job time: 28.0187 secs

ä

4; Gaps

à g

Query Match 86.9%; Score 258; DB 23; Length 54; Best Local Similarity 89.1%; Pred. No. 2.7e-13; Matches 49; Conservative 0; Mismatches 2; Indels

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Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 11, Appli
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Appli
                                                                                                                         7, 2003, 16:41:51 ; Search time 8.59284 Seconds (without alignments) 178.054 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, P
Sequence 8, Appropries No. 520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Sequence 29, Sequence 30, Sequence 31, Sequence 6, A Sequence 12, Sequence 21, Sequence 2, A Sequence 13, Sequence 18, Sequence 18, Sequence 18, Sequence 65, Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, P
Sequence 11, Sequence 11, Patent No. 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-460-269C-4
US-08-460-269C-6
US-08-460-269C-2
US-08-460-269C-2
US-08-750-624-11
US-08-750-624-11
US-08-460-268-16
US-08-460-269C-8
US-09-041-886-29
US-09-041-886-29
US-09-041-886-31
US-08-457-273B-42
US-09-041-886-31
US-08-457-273B-42
US-08-457-273B-42
US-08-457-273B-42
US-08-457-273B-42
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-273B-8
US-08-457-255-32
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                              US-09-855-754B-15
297
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Maximum DB seq length: 200000000
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Match Length DB
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106
1274
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641
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408
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                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                Scoring table:
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125
120.5
120.5
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113.5
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111.5
111.5
110.5
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65, Appl 66, Appl 4, Appll 14, Appll 21, Appl 12, Appl 12, Appl 22, Appl 22, Appll 22, Appll 23, Appll 24, Appll 26, Appll 27, Appll 28, Appll 29, Appll 20, Appll 20, Appll 20, Appll 20, Appll 20, Appll 20, Appll 20, Appll 20, Appll 20, Appll 21, Appll 22, Appll 22, Appll 23, Appll 24, Appll 26, Appll 26, Appll 27, Appll 26, Appll 27, Appll 28, Appll 29, Appll 20,			Gaps 0;	
Sequence Seq		gan, P.C.	Length 911; Indels 0; AGRELSAA 52	
US-08-478-029A-65 US-09-179-558-66 US-09-227-420-4 US-09-227-420-4 US-09-281-476-21 US-09-281-476-21 US-09-314-268-149 5352575-5 US-09-056-556-230 US-09-056-556-225 US-09-072-596-225 US-09-072-596-226 US-09-072-596-226 US-09-172-838-216 US-09-170-838-216 5470718-4 US-09-535-008-63	ALIGNMENTS	F HETEROLOGOU elano & Brani ., Sulte 1400 ., Sulte 1406 fl.0, Version 60,269C pov-2	tch al Similarity 100.0%; Score 297; DB 4; Length 9; al Similarity 100.0%; Pred. No. 8.4e-19; 52; Conservative 0; Mismatches 0; Indels GAKAPPAKRAPOPGOPOPPOPPOPPOPPOPPORPAGRELSAA	
4 4 6 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9			100.0%; ty 100.0%; ervative PQPGPQPGPOPP	PQPGPQPGPQPF
110.5 110.5 110.37.0 110.37.0 110.37.0 110.37.0 100.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9 106.5 35.9	▼ -	269C 4, 6 4, 6 11	100 cal Similarity 100 52; Conservative GAKAPPAEKPAPOPGPG	
		RESULT 1 US-08-460-269C Sequence 4, Patent NO. 6 TITLE TITLE NUMBE CORRE CORRE TOMPU COMPU TOMPU	Query Match Best Local Matches 5 Qy 1 GAR	55

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Wilson, Mary J
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                              APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROMANOS, MICHABL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922;
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM-PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284; DB 4; I
Pred. No. 1.1e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Ilhear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                   Sequence 6, Application US/08460269C Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 922 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.6%;
Best Local Similarity 89.7%;
Matches 52; Conservative (
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPG-
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                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: VA
US-08-460-269C-6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 212; DB 4;
78.8%; Pred. No. 1.9e-11;
tive 0; Mismatches 1
              NAME: LEDOVITZ, RICHALD M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: 97,067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRMEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08237716
Patent No. 5589384
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,955
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 33 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-816-4100
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Region

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Gaps
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Sequence 16, Application US/08246982A

Patent No. 5686288

APPLICANT: NacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Gusella, James F.

TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100

CITY: Washington

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
9
                                                                                                  APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 APPAPKPAPQPG-----PQPGPQ-PPQPPQPPQRQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILIG DATE: MAy 20, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.1%; Score 125; DB 6;
53.2%; Pred. No. 0.00025;
tive 0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/TOCKET NUMBER: 0609.3880002
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.29
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-246-982A-16
                                                                                                                                                                                 NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amiro acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                    :Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:3
                                                                                                                                                              PROTEIN
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                               /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127; DB 4; Length 24;
Pred. No. 1.6e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                           Score 130; DB 1;
Pred. No. 1.2e-05;
2; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sim & McBurney
6th Floor, 330 University Avenue
                                         /label- LTB sequence
                                                                                                                                                                                                                                                                                                                                                      10 PAPQPGPQPPQPPQPPQPPQRQPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                            5 PGPEIAPQPGPQPPQP-----QPEAPAPEP 32
                                                                                                                   /label= hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTONNE, NEURIL STEWART, MICHAEL I REGISTRATION NUMBER: 24,973
REMEMBENCE/DOCKET NUMBER: 1038-660
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 24 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PQPGPQPPQPPQP-----QPEAPAPQPP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 РОРСРОРРОРРОРРОРОЯ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.88;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 67.6%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: MSG IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCB
STREET: 6th Floor, 3
CITY: Toronto
                                                                                                                                                          NAME/KEY: Region
LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
                              OTHER INFORMATION:
                                                                                              LOCATION: 4..7
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                Region
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US-08-750-624-11
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NAME/KEY:
LOCATION:
                                                                              NAME/KEY:
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US-08-750-624-11
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STATE: OI
COUNTRY:
                                                                                                                                                                                                                                      US-08-237-716-11
                                                                                                                                        FEATURE:
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2200 Clarendon Blvd., Suite 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
                                                                                                                                                                                                                                                 NAME: Lebovitz, Richard M.
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28, Application US/09041886
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             CURRENT APPLICATION DATA:
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FILING DATE: 07-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.4%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.1%;
Matches 24; Conservative
                                                                 ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
                                                    USA
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Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PQPGPQPPQPPQP
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5202236-37
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                                                   Gaps
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Pred. No. 0.0045;
2; Mismatches 13; Indels 11;
                Length 3119;
                                                                                                                                                                                                                                                                                            APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                    51
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
            Score 120.5; DB 1;
Pred. No. 0.0045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA----
                                                                                    9 KPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA----
                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0609.3880003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAX-1995
CLASSIFTCATION: 514
                                                                                                                                                                                                          Sequence 16, Application US/08453265
Patent No. 5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                             MacDonald, Marcy E. Ambrose, Christine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                      1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET UNMBER: 06(
TELECOMMUNICATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
TELEFRA: (202) 371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.68;
              Query Match
Best Local Similarity 50.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3119 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.69
Best Local Similarity 50.09
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIOM TYPE: Flor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAVID M.; STRAUSBERG
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 APPAPAFAPAPALAPAPUNPNPSPPSPPSPPTPPPTPPSPPSPP 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUS SUSAN L.; MCCANDLISS; RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 120; DB 4;
Pred. No. 6.4e-05;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 6;
Pred. No. 0.00068;
0; Mismatches 17
                                                                                            APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                         REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                 LENGTH: 23 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-460-269C-8
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Score 116; DB 4; Length 530;
Pred. No. 0.0023;
2; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEGUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: |Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                              9 KPAPQPGFQPGPQPPQPPQP--PQRQPEAPAPQPPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KPAPQPGFQPGPQPPQPPQP--PQRQPEAPAPQPPAG-
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NAME: Campbell, Cathryn A.
REGISTRATICN NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
FELECOMMUNICATION INFORMATION:
                         P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-041-886-30
; Sequence 30, Application US/09041886
Patent No. 6335872
; GENERAL INFORMATION:
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKER NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEC ID NO: 29:
SEQUENCE CHAMACTERISTICS:
                                                                                                                                                                                                                                                                                          39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-849
INFORMATION FOR SEO ID NO: 30
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   LENGTH: 530 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 552 amino acida
amino acid
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                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-09-041-886-29
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TTY: San Diego
                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92122
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                                                                                                                                                                                               TOPOLOGY:
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Pred. No. 0.0022;
2; Mismatches 15; Indels
                                   TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS: ADDRESSE: Campbell 6 Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                   CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CORREWT APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                           E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORKEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%;
Best Local Similarity 45.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 513 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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STREET: 43/v.
CITY: San Diego
"mare: California
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
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5;

Gaps

14;

15;

Length 3144; Indels

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Query Match
39.1%; Score 116; DB 1;
Best Local Similarity 45.6%; Pred. No. 0.011;
Matches 26; Conservative 2; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KPAPQPGPQPGPQPPQPPQP--PQRQPEAPAPQPPAG-
                        FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 99,021
TELECOMMUNICATION INFORMATION:
      APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: May 7, 2003, 16:57:16
Job time: 23,6838 secs
                                                                                                                                                      INFORMATION: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3144 Amirical
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-246-982A-6
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Patent No. 566288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Dayso, Mablel P.
APPLICANT: Duyso, Mablel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116; DB 4; Length 589;
Pred. No. 0.0025;
2; Mismatches 15; Indels
                                                                                                                             TITLE OF INVENTION: Prospotitic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use UNBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-LJ 2626
                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/DOCKET NUBBER: P-LJ
TELECOMMUNICATION: TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SED ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 New York Avenue
                                                                                  APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 39.1%;
1 Similarity 45.6%;
26; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-041-886-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New CITY: Washington
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                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-246-982A-6
US-09-041-886-31
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us-09-855-754b-15.rapb

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Copyright (c) 1993 - 2003 Compugen Ltd.
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7, 2003, 16:53:34 ; Search time 15.5911 Seconds (without alignments) 306.927 Million cell updates/sec
OM protein – protein search, using sw model
                                                                                                          US-09-855-754B-15
297
                                      May
                                    Run on:
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1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA 52 Perfect score: Scoring table: Sequence:

349150 segs, 92025710 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

(Ggn2_6/ptodata/2/pubpaa/USOB_NEW_FUB.pep:-(Ggn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-(Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*-Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB. /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.

SUMMARIES

Description	Sequence 15, Appl		Sequence 18, Appl			17		Sequence 14. Appl			22,	Sequence 23, Appl	5,	24,	Sequence 43, Appl	43.	· Sequence 43. Appl	٠,	Sequence 47, Appl
ΩI	US-09-855-754-15	US-09-855-754-4	US-09-855-754-18	US-09-855-754-19	US-09-855-754-6	US-09-855-754-17	US-09-855-754-16	US-09-855-754-14	US-09-855-754-20	US-09-855-754-21	US-09-855-754-22	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-09-976-740-43	US-10-023-529-43	US-10-023-523-43	US-09-976-740-47	US-10-023-529-47
DB	6	σ	0	6	6	6	σ	σ	6	6	σ	6	σ	6	6	12	12	6	12
Query Match Length DB	52	911	26	28	922	52	53	49	48	52	54	42	910	39	538	538	538	550	550
Query Match	100.0	100.0	96.0	92.6	95.6	91.2	90.1	89.7	87.5	87.2	86.9	71.4	71.4	64.5	41.4	41.4	41.4	40.9	40.9
Score	297	297	285	284	284	271	267.5	266.5	260	259	258	212	212	191.5	123	123	123	121.5	121.5
Result No.	1	7	m	4	ស	9	7	80	6	10	. 11	12	13	14	15	16	17	18	19

Sequence 47. Appl	Sequence 3, Appli	-	Sequence 7, Appli	Sequence 2, Appl1	Sequence 1002, Ap	Sequence 1002, Ap	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 9, Appl1	Sequence 160, App	Sequence 5, Appli	Sequence 4, Appl1	Sequence 32, Appl	Sequence 62, Appl	Sequence 2, Appli	_	Sequence 21, Appl	Sequence 125, App	Sequence 70, Appl	Sequence 967, App	Sequence 1444, Ap		. 0	Sequence 6, Appli
12 US-10-023-523-47	9 US-10-171-384-3	10 US-09-823-240-2	10 US-09-904-987-7	9 US-09-959-987-2	9 US-09-925-299-1002	10 US-09-925-299-1002	9 US-10-171-384-1	9 US-10-077-584-4	9 US-10-020-215-2	9 US-10-077-584-9	10 US-09-765-272-160	9 US-10-067-457-5	10 US-09-850-887-4	12 US-10-042-417-32	9 US-09-298-523B-62	9 US-09-298-523B-2	10 US-09-823-240-10	10 US-09-910-087-21	9 US-10-072-036-125	10 US-09-791-171-70	10 US-09-764-864-967	10 US-09-925-300-1444	9 US-10-038-010-4	9 US-10-001-873-50	9 US-09-978-167-6
550	827	802	1543	641	647	647	824	171	1274	68	641	863	274	197	701	707	380	509	635	999	316	531	638	1134	578
40.9	40.9	40.7	39.1	38.9	38.9	38.9	38.2	38.0	37.9	37.7	37.5	37.5	37.4	37.2	37.2	37.2	37.0	37.0	37.0	37.0	36.9	36.9	36.9	36.9	36.7
121.5	121.5	121	116	115.5	115.5	115.5	113.5	113	112.5	112	111.5	111.5	111	110.5	110.5	110.5	110	110	110	110	109.5	109.5	109.5	109.5	109
50	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                      APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVERVION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERVION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERVION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERVION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000 .
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PAPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATEGIL VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURGAUX-EDIDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 297; DB 9;
llarity 100.0%; Pred. No. 2.4e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
Sequence 15, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches | 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 15
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/855,754
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOSHIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISSEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/9855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2000-05-25
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FILE REFERENCE: 0495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 1.7e-13;
0; Mismatches 0; Indels
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Pred. No. 2.6e-13;
; Mismatches 0;
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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Best Local Similarity 92.9%;
Matches 52; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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LENGTH: 56
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLICEPITLES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPILA, THERR USE IN DIAGNOSTICS, AND I
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60,206,969
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                                                                                                                                                                                                                                                     Score 284; DB 9;
Pred. No. 2e-13;
0; Mismatches 0;
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Pred. No. 2e-12;
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CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                            , ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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89.7%;
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1 Similarity 89.7%;
52; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                   NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Matches 52; Conserv
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Best Local Similarity
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; ORGANISM: Bordetella bronchiseptica US-09-855-754-20
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US-09-855-754-21
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BORNSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                 Query Match 89.7%;
Best Local Similarity 94.2%;
Matches 49; Conservative
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Matches 48; Conservative
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PRIOR FILING DATE: 2000-0
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SOFTWARE: Patentin Ver.
SEQ ID NO 21
LENGTH: 52
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US-09-855-754-20
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US-09-855-754-21
       US-09-855-754-14
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TITLE OF INVENTION: POLYEPHIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: RANDOMCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSELIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
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Publication No. US20020192237A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EDDE, CAROLINE
APPLICANT: BUSCO-MACLOUF, NICOLE
TITLE OF INVENTION: PCLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE REPERENCE: 04455-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                                                      Length 59;
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Pred. No. 1.4e-12;
0; Mismatches 0;
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85.0%; Pred. No. 2.6e-12;
iive 0; Mismatches 0;
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                                                                   TYPE: PRT; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
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Publication No. US20020192237A1
GENERAL INFORMATION:
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                                                                                                                                                              Query Match 91.2%;
Best Local Similarity 96.2%;
Matches 51; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
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Matches 51; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 14
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LENGTH: 59
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITTILE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITTILE OF INVENTION: BRONGTELLA PARAPERTUSSIS, AND BORDETELLA PARAPETUS OF INVENTION: BRONGTISEPTICA, THEIR USE IN DIAGNOSTICS, AND FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/985,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
SOFTWARE: PATENTIN PATENTIN PATENTIAN PATE
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERFACTINI IN BONDETELLA PERFUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
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Score 266.5; DB 9;
Pred. No. 2.7e-12;
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92.3%; Pred. No. 7.2e-12;
11ve 0; Mismatches 0;
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92.5%; Pred. No. 8.9e-12;
ive 0; Mismatches 2;
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Matches 49; Conservative
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Best Local Similarity
Matches 38; Conserv
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US-09-976-740-43
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US-09-855-754-24
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LENGTH: 39
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
                                                                                                                                                                                                                  APPLICANT: BOUTSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYTEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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  22
                       1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPEAPAPQPPAGRELSAA 42
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. 1.1e-11; Indels
1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPPQP-PQRQPEAPAPQPPAGRELSAA
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Pred. No. 1.1e-08;
0; Mismatches 1;
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Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella bronchiseptica US-09-855-754-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CARCLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                      Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.4%;
Best Local Similarity 78.8%;
Matches 41; Conservative
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Best Local Similarity 89.1%;
Matches 49; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 24
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LENGTH: 42
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TITLE OF INVENTION: BORDETELLA PRARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, PHEIR USE IN DIAGNOSTICS, AND INTELE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 0495-0206-00000
CURRENT APPLICATION NUMBER: U5/09/855,754
CURRENT APPLICATION NUMBER: U5/09/855,754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 212; DB 9;
Pred. No. 1.4e-07;
0; Mismatches 1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/09976740 Publication No. US20020194633A1
                                                                              CAROLINE
Sequence 5, Application US/09855754
Publication No. US20020192237A1
                                                                                                          GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754-5
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Best Local Similarity 78.8%;
Matches 41; Conservative
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                                                  GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE,
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 5
LENGTH: 910
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Search completed: May 7, 2003, 17:30:50 Job time: 15.5911 secs

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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-855-754B-15 297 Title: Perfect score: Scoring table: Sequence:

Run on:

22

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	68K Outer membrane		bra	hypothetical 47.8K	ໝ	proline-rich prote	sulfated surface q	nuclear protein EB	hypothetical proli	cysteine-rich exte	proline-rich prote	hypothetical prote	·	chitinase (EC 3.2.	UL36 protein - hum	hypothetical prote		_	hypothetical prote		hypothetical prote	u	protein-tyrosine-p	cysteine-rich exte	acrosin (EC 3.4.21	hypothetical prote			
SUMMARIES	a	A47675	S15204	A32560	JC2301	T10798	S16748	A33647	S42442	A34043	A48232	S21961	T48814	A86335	S51939	ММВЕН6	AE2295	T17547	107907	T10340	C96623	н83619	T06291	T14355	B48232	S47538	T02632	B96534	A71416	T31611
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đ	Query Match	100.0	92.6	71.4	51.0	47.5	47.3	46.1	45.8	45.5	45.5	44.4	44.4	43.9	43.8	43.6	43.4	43.4	43.3	43.1	43.1	42.8	42.8	42.4	42.3	42.3	٠	41.2	41.2	41.2
	Score	297	284	212	151.5	141	140.5	137	136	135	135	132	132	130.5	130	129.5	129		128.5	128	128	127	127	126	125.5	125.5	123	122.5	122.5	122.5
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glyceraldehyde-3-p	pistil extensin-li	extensin-like prot	extensin - Volvox	extensin-like prot	proline-rich prote	cappuccino dene pr	unknown protein [1	hypothetical prote	hypothetical prote	spliceosome-associ	protein F2401.6 [1	proline-rich prote	requiatory factor	pistil extensin-li	proline/lysine-ric
149681	JQ1696	T10741	S22697	JQ1686	T17531	T13286	G86441	T24470	T19069	JC5437	A96650	T17737	A35913	P00476	T17908
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440	426	461	464	151	412	1058	1201	165	379	388	70	288	979	154	496
41.1	6.04	40.6	40.6	40.4	40.2	40.1	40.1	39.9	39.9	39.9	39.7	39.7	39.7	39.6	39.6
 122	121.5	120.5	120.5	120	119.5	119	119	118.5	118.5	118.5	118	118	118	117.5	117.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1	
	A47675	
	68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica	chiseptica
	C;Species: Bordetella bronchiseptica	•
	C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999	ange 08-Oct-1999
	C; Accession: A47675	
	R;L1, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G.	es, I.G.
-	J. Gen. Microbiol. 138, 1697-1705, 1992	
	Artitle: Cloning, nucleotide sequence and heterologous expression of the protective o	ession of the protective o
-	A; Reference number: A47675; MUID:92407514; PMID:1527510	0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	A; Contents: CN7531	
	A; Accession: A47675	•
	A;Status: preliminary	
	(A) Molecule type: hucleic acid	
••	A; Residues: 1-911 <li1></li1>	•
	A; Cross-references: GB:X54815; GB:S46416; NID:q39396; PIDN:CAA38584.1: PID:q39397	CAA38584.1: PID:q39397
	A:Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)	, NCBIP:113319)
	Ouerv Match 100 08 Sooms 207: DB 2: Iconth 011:	h 011.
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pertactin - Bordetella parapertussis
N;Alternate names: outer membrane protein P70
C;Species: Bordetella parapertussis
C;Species: Bordetella parapertussis
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999
C;Accession: S15204; S14659
R;Li, L.J.; Dougan, G; Novotny, P.; Charles, I.G.
Mol. Mcrobiol. 5, 409-417, 1991
A;Title: P,70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A;Reference number: S15204; MUID:91251771; PMID:2041476
A;Accession: S15204 . <u>අ</u>

A Molecule (Lype: DNA A; Residues: 1-922 <LIL> A; Cross-references: EMBL:x54547; NID:g39761; PIDN:CAA38419.1; PID:g39762 C; Genetics: A; Gene: prn C; Keywords: membrane protein

Gaps 9 Score 284; DB 2; Length 922; Pred. No. 3.3e-12; 0; Mismatches 0; Indels Query Match 95.6%; Best Local Similarity 89.7%; Matches 52; Conservative δ

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52 ---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 1 GAKAPPAPKPAPQPGPQPG---

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C; Species: Brassica napus (rape)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C; Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C; Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
R; Roberts, M.R; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991
A; Description: Cloning and characterization of a proline-rich gene expressed specific A; Reference number: S16748
A; Accession: S16748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Volvox carteri
C; Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Accession: A33647, R; Wenzl, S; Engel, J; Sumper, M.
J; Cell Biol. 109, 3493-3501, 1989
A; Title: The extracellular matrix of Volvox carteri: molecular structure of
A; Reference number: A33647; MJD:90094551; PMID:2689458
A; Recession: A33647
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear protein EBNA2 - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: 842442, S32988; S42447
R;Sample, J; Hummel, M; Braun, D; Birkenbach, M; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KAPPAPKPAPQPGPQPGPQPPQPPQ-------PPQPPQRQPE---APAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-45 CERT-
A;Cross-references: GER:S51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Reywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 140.5; DB 2; Length 449; llarity 44.3%; Pred. No. 0.005; Conservative 4; Mismatches 13; Indels 17
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                                                Score 141; DB 2; Length 599;
Pred. No. 0.0058;
1; Mismatches 17; Indels
C; Keywords: extracellular matrix; glycoprotein; pheromone
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A;Residues: 1-449 <ROB>
A;Cross-references: EMBL:X60376; NID:g22596; PID:g22597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sulfated surface glycoprotein 185 - Volvox carteri
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                                                         47.5%;
55.0%;
                                                            Query Match
Best Local Similarity 55.0
Matches 22; Conservative
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27; Conserv
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Matches 2
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A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-fre
                                                                                                                                                                                                                                                                   R.Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989

Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989

A;Title: Molecular cloning and characterization of protective outer membrane protein P.6

A;Reference number: A32560; MUD:89264462; PMID:2542937

A;Rosession: A32560

A;Molecule type: DNA

A;Rosidues: 1-910 CCHA>

A;Rosidues: 1-910 CCHA>

A;Rosidues: 1-910 CCHA>

A;Note: it is uncertain whether Met-1 or Met-3 is the initiator

C;Keywords: membrane protein

F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical 47.8K protein - Pneumocystis carinii
N;Alternate names: ORF-3
C;Species: Pneumocystis carinii
C;Species: Dan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
K;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C.Accession: T10798
R.Godl, K.: Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin
A;Reference number: 217154; MUID:97162277; PMID:9009264
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAN06706.1; PID:d1007278;
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                                                                                                                                                      outer membrane protein P.69 precursor - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
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   GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
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Best Local Similarity 50.8%; Pred. No. 0.00092;
Matches 30; Conservative 1; Mismatches 9; Indels 19
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Pred. No. 1.7e-07;
0; Mismatches 1; Indels
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78.8%;
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Matches 41; Conservative
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A; Residues: 1-599 <GOD>
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A; Residues: 1-430 <WAD>
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Length 209;

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A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding novel e
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474; MUID:93005740; PMID:1392607
A;Accession: RABA
A;Residues: BABL: Z4020; NID:919918; PID:919919
A;Experimental source: BABL: Z4020; NID:919918
C;Superfamily: glutelin stigma, style; strain Petit Havana SR1
C;Superfamily: glutelin attrix; fertilization; glycoprotein
C;Superfamily: glutelin sequence #status predicted <SIG>
F;20-209/Product: cystelne-rich extensin-like protein 1 #status experimental <AMAT>
E7:146/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity 55.8<sup>†</sup>
Matches 24<sup>‡</sup> Conservative
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A; Introns: 281/3
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A; Realdues: 1-487 < FARS
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
A; Cross-references: EMBL: V01555; NID: 959074; PIDN: CAA24877.1; PID: 91632787
B; Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A; Fithe: UZ region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2.
A; Facterence number: S42447; MUID: 85063846; PMID: 6209719
A; Accession: S42447
A; Molecule type: DNA
C; Cross-references: EMBL: K03333; NID: 9330443; PIDN: AAA45903.1; PID: 9330444
C; Superfamily: hydroxyproline-rich glycoprotein
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C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
R;Mu, H; Zou, J; May, B; Gu, O; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a;Reference number: $42440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C;Species: Owenia fusiformis
C;Species: Ovenia fusif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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0.011;
ches 20;
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Pred. No. 0.0047;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                             R;Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A;Reference number: 832973
AAccession: 832988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.5%;
Matches 23; Conservative
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Best Local Similarity 53.5%;
Matches. 23; Conservative
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A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M32217
A;Accession: B34043
                                                                                                                                             A; Molecule type: mRNA A; Residues: 1-487 <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-141 <BAK>
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A; Residues: 1-209 < WUA>
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                                                                                                       A; Accession: S42442
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proline-rich protein APG - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 (C.) Accession: S2196! R. R. Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991 A.Description: Cloning and characterization of a proline-rich gene expressed specific A. Reference number: S16748 A. Accession: S21961 A. Residues: 1-534 (-ROB) A. Residues: 1-534 (-ROB) A. Cross-references: EMBL:X60377; NID:922599; PID:922599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cipacies: Neurospora crassa
Cipacies: Neurospora crassa
Cipacesion: T48814
R.Schulte, U.; A48814
R.Schulte, U.; A48814
A.Recession: T48814
A.Recession: T48814
A.Recession: T48814
A.Recession: T48814
A.Residues: 1-1922
A.Re
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                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Indels
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                                                                                                                                                                                                                                                                                             5 PPAPKPAPQPGPQPGPQP-PQPPQPPQP-PQRQPEAPAPQPPA 45
45.5%; Score 135; DB 2;
55.8%; Pred. No. 0.0064;
11ve 4; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No. 0.021;
3; Mismatches. 1
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Matches 26; Conservative
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Length 1952;

DB 2;

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RingGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P. J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUD:88274327; PMID:2839594
A;Sterence number: A30083; MUD:88274327; PMID:2839594
A;Recension: 130085
A;Recension: I30085
A;Molecule type: DNA
A;Residues: 1-3164 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
                                                                                                                                                                                                                                     C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: I30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2939 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPGPG 2982
6 PAPKPAPQPGPQPGPQP-PQP-PQP-PQP-PQRQPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                               UL36 protein - human herpesvirus 1 (strain 17)
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Best Local Similarity 66.7%;
Matches 30; Conservative
                                                                                                                                                                                                             C; Species: human herpesvirus 1
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Job time : 10.7445 secs
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                                                                                                                     RESULT 15
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Date: 28-oct.1996 *sequence_revision 07-Feb-1997 *text_change 10-Jul-1998
C;Accession: S51939; S72315; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A. Plant Mol. Biol. 27, 211-216, 1995
Plant Mol. Biol. 27, 211-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
A;Title: A proline-rich chitinase from Beta vulgaris.
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A;Residues: 1-1137 <STO>
A;Cross-references: GB:AE005172; NID:g8778985; PIDN:AAF79900.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                  T20H2.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
                                    Gaps
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Note: the authors translated the codon TGC for residue 416 as Gly
Accession: S72315
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Pred. No. 0.024;
2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 KPPPAAPSPSPCPSPPRRQPKPQPKPVPPPACPPTPPKPQPKPAPPPEPKPA 155
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                                    Indels
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C; Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted <SIG>
F;2-439/Porduct: chitinase #status predicted <MAT>
F;183-423/Domain: plant chitinase homology <PCH>
                                                                                                                           5 PPAPKPA-PQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
      Pred. No. 0.057;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chitinase (EC 3.2.1.14) precursor - beet
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      Best Local Similarity 58.5%;
Matches 24; Conservative
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Residues: 191-397 <BER2>
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Matches 27; Conserv
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Residues: 1-439 <BER>
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Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
Molecule type: DNA
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Gaps

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Length 3164; Indels

DB 1; æ

Score 129.5; DE Pred. No. 0.12; 2; Mismatches

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:49; Search time 5.0494 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-15 297 1 Garappapkpapgpgpgp......QrQpeapapgppagrelsaa 52 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

													-																					
	Description	35 bordetella	28 bordetella	33 bordetella	3 brassica na	37 volvox cart		_	32 arabidopsis		-	homo sa	-	-	1 mus musculu	11 rattus norv	_	21 emericella	11 nicotiana t	35 homo sapien	12 caenorhabd1	20 drosophila	70 homo sapien	_		24 mus musculu	50 herpesvirus	_	_	99 ureaplasma	6 herpesvirus	_	_	15 plasmodium
	esc	00303	P24328	P14283	P40603	P21997	P12978	P21260	P40602	P10220	083949	927	P48038	9bdJ60	P02831	P51111	064467	P78621	003211	060885	009442	241	P22670	063943	414	070324	P25050	P42858	P05142	9pr	P22576	P58840	P05143	P0691
SUMMARIES	QI	RT_BORBR	PERT_BORPA P	E		Æ		FU					_RABIT		OUSE												S7				HSVSC	HUMAN	MOUSE	CSP_PLABE P
	DB	1	-	-	-		Н	Н	Н	Н	-	Н	н	~	Н	-	-	-	-	-	-			-	-	-	-	1	-	-	-	-	-	-
	Length	911	922	910	449	485	487	141	534	3164	875	2004	431	555	443	3110	440	1790	426	1362	379	1059	979	514				m	261				296	339
de	Ouery Match	100.0	92.6	71.4	7	46.1	2	•	43.9	e.	щ.	ä				41.2	41.1		ö	0	go.	30	on o	σ,	σ,	2	S)	a)	38.9	₿	∞ .	8	38.6	38.6
	Score	297	284	212	140.5	137	136	135	130.5	129.5	128	127.5	125.5	125	122.5	122.5	122	122	121.5	120	118.5	118.5	118	117	117	116.5	116	116	115.5	115.5	115	115	114.5	114.5
	Result No.	н	7	m	4	io.	φ	7	co	σ	10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29	30	31	32	33

P23093 plassmodium P06914 plasmodium Q99014 trichhoderma Q05859 mus musculu Q05860 mus musculu P08001 sus scrofa P42768 homo sapien P09791 trypanosoma P42859 mus musculu Q15428 homo sapien P93329 medicago tr	
CSP_PLABA CSP_PLAYO KPCL_TRIRE FM14_MOUSE FM14_MOUSE ACRC_PIG MASP_HUMAN CIRF_HUMAN CIRF_HUMAN PARB_TRYBB HD_MOUSE S3A2_HUMAN NO20_MEDTR	
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347 1139 1206 1468 415 502 757 129 3119 464	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li L.J., Dougan G., Novotny P., Charles I.G.; "P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . MICTOBIOL. 5:409-417(1991).
FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MADIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
SUBUNIT: MONOMER.
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
           3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERTACTIN (P.70).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                          ö
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                       Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                                                                                          Indels
                                                     3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                            Score 297; DB 1;
Pred. No. 5.5e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CN2591;
MEDLINE=91251771; PubMed=2041476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rik; S14659; S14659.
InterPro; IPR004899; Pertact_sup.
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0
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01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                     ..
Έ
                                                                                                              100.0%;
1larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03212; Pertactin; 1.
                                                                                   93995
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647
922
262
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                                                                                  911 AA;
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONCENTRATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=519;
                                                                                                                  Local S...
52;
                                                                                                                                                                                                                                                                      PERT_BORPA
P24328;
                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella.
                                                                    DOMAIN
SEQUENCE
                                                                                                               Query Match
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PROPEP
SITE
SITE
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                                        REPEAT
                                                        REPEAT
                            REPEAT
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                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordecella pertussis.",
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I - FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
                                                                                                                                                                                                                                                        621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                             X 3 AA APPROXIMATE REPEATS OF P-Q-P 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                           25
                LINES).
1 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPGPGPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGKELSAA
                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                            Length 922;
                                                                                                                                           Score 284; DB 1; Length 92.
Pred. No. 3.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin precursor (Outer membrane protein P.69) (P.93). PRN OR OMP69A.
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                               4 (APPROXIMATE)
9 X 3 AA APPROX
                                                                                                                                                                                                                                                                                                                                         910 AA.
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89264462; PubMed=2542937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 264 AND 332.
MEDLINE-92407514; Pubmed-1527510;
                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                             95178 MW;
                                                                                                                                                            95.68;
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                               290
275
275
280
285
603
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                                                                                                                             922 AA;
                                                                                                                                                                              Similarity
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                               266
266
271
271
281
575
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                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994
                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                       PERT_BORPE
P14283;
                                                                                                                               SEQUENCE
                                                                                                                                                             Query Match
                                                                                                                                                                              Local
                               DOMAIN
REPEAT
                                                                                                              DOMAIN
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                                                                                                                                                                                            Matches
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SELLETERS
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Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3067;
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                             X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                 CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                           (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                71.4%; Score 212; DB 1; Length 910; 78.8%; Pred. No. 7.4e-07; 1ve 0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQRPQPEAPAPQPPAGRELSAA
                                                                                             PERTACTIN (P.69).
                                                                                                                                                                                 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                         449 AA.
                                                                  membrane; Signal; Virulence; Repeat.
                                                                                                        POTENTIAL
       InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001087; Lipase_GDSL
                                             PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                             93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                    41; Conservative
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           Brassica napus (Rape).
                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                             910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              CBI_TaxID-3708;
                                                                                                                                                                                                                                                                                                                                         APG_BRANA
P40603;
                                                                                                                                                                                                                                                                                                                                                                                                   OR CEX
                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                                                Query Match
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APG_BRANA
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J. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. 109:3493-3501(1989).
I. Cell Biol. The Extracellular matrix (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOWERIC PRECURSOR OF THIS SUBSTITUTE (C3Z STRUCTURE). THE CONALENT (CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
I. PIM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                       3 KAPPAPKIYAPQPGPQPGPQPPQPPQ-------PPQPPQRQPE---APAPQPPA 45
                                                                                                                                                                                                                                                                                                             7 КРРРКРОРКРОРАРТРЯРСРРОРКРОРКРРАРТРЯРСРРОРКРОРКРОРАРДЯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-f. Nagariensis / HK10;
MEDILTE-9004551; PubMed-2689458;
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carter1: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                             Length 449;
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                                                                                                                                                                                          Indels
                                                            9EFB6A3AB28EEA15 CRC64;
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                                                                                                                      47.3%; Score 140.5; DB 1;
44.3%; Pred. No. 0.0091;
11ve 4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PPAPKPARQPGPQPGPQPPQPPQPPQRQPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 1851e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 AA.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=f. Nagariensis / HK10;
                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfation; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO
                                                         449 AA; 48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X51616; CAA35953.1; -. PIR; A33647; A33647.
                                                                                                                                                        Local Similarity 44.3%; tes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.00
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 AA;
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Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                  45.5%;
                                                                                                                                                                                                                                                                                            23; Conservative
                                                                                                                                                                                                                                         141 AA;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Owenia fusiformis.
                                     NCBI_TaxID-6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
                                                                                                                                                                                                DOMAIN
DNA_BIND
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                              MEDITINE-84270667; PubMed-6087149;
MEDITINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glisson T.J., Harfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.,
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                             Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
Jurol. 65.2545.2554(1991).
-i- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                    MEDLINE-90266473; Pibmed-2161150;
Petti L., Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01618; -.
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 356 6 X 2 AA TANDEM REPEATS OF R-G, 487 AA; 52544 MW; DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%; Score 136; DB 1; Length 487;
llarity 53.5%; Pred. No. 0.018;
Conservative 0; Mismatches 20; Indels
                                                                                                                   Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PPLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPQR 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proline-rich protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 AA
                          487 AA
                                                                                                                                                                                                                                                                                 [2]
SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V01555; CAA24877.1; ALT_INIT.
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPRO_OWEFU STANDARD; PR P21260; P21261; OI-MAY-1991 (Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last seque) 01-NOV-1995 (Rel. 32, Last annot: Hypothetical proline-rich protein
                                                                                                                                                                                                                                                                   Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- PTM: PHOSPHORYLATED.
                          STANDARD;
                                                                                           EBNA-2 nuclear protein.
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF LMP-1
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Local Si.
23;
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Matches
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             EBN2_EBV
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BUTTE

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APG_ARATH
APG_ARATH
STANDALL,
APG_ARATH
ACTION APG_STAIL4; GOLUNG;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-70N-2002 (Rel. 41, Last sequence update)
DT 15-70N-2002 (Rel. 41, Last annotation update)
DT 15-70N-2002 (Rel. 41, Last annotation update)
DF ARTON APG OR ATGOLOGO NEAL AND APG APG OR ATGOLOGO NEAL AND APG APG OR ATGOLOGO NEAL APG APG OR ATGOLOGO STANDAL AND APG APG OR ATGOLOGO STANDAL APG APG OR APG
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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Bull J.E., Chan L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A. Chung W.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
A. Chung W.K., Coll J., Haas B., Hansen N.F., Hughes B., Fujii C.Y.,
A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
A. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
A. Lin X., Liu S.X., Lie A., Lee J.M., Lenz C.A., Lii J.H., Li Y.-P.,
A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A. Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
A. H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
A. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
B. Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                          MEDILINE=90147742; PubMed=2105723;
MEDILINE=90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Biochem. Biochem. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94004980; PubMed-8401599; Sobberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; "Gametophytic and sporophytic expression of an anther-specific
Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
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H-T-H MOTIF (POTENTIAL).
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Pred. No. 0.0084;
0; Mismatches 2
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MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; DNA-binding.
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FUNCTION: TEGUMENT PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                        CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                            STRAIN—cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
*RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the Storosortium (Salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-! TISSUE SPECIFICITY: FOUND IN SPOROHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-88274327; Pubmed-2839594;

MEDGOCH D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,

MCNab D., Perry L.J., Scott J.E., Taylor P.;

"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                           MATURATION.
SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
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4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KAPPAPKPAPQPGPQPGPQP---PQPPQPPQPPQRQPE-APAPQP-PA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S -> P (IN REF. 1)
E -> A (IN REF. 1)
E -> H (IN REF. 1)
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01-WAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                          gene model prediction.
Nature 408:816-820(2000).
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                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10299;
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ACT_SITE
CONFLICT
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyla pseudotsugata baculovirus DNA
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24; EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              083949; Q65364; O10323; O100323; Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hyporhetical, 98.6 kba protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; d5DNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1300; PubMed=9126251;
Russell R.R., Funk C.J., Evans J., Harwood S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIrology 210;372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 X 2 AA TANDEM REPEATS OF W; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPKPAPOPGPOPGPOP-POP-POP-POP-POROPEAPAPOPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129.5; DB
Pred. No. 0.17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          875 AA
                                                                                                                                                                                                                                                                                                                                                                        PIR; 130085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; Pubmed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2911 2980 35
3164 AA; 335857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.68;
                                                                                                                                                                                                                                                                                                                                           EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97271300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ahrens C.H., Ru
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudosugata!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOG6_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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DOMAIN
                                     DOMAIN
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                                                                                                                                                                                                                                                                                                         ACRO_RABIT
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                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chagarit R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelana F., Volinia S., Watnore A. E., Housman D. E.; "The translocation t(8;16)(p11;p13) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Mat. Genet. 14:33-41(1996).

-I. FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i-SUBCELLULAR LOCATION: Nuclear.
-i-DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL
TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE WRELOID LEUKEMIA.
-i-SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
-i-SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translocation; Zinc-finger; Repeat;
                                                                                                                                                    5 PPAPKPA-----PQPGPQPGPQPPQPPQPP----QPPQRQPEAPAP--QPP 44
                                                                                                      Score 128; DB 1; Length 875;
Pred. No. 0.084;
3; Mismatches 10; Indels
                                                                     86 91 POLY-PRO.
875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                   2004 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SWART; SW00245; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_1; 1.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96376968; PubMed-8782817;
                                                                                                                                                                                                                                                          (Rel. 36, Created)
         EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; IFOS.
                                                                                                      43.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U47742; AAC50662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roto-oncogene; Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:13013; ZNF220.
                                                                                                                               27; Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
313
379
                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          .5-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601408
                                                                                                                                                                                                                                   MOZ_HUMAN
092794:
                                                                               SEQUENCE
                                                                                                                               Matches
                                                                                                                                                                                                                      MOZ_HUMAN
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SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Mew Zealand white; TISSUE-Testis;
STRAIN-Mew Zealand white; TISSUE-Testis;
MEDLINE-9436861; Pubmed-8086468;
Richardson R.T., O'Rand MG;
Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin related cDNA.";
Proproacrosin related cDNA.";
Plochim. Biophys. Acta 1219:215-218(1994).
IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY.
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                                                                                                                                                                                                                                                                    GLN/PRO-RICH.
MET-RICH.
BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                       9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PPAPKP----APQPGPQPGPQPPQP-PQPPQPQRQPEAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFIDE BONDS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.5; DE
Pred. No. 0.16;
1; Mismatches
                                                                                                                                   GLU-RICH.
GLU-RICH.
                                                                                                    POLY-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                 POLY-GLU
                                                                                                                                                                                                     POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00089; trypsin, 1.
PRINTS, PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    2004 AA; 225054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
995
1026
1078
1150
1150
1302
1414
1597
1704
                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACRO_RABIT
P48038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACROSOME
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DEVELOPMENTAL STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL PRELIMINARY SEQUENCE FROM N.A. MEDLINE-91017504; PubMed-1699225; Adair W.S., Apt K.E.; "Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-i- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                               Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
1 16 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
(BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                         SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21159092; PubMed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSFECTION (NO.0027; Created)
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AKAPPAPKPAPQPGPQ-----PGPQPPQPPQPPQPPQRDPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 125.5; DB 1; Leus-
Pred. No. 0.071;
Traffhes 20; Indels
                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY STEARGE RELAY SYSTEM (BY STEARGE RELAY SYSTEM (BY STEARGE CHARGE RELAY SYSTEM (BY STEARGE)
                                                                                                         (BY
                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .
N-LINKED (GLCNAC. . .
                                                                                                      ACROSIN LIGHT CHAIN ACROSIN HEAVY CHAIN PRO-RICH.
                                                                                                                                                                     SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: Associates with GP2 and GP3.
-1- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                               SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
      TRYPSIN_HIS; 1.
TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                     288
152
160
87
87
                                                                                                                                                                                                                                                                       223
264
                                                                                                                                               431
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                                                                                                                                                                                                                                                                                                                                                                                                               431 AA;
PROSITE; PS00134;
PROSITE; PS00135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3055;
                                             Hydrolase;
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ACT_SITE
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DISULFID
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CARBOHYD
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The homeo domain of a murine protein binds 5' to its own homeo box."; roc. Natl. Acad. Sci. U.S.A. 83:9532-9536(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 185-258 FROM N.A.
MEDLINE-85024859; PubMed-6091896;
McGinnis W., Hart C.P., Gehring W.J., Ruddle F.H.;
Molecular cloning and chromosome mapping of a mouse DNA sequence homologous to homeotic genes of Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                              VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
6A584A90465502F5 CRC64;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87092283; PubMed-2879282;
Fainsod A., Bogarad L.D., Ruusala T., Lubin M., Crothers D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruddle F.H., Hart C.P., McGinnis W.; "Structural and functional aspects of the mammalian homeo-box
                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 555
                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c;
Hofmann M., Boehm T.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 APPAPKPAPQPGPQPPGPQPPQP----PQPPQRQPEAPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                  Score 125; DB 1.
Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P02831; Q61197;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
HOXA3 OR HOXA-3 (HOX-1.5) (MO-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 AA
                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                      POLY-PRO.
                                          InterPro: IPR002965; P_rich_extensn.
InterPro: IPR003802; Pistil_extensin.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
Glycoprotein; Repeat; Signal.
EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSulteDB; Q9FPQ6; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ICR Swiss;
MEDLINE=96323206; PubMed=8710855;
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                                                                                                                                                                                                                                                                                                                                                                                  42.18;
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                                                                                                                                                                                                                                                                                                         493
555 AA;
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es 25; Conserv
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CARBOHYD
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                            - I- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC FOSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

SPECIFIC FOSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

I- SUBCELLULAR LOCATION: Nuclear

- ENVELOPMENTAL STREESE EXPRESSED IN A SPATIALLY RESTRICTED MANNER IN EMBRYOS 8.5 DAYS P.C., EXPRESSION IS LIMITED TO THE CNS WITH AN ANTERLOR BOUNDARY IN THE HINDBRAIN AND EXTENDING POSTERIORLY THROUGH CANDAL REGIONS OF THE SPINAL CORD. THE SAME SPATIAL EXPRESSION IS SEEN IN EMBRYOS 9.5 TO 12.5 DAYS P.C., SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50073; ANTENNAPEDIA; 1.
HOMEOBOX; UNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
PROPING PROFICE.

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PROFICE.
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A -> G (IN REF. 3 AND 4).
SA -> RP (IN REF. 3 AND 4).
C -> M (IN REF. 3 AND 4).
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               Fainsod A., Awgulewitsch A., Ruddle F.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6C0E184B0F6F2D40 CRC64;
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ANTP-TYPE HEXAPEPTIDE.
HOMEOBOX.
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InterPro; IPR001356; Homeobox.
MEDLINE-88030407; PubMed-2444477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 34, Created)
(Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46429 MW;
                                                  embryogenesis.";
Dev. Biol. 124:125-133(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y11717; CAA72404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U56399; AAC52778.1; -. EMBL; K02591; AAA37822.1; -. PIR; A03315; A03315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AA;
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15-DEC-1998
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HD_RAT
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                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE-94100980; PubMed=8275091;
MEDLINE-94100980; PubMed=8275091;
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K.,
Swarcop M., Kaatz K.W., Collins F.S., Albin R.L.;
"Widespread expression of the human and rat Huntington's disease gene in brain and nonneural tissues.";
Nat. Genet. 5:259-265(1993).
-!- FUNCTION: MAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR VESICLE FUNCTION.
                     Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hash Hamelster H., Epplen J.T., Aless O., "Expression of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
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POLY-GLU.
MW; 33C357E8FC141550 CRC64;
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Pred. No. 0.45;
1; Mismatches
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POLY-PRO.
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Job time : 6.0494 secs
                                                                                                                                   Hum. Mol. Genet. 4:1173-1182(1995)
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MEDLINE-96133292; PubMed-8528205;
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Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
                                                                                                                                                                                SEQUENCE OF 1773-1926 FROM N.A.
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Hes 28; Conserv
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OM protein - protein search, using sw model

May 7, 2003, 16:38:52 ; Search time 26.5758 Seconds (without alignments) 403.166 Million cell updates/sec Run on:

US-09-855-754B-15 297

Title: Perfect score: Sequence:

1 GAKAPPAPKPAPQPGPGPGP......QRQPEAPAPQPPAGRELSAA 52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_archea:* sp_bacteria:* sp_fungi:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

		æ				
Result No.	Score	Query Match	Juery Match Length DB	DB	OI	Description
1	297	100.0	107	. 7	Q9K5H5	09k5h5 bordetella
7	297	100.0	200	7	O9ALP9	
m	297	100.0	911	~	09L4E2 .	
4	286.5		109	7	Q9K5H1	_
2	286.5		215	~	O9ALO4	_
9	285		111	7	Q9K5G9	
7	285	96.0	122	~	Q9KJX9	09kjx9 bordetella
80	285		252	7	Q9ALQ2	09alq2 bordetella
6	284		111	~	Q9K5G7	
10	283		115	~	Q9K5H3	
11	266.5	89.7	104	~	09к5н9	_
12	266.5	89.7	105	7	Q9K5H7	09k5h7 bordetella
13	266.5	89.7	115	7	Q9KJY1	_
14	266.5	89.7	115	7	Q9KJY0	_
15	266.5	89.7	198	~	ованью	Ogahpo bordetella
16	260	87.5	105	7	O9K5G5	O9k5a5 bordetella

Q9k5g4 bordetella	Q9k5g1 bordetella	Q9alp3 bordetella		-	_		_		Q9s6n0 bordetella		O69259 bordetella		_	_	Q8rsu0 bordetella	Q9uvdl pneumocysti	_	09p944 pneumocyst1	Q96vi4 pneumocyst1		ᇨ	P93797 volvox cart		091le9 rattus norv	OStly6 dictyostel1	069023 human herbe	O13305 pneumocysti	Q9rcx9 streptomyce
Q9K5G4	Q9K5G1	Q9ALP3	Q9ALP7	Q9ALQ0	Q9ALP5	Q9AIX8	6M9S60	Q9S3M8	08980	Q9S6N1	069259	088143	Q93L98	069257	Q8RSU0	Q90VD1	001823	Q9P944	096VI4	Q93L97	Q9ULL5		Q8S7Y7		Q8T1Y6	069023	013305	Q9RCX9
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87.2	86.9	84.8	83.3	78.8	76.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	64.5	64.5	51.7	51.0	7	18	48.3	8.0	47.5	47.5	9.9	46.5	46.5	46.3	46.1
259	258	252	247.5	234	227	212,	212	212	212	212	212	212	212	191.5	191.5	153.5	151.5	146	74	143.5	142.5	14	141	138.5	138	138	137.5	m
17	18	13	20	21	22	23	24	52	56	27	. 28	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

1ca	Gaps
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ence update) tation update) s bronchisepticus). ision; Alcaligenaceae; laion; Alcaligenaceae; and Bordetella bronchiseptica.";	Length 107; Indels
Created) Last sequence update) Last sequence update) Last annotation update) Last sequence updat	DB 2; 4e-18; 0;
107 AA) quence up notation nes bronc ivision; f Pertact , and Bor	ore 297; ed. No. 1. Mismatches
Created) Last sections and sections of sections of sections of sections of sections of sections.	Score Pred.
PRELIMINARY; (TIEMBLEI 15, C1 (TIEMBLEI 11, L2 (TIEMBLEI 21, L2 P.68) (Fragment). bronchiseptica (Alc roteobacteria; better 518; com N.A. (Com N.A. (Com N.A. (Com Separed Registration) (Com Separed Registrat	100.0%; 100.0%; ative 0
(Trembline) (Tremb	100 sal Similarity 100 452; Conservative
9K5H5; 1-OCT-2000 1-OCT-2000 1-OCT-2000 1-OCT-2000 1-OCT-2000 1-OCT-2000 ertactin (RN. Ordetella acteria; FOLT-INC COLT-INC EDILNE-203 OURSIAN POLYMOLPHI MEDI, AJ256 MEDI, AJ256 NEPPO; InterPro;	Query Match Best Local Similarity Matches 52; Conserv
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Gaps

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Q9ALP9

RESULT 2

29ALP9

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Boursaux Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertuasis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4817(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 74,
                                                          DB 2; Length 109;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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EMBL, AX007263; AAG38439.1; InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR004895; Pertactin.
InterPro; IPR004895; Pertactin.
InterPro; IPR004895; Pertactin. 1.
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0; Indels
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109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                               09K5H1,
01-0CT-2000 (TrEMBLrel. 15, Created)
10-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Pred. No. 1.1e-17;
0; Mismatches 0;
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  Mismatches
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MEDLINE=20359389; PubMed=10899896;
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PRINTS; PR01217; PRICHEXTENSN.
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98.1%;
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    Conservative
                                                                                                                                                                                  PRELIMINARY;
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les 52; Conserv
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SEQUENCE
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EMBL: AJZ45927; CABB2515.1; ...
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertactin.vir.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).

EMBL; AY007271; AAG3847.1;
Interpro; IPR00399; pertactin.
Interpro; IPR004899; Pertactin.
Interpro; IPR002965; P_rich_extensn.
PRIMTS; PR01482; PERTACTIN.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01482; PERTACTIN.
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20826 MW; 9F3AC6E4128942E6 CRC64;
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Last annotation update)
                                                                                                      (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
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100.0%; Score 297; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 52; Conservative 0; Mismatches 0;
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Pred. No. 8.2e-18;
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                                                  PRT;
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MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
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200 AA;
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Best Local Similarity
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01-JUN-2002
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Pertactin.

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RESULT 3

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SEQUENCE

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InterPro; IPR002965; P_rich_extensn.
           Pfam; PF03212; Pertactin; 1. PRINTS; PR01217; PRICHEXTENSN.
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Q9K5G7
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250087; CAB76441.1; InterPro; IPR004899; Pertact_sup.
InterPro; IPR00265; P_rich_extensn.
Pr03212; Pertactin; 1.
                                                     Gaps
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Keil D.J., Fenwick B.;
Variability in the pertactin genes of Bordetella bronchiseptica
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR156773; ARR82397.1; -.
InterPro; IPR004899; Pertact_sup.
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                                                                                   140 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPGRELSAA 192
                                                                       1 GAKAPPAPKPAPQPGPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 52
                               DB 2; Length 215;
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                    Indels
 215
22327 MW; 5C21D45CF784B4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA; 11416 MW; 5140669692808F8E CRC64;
                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                              Query Match 96.5%; Score 286.5; DB 2; Best Local Similarity 98.1%; Pred. No. 1.9e-17; Matches 52; Conservative 0; Mismatches 0;
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MEDLINE=20359389; PubMed=10899896;
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NON_TER 11 11 11 SEQUENCE 111 AA; 11416 MW;
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 215 2
215 AA;
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NON_TER
SEQUENCE
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Q9KJX9;
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                                                                                                                                                                                    42 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 97
                                                                                                   . 4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordet ella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
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                                                       Length 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 252
252 AA; 26107 MW; 368C142508D77057 CRC64;
122 AA; 12395 MW; RED00966A40FF994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              01-007-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P 68) (Fragment).
                                                    Query Match 96.0%; Score 285; DB 2; L
Best Local Similarity 92.9%; Pred. No. 1.6e-17;
Matches ; 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.0%; Score 285; DB 2; Best Local Similarity 92.9%; Pred. No. 3e-17; Matches 52; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                  252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bronchiseptica Pertactio.";
Infect. Immul. 69:1917-1921(2001).
EMBL; AXO0765; AXG38441.1;
Interpro; IPR003992; pertactin.
Interpro; IPR004899; pertact.
Interpro; IPR004899; Pertact.
Pfam; PP03212; PertactLin.
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                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin (Fragment).
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Length 104;

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pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJJS50077; CAB76431.1; --
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20359389; PubMed=10899896;

Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250079; CAB76433.1; -.

InterPro; IPR004899; Pertact_sup.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 52
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0170N-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
                                                                                                                                                                                                                                                                                                                  104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.7%; Score 266.5; DB 2
94.2%; Pred. No. 5.2e-16;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                         Score 266.5; DB 2
Pred. No. 5.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 AA
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                            Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                      MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                         89.78;
94.28;
                                                                                                                                                                                                                                                Pfam; PF03212; Pertactin; 1.

NON_TER 104 104

SEQUENCE 104 AA; 10714 MW
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                                                                                                                                                                                                                                                                                                                                                                                                   49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                   NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=518;
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  Bordetella
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NON_TER
SEQUENCE
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Q9KJY1
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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09K5H7
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertusis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4015.4017(2000).
EMBL: AJ550089; CAB76443.1; InterPro; IRR004899; Pertact_sup.
InterPro; IPR004899; Pertact_sup.
Pfam: PF031212; Pertactin; 1.
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                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                     8;
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                                                                                                                                                                                                                                                                                          Score 284; DB 2; Length 111;
Pred. No. 1.8e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.3%; Score 283; DB 2; Length 115;
86.7%; Pred. No. 2.3e-17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                     111 AA; 11453 MW; 9B67012D3B9AEECA CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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MEDLINE-20359389; PubMed-10899896;
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                                                                                                                                                                                     PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                            95.6%;
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Best Local Similarity
Matches 52; Conserv
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Matches
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Register K.B.;
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Keil D.J., Fenwick B.;
Variabhlithy in the pertactin genes of Bordetella bronchiseptica
"Variabhlithy in the pertactin genes of Bordetella bronchiseptica
amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF155772; AFR82396.1;
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
NON_TER
                                                         Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                           89.7%; Score 266.5; DB 2; Length 115; 94.2%; Pred. No. 5.6e-16; 1ive 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 266.5; DB 2; Length 115;
Pred. No. 5.6e-16;
0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                         42 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQPPQRPAPAPQPPAGRELSAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPQPGRAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                       Submitted (JÜN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF156771; AAF82395.1; -.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                     115 AA; 11693 MW; FA3A76596F7097EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Q9KJY0;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Pertactin (Fragment).
                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                      llarity 94.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 89.7%;
Local Similarity 94.2%;
Nes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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mes 49; Conserv
                                 SEQUENCE FROM N.A.
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           WCBI_TaxID=518;
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09AHP0;
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Matches
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Matches
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                       "Novel Genetic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20575 MW; AC940EC331A725AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.7%; Score 266.5; DB 2; 94.2%; Pred. No. 8.7e-16; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                      EMBL: AF298590; ARK16691.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004999; Pertact_sup.
InterPro; IPR004999; Pertact_sup.
Pfan: PF03212; Pertactin; 1.
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                                                                                                                                                            MEDLINE-21117018; PubMed-11179374;
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PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 198 198
SEQUENCE 198 AA; 20575 MW;
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Matches 49; Conservative
                                                                                                                SEQUENCE FROM N.A.
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Job time: 27.5758 secs
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B. bronchiseptica

B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica Bordetella pertuss Bordetella pertuss

AAE16183 AAE16201 AAE16200 AAE16199 AAE16199 AAE16199 AAE16194 AAE16184 AAE16184

Novel human diagno Novel human diagno Drosophila melanog Peptide 683 derive Novel human diagno Human polypeptide

AAR11737 ABG27250 AAO02124 ABG21919 AAR28150 AAR11739

Novel human diagno Sugar beet chitina Peptide BBOS deriv Streptococcus pneu Streptococcus pneu Herbicidally activ

AAW14573 AAW14569 ABB93838

AAW14570 AAW14574 ABB78538 AAE14305

AAC22949 AAP82971

AAW37148

Streptococcus pneu Streptococcus pneu Ser-Pro-Pro-Pro-Pr

Sugarcane proline Drosophila melanog

Arabidopsis thalia

Bioadhesive precur Mammallan Ena (Men

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                       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:

26-MAR-2002 AAE16195;

B. bronchiseptica strain II-3 pertactin outer membrane protein region II.

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

(INSP) INST PASTEUR

Suiso-maclouf N, Boursaux-eude C;

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

B. bronchiseptica Description AAR25578 AAE16185 AAR16197 AAR14321 AAE16196 AAE16194 AAR14320 AAE16195 AAE16198

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AAE16195 standard; peptide; 60 RESULT 1

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(first entry)

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DB

Length

Query Match 1

Score

Result Š

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

25-MAY-2000; 2000US-206969P

WPI; 2002-097639/13.

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in builtying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AA;
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96.9%; Score 331.5; DB 2
98.3%; Pred. No. 1.6e-17;
11ve 0; Mismatches 0
                               59; Conservative
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Best Local Similarity
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- 1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59 à 셤

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AAE16198 standard; peptide; 58 AAE16198; RESULT 2

26-MAR-2002 (first entry)

B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica,

WO200190143-A2.

29-NOV-2001.

91WO-GB02302 90GB-0027901

23-DEC-1991; 21-DEC-1990;

WO9211292-A.

(WELL) WELLCOME FOUND LID.

Charles IG;

WPI; 1992-250033/30. N-PSDB; AAQ26509.

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

forPolypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fulds, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Bordetella in a material. The present sequence is B. bronchiseptica
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te= "contains 9 direct repeats of Pro-Gln-Pro"
                                                                                                                                                                                                                                                                                                       /note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                  260..262
/note= "motif associated with cell-cell adhesion"
                                                                                                                                                                                          Whooping cough; P70 antigen; P95 precursor protein; vaccination.
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re- "contains 5 direct, tandem repeats"
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                                     Score 298.5; DB 2
Pred. No. 3.6e-15;
0; Mismatches 0
       pertactin outer membrane protein region II.
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Matches 57; Conservative
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comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen Acellular vaccine for immunisation against whooping cough -

Claim 1; Fig 1; 20pp; English.

recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the bamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (#P95) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kb. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino A cosmid library was constructed by transforming E.coli HB101 with

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1 САКАРРАЗКРАРОРСРОРСРОРСРОРСРОРСРОРОРОРОРОРОВ-РЕАРАРОРАСКЕТSAA 59
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                              RESULT 5
                                                                                         AAE16197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR14321
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                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 4jycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                     Gaps
                                                                                                                                                                                                                                Bordetella parapertussis pertactin outer membrane protein, p.70.
                                                                 .;
;
                                             Length 922;
                                                                 Indels
                                            DB 13;
                                           Score 298.5; DB 13;
Pred. No. 2.6e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
254..304
/note= "Pertactin region I"
554..63.
/note= "Pertactin region II"
acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                   ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                AAE16185 standard; Protein; 922
                                           87.3%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                      Ouery Match
Best Local Similarity 95.0
Matches 57; Conservative
                                                                                                                                                                                                                                                                                       Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                      922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD26442
                                                                                                                                                                                                                                                                                                                                                                             WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2001
                       Sequence
                                                                                                                                                                                      AAE16185;
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                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                      AAE16185
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SXC
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The present invention relates to Bordetella bronchiseptica pertactin (outer, membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of &b in those meterials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                 B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                               Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294.5; DB 23;
Pred. No. 6.7e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ż
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AAE16197 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  W0200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2001
                                                                     AAE16197;
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Score 298.5; DB 23; Length 922; Pred. No. 2.6e-14;

87.3%; 95.0%;

Query Match Best Local Similarity

outer membrane protein; vaccine; Bordetella infection;

(first entry)

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B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin
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                                                                                                                                                                                                  therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                Suiso-maclouf N, Boursaux-eude C;
                                                        AAE16196 standard; peptide; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                        23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                 Pertactin; PRN;
                                                                                                                                                                                                                                                            WO200190143-A2.
                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                          29-NOV-2001
                                                                                       AAE16196;
                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptice P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 283.5; DB 12; Length 922;
Pred. No. 3.1e-13;
0; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                                                          Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     595.597
                                                                                                                                                                                                      281..285
/label= ren
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/label= repeat
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Best Local Similarity 91.7%;
Matches 55; Conservative
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20-JAN-1992 (first entry)
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/label= re
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'label= re
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/label= re
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/label= re
                                                                                                                                                                                                   76..280
7abel= re
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                                                                                                                                       266..270
/label- r
                                                                                            parapertussis.
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                              Pertactin antigen P.70
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                                                                                          Bordetella
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                                                                                                                          Key
Peptide
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Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 53;
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80.1%; Score 274; DB 23;
Best Local Similarity 86.7%; Pred. No. 1.9e-13;
Matches 52; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA;
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3;

Gaps

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prn proteins.
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                                                                                                                                           WO9115571-A
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                                                                                               Peptide
                                                                      Peptide
                Peptide
                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 78.2%; Score 267.5; DB 23; Length Similarity 85.0%; Pred. No. 5.5e-13; 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; Pichia; B. pertussis; B. parapertussis.
therapy; antibiotic; antibacterial; region II.
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266..270
/label- repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR14320 standard; Protein; 911 AA
                                                                                                                                                                                                  Boursaux-eude C;
                                                                                                                                                                                                                                                                                                              Claim 26; Fig 1c; 47pp; English.
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574..576
/label repeat
578..580
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/label= repeat
                                                                                                             23-MAY-2001; 2001WO-EP06457.
                                                                                                                                        25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica.
                          Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin antigen P.68.
                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                            WPI; 2002-097639/13.
                                                                                                                                                                                                 Suiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA;
                                                    WO200190143-A2
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                                                                                29-NOV-2001
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Pichia microorganisms are transformed for the expression of pertactin anitigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively, or the B. pertussis P.59 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%; Score 267.5; DB 12; Length 911; 85.0%; Pred. No. 4.3e-12; 1ve 0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260..262
/label= RGD_tripeptide
701..703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266..279
/label= Repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570..589
/label= Repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR26503 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1B; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          (WELL ) WELLCOME FOUNDATION LTD.
581..583
/label= repeat
584..586
/label= repeat
                                                                                         587..589
/label= repeat
599..601
/label= repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35..632 · /label= P.68
                                                                                                                                                                                                                                                                                                                91WO-GB00487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 85.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetalla bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-325214/44.
N-PSDB; AAQ14319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          911 AA;
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The present invention relates to Bordetella bronchiseptica pertactin (cuter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin natibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, alycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as bloogical and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.2%; Score 267.5; DB 2
85.0%; Pred. No. 4.3e-12;
iive 0; Mismatches 0
                                                                                                                                                                                                                       Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boursaux-eude C;
Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE16201 standard; peptide; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N,
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE16201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rininitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 267.5; DB 13; Length 911;
Pred. No. 4.3e-12;
0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
/label- RGD_tripeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.2%;
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                                                                                                                                             92WO-GB00561
                                                                                                                                                                                             91GB-0006568
                                                                                                                                                                                                                                        (WELL ) WELLCOME FOUND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entire P.94 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                         WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200190143-A2
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                                                                                                                                                                                             27-MAR-1991;
                                                                                                                                                27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                WO9217587-A
                                                                                             15-0CT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2001
                                                                                                                                                                                                                                                                                              Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16183;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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Gaps

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ä;
vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodgical and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPPQPPQP-PQPPQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                   Score 249.5; DB 23; Length
Pred. No. 1.1e-11;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                   ch 73.0%;
1 Similarity 81.7%;
49; Conservative
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                             54 AA;
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                           Matches
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 B. bronchiseptica strain II-1 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II. Ą AAE16193 standard; peptide; 49 23-MAY-2001; 2001WO-EP06457 (first entry) Bordetella bronchiseptica WO200190143-A2 26-MAR-2002 29-NOV-2001 AAE16193; **AAE16193** RESULT

Guiso-maclouf N, Boursaux-eude C; 25-MAY-2000; 2000US-206969P (INSP) INST PASTEUR WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antipens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. The present invention relates to Bordetella bronchiseptica pertactin

49 AA; Sequence

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AAE16199 standard; peptide; 48

RESULT 15

AAE16199 ID AAE1

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    B. bronchiseptica strain II-θ pertactin outer membrane protein region II.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens can be used for qualitative or quantitative determination of Bordefella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                              1 GAKAPPARKPARQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Length 52;
     Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 242.5; DB 23;
Pred. No. 3.4e-11;
1; Mismatches 3;
 Score 247; DB 23;
Pred. No. 1.6e-11;
0; Mismatches 0
                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                               AAE16200 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%;
Llarity 81.4%;
Conservative
                                                                                   72.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica.
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP |) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-097639/13.
Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                  WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2001
                                                                                                                                                                                                                  AAE16200;
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                                                                                                                                                    RESULT 14
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Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the artigens can be used for qualitative or quantitative or quantitative or quantitative of pertactin outer membrane protein region II.
                                                                                B. bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                     23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                       25-MAY-2000; 2000US-206969P
                                                26-MAR-2002 (first entry)
                                                                                                                                                                   Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-097639/13.
                                                                                                                                                                                                 WO200190143-A2
                                                                                                                                                                                                                                     29-NOV-2001.
              AAE16199;
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pertactin

Bordetella bronchiseptica

Score 240.5; DB 23; Length 48; Pred. No. 4.5e-11; 0; Mismatches 0; Indels 13; Gaps 70.3%; 78.3%; Ouery Match 70.35
Best Local Similarity 78.35
Matches 47; Conservative

48 AA;

Sequence

5

1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQRPQR-PEAPAPQPPAGRELSAA 59

ò a Search completed: May 7, 2003, 16:47:06 Job time : 31.6559 secs

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RESULT 1
US-08-460-269C-6
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Sequence 12,
Sequence 12,
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                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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S-07-609-716-65
S-08-478-0294-65
S-08-961-083-160
S-09-314-268-134
S-08-642-255-33
S-08-475-411A-66
S-08-475-411A-66
S-08-475-418-66
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S-202236-3
US-09-109-841-2
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US-08-961-083-16
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US-08-961-083-16
US-08-961-083-16
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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seq length: 200000000
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Sequence 73, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 31, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 16, A
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MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: LIBM PC COMPATIBLE
COMPUTER: DEALER : PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORREY/AGGNT INFORMATION:
NAME: LEDOVITZ, Richard M.
REGISTRATION NUMBER: 37,067
REEFERNEC/POCKET NUMBER: 37,067
REEFERNEC/POCKET NUMBER: 37,067
REEFERNEC/FOCKET NUMBER: ORDOV-2
TELEFPACE (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
LENGTH: 922 amino acids
LENGTH: 922 amino acids
"NPDE: Ami
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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US-09-535-008-77
US-09-041-886-28
US-09-041-886-29
US-09-041-886-31
US-09-041-886-31
US-08-246-982A-6
US-08-457-255-6
US-08-457-275-6
US-08-556-419-21
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Pred. No. 2e-18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-041-886-15
-08-750-624-11
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.3%;
Best Local Similarity 95.0%;
Matches 57; Conservative
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         1679
1681
1681
1682
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3144
31444
31444
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3119
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APPLICATION NUMBER: US/08/460,269C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY 1990
                                                                                                                                 TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     LENGTH: 910 amino acids
                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                                                                       59.5%;
69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.55
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUSAN L.; MCCANDLISS, RUSS; WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5202236-3; Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 334.
5202236-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARL INFORMATION: CIARE, JEFFREY J.
ROWANOS, MICHAEL A.
ROWANOS, EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.2%; Score 267.5; DB 4; Length 911;
85.0%; Pred. No. 8.2e-16;
1.ve 0; Mismatches 0; Indels 9
                                                                                                                         ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                       Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37, 067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Ze
STREET: 2200 Clarendon Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                           Sequence 4, Application US/08460269C Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 911 amino acids TYPE: amino acid
                                                                                                      APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                                                                                                 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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4 APPAP------KPA-PQPGPQ--PGPQPGPQPGPQPPQPPQPPQRPEAPAPQPP 51
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                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                          Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, N E.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TILLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                        Score 203.5; DB 4;
Pred. No. 2.1e-10;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 140.5; DB 6
Pred. No. 1.9e-05;
0; Mismatches 19
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                         ) MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
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Gaps

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NAME: Wilson, Mary J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-237-716-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                   4 APPAP------KPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                11;
                                                                                                          Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1274;
                                                                                                      Score 138.5; DB 6; Length 3 Pred. No. 2.8e-05; 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAP----GPQPRPAPQPGPQPGPQPGPQP----GPQPPQ--
                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09095443

Patent No. 6342593

GENERAL INFORMATION

APPLICANT: Plowman, Gregory

APPLICANT: Peles, Eior

TITLE OF INVENTION: DFAGNOSIS AND TREATMENT

TITLE OF INVENTION: OF ALP RELATED DISORDERS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 613 West Fifth Street

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 136; DB 4;
Pred. No. 0.00014;
1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.6" Actoratiole COMPUTER: IBM COMPACTION WINDER: US/09/095,443 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/049,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J. REGISSTRAITON UNMBER: 32,327 REFERENCE/DOCKET UNMBER: 32,327 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-1510
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                          illarity 44.18;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 43.6%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FILING DATE: 13-SEP-1984
;SEQ ID NO.37:
; LENGTH: 331
5202236-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 QPP--QPPQRPEAPAPQP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-095-443-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Los Angeles
: California
                                                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                               RESULT 6
US-09-095-443-2
                                                                                                                                                                                                                       셤
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATE: Delabs/MS-DOS
CURRENT APPLICATION DATA: US/08/237,716
FILING DATE: US/08/237,716
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                    4-Glucanases From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%; Score 134; DB 4;
45.1%; Pred. No. 9.3e-05;
tive 8; Mismatches 18
                                                                   APPLICANT: Bjornvad, Mads E.
APPLICANT: Hatakeyama, Mariko
APPLICANT: Hatakeyama, Mariko
APPLICANT: Hatakeyama, Mariko
APPLICANT: Hatakeyama, Mariko
APPLICANT: Nielsen, Jack B.
TITLE OF INVENTION: Endo-Beta-1, 4-Glucanase
TITLE OF INVENTION: Saccharothrix
FILE REFERENCE: 5195.200-US
CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 0846/97
EARLIER PILING DATE: 1997-07-01
EARLIER PILING DATE: 1997-07-01
EARLIER PILING DATE: 1997-07-01
EARLIER FILING DATE: 1997-07-13
EARLIER FILING DATE: 1997-07-13
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
IIILE OF INVENTION: FUSION PROTEINS
WOMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UNN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-UNN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Saccharothrix australiensis
US-09-109-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08237716
Patent No. 5589;84
GENERAL INFORMATION:
Sequence 2, Application US/09109841
Patent No. 6207436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.1
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201
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Gaps

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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAG 53
                                                                                                                                                          Score 130.5; DB 1; Length 60;
Pred. No. 3e-05;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 60;
                                                                                                                                                                                                                                                                                                 APPLICANT: Fields, Gregg B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned,
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CAPPELLO, JOSEPh
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,140
FILING DATE: US/03-UUL-1996
CLASSIFICATION: 5.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 130.5;
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5726243west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
                                                                                                                                                                                                                                               Sequence 12, Application US/08675140 Patent No. 5726243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 60
FELECOMMUNICATION: INFORMATION:
                                                  38.2%;
49.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: ....
575-7-1
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 unknown
                                                    Query Match
Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 26; Conserve
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 55402
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; TOPOLOGY:
US-08-534-342-12
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US-08-642-255-32
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                             /label= P69 BB05 epitope of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fields, Gregg'B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned,
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 132.5; DB 1;
Pred. No. 1.2e-05;
3; Mismatches 2;
                                                                                                                                                                                                                                                   /label= LTB sequence
                                                                                                                                                                                                                                                                                                                        /label= hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PGPQPGPQPGPQPPQPPQPPQRPEAPAPQP 50
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                                                                                                                                                                                                                                                                                                                                                                                                             pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Merchant & Gould
: 3100 No. 5576419west Center
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-UUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08534342
Patent No. 5576419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33,977
                  TELECOMMUNICATION INFORMATION TELEPHONE: 703-816-4000
                                                                        11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.79
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mueting, Ann M. REGISTRATION NUMBER:
                                                  TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                           SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Region
COCATION: 10.31
OTHER INFORMATION:
US-08-237-716-11
                                                                                                                                                                                                                                  LOCATION: 1.2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                   LOCATION: 4..7
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                    NAME/KEY: Region
                                                                                                                                                                                                                NAME/KEY: Region
                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fields
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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313 GPPGPPGPPGPPGPPGPPGPPGPAGPVGSPGAPGPPGPPGPPGPPGPPGPPGPPGPPGPP 372
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                                                                                                                                                                                                                                                                                                                             Score 130; DB 1; Length 408;
Pred. No. 0.00017;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Appilication US/08475411A
Patent No. 6140072
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San'Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FALLABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PION APPLICATION DATA:
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REGISTRATION NUMBER: 20015
REFERENCE/JOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICÁTION INFORMATION:
TELEFRONE: 415-781-1989
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-0CT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/269,429 FILING DATE: 09-NOV-1988
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                           Query Match 38.0%;
Best Local Similarity 47.5%;
Matches 29; Conservative (
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                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-07-609-716-65
                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-475-411A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Pred. No. 0.00014;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPEDIBENCE ADDRESS:
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: San Francisco
: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400 n Prancisco
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06.NOV-1990
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-609-716-65
Sequence 65, Application US/07609716
Patent No. 514581
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277-299 FHT UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.0%;
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NAME: Rowland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 330 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 47.5
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111
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                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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24; Indels

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6 PAPKPAP-OPGPOPGP-OPGPOPGPOPPOP---POPPOPPORPEAPAPOP----PAGREL 56
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 160, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Chol et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 641;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Dishette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.6%; Score 128.5; DB 4; Best Local Similarity 48.4%; Pred. No. 0.00034; Matches 30; Conservative 3; Mismatches 20;
                                            38.0%; Score 130; DB 4;
47.5%; Pred. No. 0.00017;
tive 0; Mismatches 24;
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Job time : 10.8405 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                         Query Match
Best Local Similarity 47.57
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           US-08-961-083-160
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    US-08-478-029A-65
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8
                                                                                                                                                                             Length 408;
                                                                                                                                                                                                                         24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TILLE OF INVENTION: Functional Recombinantly Prepared
TILLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                             Score 130; DB 4;
Pred. No. 0.00017;
0; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTK TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPATORION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,029A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
1S-08-478-029A-65
Sequence 65, Application US/08478029A
Patent No. 6184348
                                                                                                                                                                           Query Match 38.0%;
Best Local Similarity 47.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 408 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     single
                                                                                                          ; MOLECULE TYPE: protein US-08-475-411A-65
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                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                          linear
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                                                                                        TOPOLOGY:
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COUNTRY:
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7, 2003, 16:53:34; Search time 17.6899 Seconds (without alignments) 306.927 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPGP.....PQRPEAPAPQPPAGRELSAA 59
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                              349150 seqs, 92025710 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                  Title:
Perfect score:
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                                                                                                                                                                                                                                           Sequence:
                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:/

/cgn2_6/ptodata/2/pubpaa/us0b_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/Us09_NEW_PUB.pep:*

ptodata/2/pubpaa/US08_NEW_PUB.pep:

Published_Applications_AA:

Database :

/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pe

	Description	Sequence 16. Appl	10	9	18,	17,	15,	4. A	22	14	21,	20,	23	, N	24	7		m	Sequence 43. Appl	C/I
SUMMARIES	ID	US-09-855-754-16	US-09-855-754-19	US-09-855-754-6	US-09-855-754-18	US-09-855-754-17	US-09-855-754-15	US-09-855-754-4	US-09-855-754-22	US-09-855-754-14	US-09-855-754-21	US-09-855-754-20	US-09-855-754-23	US-09-855-754-5	US-09-855-754-24	US-09-823-240-2	US-09-976-740-43	US-10-023-529-43	US-10-023-523-43	US-09-959-987-2
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æ	Query Match	100.0	87.3	87.3	86.1	83.2	78.2	78.2	73.0	72.2	70.9	70.3	59.5	59.5	53.5	40.9	40.1	40.1	40.1	39.8
	Score	342	298.5	298.5	294.5	284.5	267.5	267.5	249.5	247	242.5	240.5	203.5	203.5	183	140	137	137	137	136
	Result No.	1	7	e	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19

Sequence 1002. Ap	Sequence 1002, Ap	Sequence 2, Appl1	Sequence 47, Appl	Sequence 47. Appl	Sequence 47, Appl	Sequence 4. Appli	Sequence 70. Appl	Sequence 160, App	Sequence 3, Appli	Sequence 62, Appl	Sequence 2. Appli	Sequence 34988. A	Sequence 36844, A		Sequence 4, Appli	Sequence 7. Appli	Sequence 967. App	Sequence 17, Appl	Sequence 10936. A	Sequence 61, Appl	Sequence 1. Appl1	Sequence 60, Appl	Sequence 43644. A	Sequence 10. Appl	Sequence 125, App	
9 US-09-925-299-1002	10 US-09-925-299-1002	9 US-10-020-215-2	9 US-09-976-740-47	12 US-10-023-529-47	12 US-10-023-523-47	10 US-09-850-887-4	10 US-09-791-171-70	10 US-09-765-272-160	9 US-10-171-384-3	9 US-09-298-523B-62	9 US-09-298-523B-2		10 US-09-864-761-36844	0	9 US-09-824-574-4		10 US-09-764-864-967	0	10 US-09-815-242-10936	9 US-09-298-523B-61	9 US-09-298-523B-1	9 US-09-298-523B-60		10 US-09-823-240-10	9 US-10-072-036-125	
647	647	1274	550	550	550	274	999	641	827	701	707	171	171	416	1647	1543	316	274	1333	069	691	929	132	380	635	
39.8	39.8	39.B	39.6	39.6	39.6	39.0	38.2	37.6	37.6	37.4	37.4	37.1	37.1	36.7	36.4	36.3	36.1	35.8	35.7	35.4	35.4	35.4	35.1	34.9	34.9	
136	136	136	135.5	135.5	135.5	133.5	130.5	128.5	128.5	128	128	127	127	125.5	124.5	124	123.5	122.5	122	121	121	121	120	119.5	119.5	
20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PERTUGSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 1205-00000
CURRENT APPLICATION NUMBER: 1206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOORSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAFKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPAPAGRELSAA 59
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Ouery Match

Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Borcetella bronchiseptica
Sequence 16, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Aprilication US/09855754
Publication No. US20020192237A1
                                                                                APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                         GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                  2000-05-25
                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 59
TYPE: PRT
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RESULT 6
US-09-855-754-15
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APPLICANT: BUSO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BOLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENE COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BORDETELLA PARABERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILLING DATE: 2001-09-10
PRIOR PILLING DATE: 2000-05-25
PRIOR FILLING DATE: 2000-05-25
SUPPRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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Pred..No. 1.2e-13;
0; Mismatches 0;
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Pred. No. 1.1e-12;
0; Mismatches 0;
                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica US-09-855-754-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09855754 Publication No. US20020192237A1
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95.0%;
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Best Local Similarity 95.0%;
Matches 57; Conservative
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                  SEQ ID NO 19
LENGTH: 58
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: BUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: INMUNOSENIC COMPOSITIONS

FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: U3(99/855,754

CURRENT FILING DATE: 2001-09-10
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APPLICANT: BOURSAUX-BUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYWORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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Pred. No. 8.7e-13;
0; Mismatches 0;
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Pred. No. 2.1e-13;
0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/855,754
                         CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Bordetella bronchiseptica US-09-855-754-17
                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Sequence 17, Application US/09855754
; Publication No. US20020192237A1
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Best Local Similarity 91.7%;
Matches 55; Conservative
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Best Local Similarity 88.1%;
Matches 52; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 52
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
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Gaps

SOFTWARE: Patentin Ver. 2.1

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 12,09/96155,754
CURRENT FILLING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: USA/09/855,754
CURRENT FILLING DATE: 2001-09-10
                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                Length 54;
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                                                                                          Indels
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                                                DB 9;
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                             Score 249.5; DB 9:
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Pred. No. 2.2e-10;
                                                                    Pred. No. 1.76
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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US-09-855-754-21
                                                                                                                                                                                                                                                                    S-09-855-754-14
Sequence 14, April:cation US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOUESAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLF
                                           73.0%;
81.7%;
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Matches 48; Conservative
                                                                                          Conservative
                                           Query Match
Best Local Similarity
Matches 49; Conserv
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US-09-855-754-21
US-09-855-754-22
                                                                                     49;
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LENGTH: 52
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APPLICANT: BORSAUX-EUDE, NICOLE
APPLICANT: BORSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PRATACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILLNG DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                                                                         APPLICANT: GUISO-MACLOUF, CANCELLAND APPLICANT: GUISO-MACLOUF, CANCELLAND APPLICANT: GUISO-MACLOUF, CONTAINING POLYMORPHISMS OF THE REPEATIVE OF INVENTION: BORDEFELLA PARAPETUSIS, AND BORDEFELLA TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

FILE REFERENCE: 03465-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT APPLICATION NUMBER: 60/206,969
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                                                                                                                                                           DB 9; Length 52;
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Pred. No. 1.1e-10;
0; Mismatches 0;
                                                                                                                                                       Score 267.5; DB 9;
Pred. No. 1.1e-11;
0; Mismatches 0;
                                                                                  ; ORGANISM: Bordetella bronchiseptica US-09-855-754-15
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US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
                                                                                                                                                       78.2%;
ilarity 85.0%;
Conservative
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1 Similarity 85.0%;
51; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Best Local Similarity
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LENGTH: 54
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Matches
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US-09-855-754-24
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LENGTH: 910
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US-09-823-240-2
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LENGTH: 39
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 01495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 020-05-25
                           1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
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Pred. No. 5.8e-10;
0; Mismatches 0;
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Pred. No. 1.3e-07;
1; Mismatches 0;
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CURRENT PELLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: G6/206,969
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN OF SEQ ID NOS: 24
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US-09-855-754-23
                                                                                                                                                    Sequence 20, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                      CAROLINE
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69.58;
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Best Local Similarity 78.3%;
Matches 47; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 41; Conserv
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US-09-855-754-20
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US-09-855-754-23
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT PELLING DATE: 2001-09-10
PRIOR PELLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 24
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 1.5e-06;
1; Mismatches 0;
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64.4%; Pred. No. 2.6e-06;
iive 1; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
Sequence 5, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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; Patent No. US20020048813A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.5%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.4*
Matches 38; Conservative
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SOFTWARE: PatentIn Ver.
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7, 2003, 16:41:02 ; Search time 11.0562 Seconds (without alignments) 513.008 Million cell updates/sec
                                                                                                                                                                       US-09-855-754B-16
342
1 GARAPPAPKPAPQPGPQPGP......PORPEAPAPQPPAGRELSAA 59
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		pertactin - Bordet	E	outer membrane pro	hypothetical prote		hypothetical 47.8K	Q)	hypothetical proli	sulfated surface q	UL36 protein - hum	hypothetical prote	ᆽ	cysteine-rich exte	proline-rich prote	immediate-early pr	proline-rich prote			nuclear protein EB	T20H2.9 protein -	proline/lysine-ric	proline-rich prote	ORF2 protein - sai	proline-rich prote	proline-rich prote	procyclin homolog	proline-rich prote	chitinase (EC 3.2.	당
SUMMARIES	£1	S15204	A47675	A32560	AE2295	S16748	JC2301	T10798	A34043	A33647	ММВЕН6	н83619	A48232	B48232	S21961	EDBEIF	T17737	T24470	T14355	S42442	A86335	T17908	T17531	B34770	T17815	C29149	T17557	T17636	S51939	വ
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di	Query Match	87.3	78.2	59.5	47.2	٠	47.1	٠	46.2	46.2	46.2		٠	45.2	•	44.0	43.7	•	٠	•	•	43.3	٠	٠	٠	•	42.7	42.7	42.7	42.5
	Score	298.5	267.5	203.5	161.5	161.5	161	161	158	158	158	157	156.5	154.5	153.5	150.5	149.5	149	149		148.5	148	147.5	147	146.5	146	146	146	146	145.5
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	332 332 332 332 332 332 344 444 547 547 547 547 547 547 547 547 5	145 145 144 144 141 141 141 139 139 138 138 138 138 138		44444444444444444444444444444444444444	240 240 317 431 421 426 875 11585 11789 11749 11749 1188 1188	00000000000000	B24264 A24264 A24264 A28996 A27538 A201696 T10340 T31611 A26036 T17547 S75138 S14959 C41132	proline-rich prote proline-rich prote proline-rich prote acrosin (E. 3.4.21 platil extensin-li hypothetical prote extensin- volvox hypothetical prote procyclic acidic r hydroxyproline-rich prote proline-rich prote hypothetical prote hypothetical prote collagen-related p
							ALIGNMENTS	4
,	RESULT 1 S15204 pertactin - Bordetella parapertussis Nyalternate names: outer membrane pr C; Species: Bordetella parapertussis C; Date: 07-Apr-1994 #sequence_revisit C; Accession: \$15204; \$14659 R; Li, L.J.; Dougan, G.; Novotny, P.; M. Microbiol. 5, 409-417, 1991 A.Title: P.70 pertactin, an outer-me A; Reference number: \$15204; MUID: 912 A; Molecule type: DNA A; Residues: 1-922 < LILL> A; Cross-references: EMBL: X54547; NID C; Genetipen C; Keywords: membrane protein	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	Bordet names: ordete pr-199 Sol520 Sol520 Dert number S1520 rences	Bordetella paraperti names: outer membrai nordetella parapertu pr.1994 #sequence_rv S15204; 814659 Dougan, G.; Novotny ol. 5, 409-417, 199 0 pertactin, an oub number: 815204; MUI s15204 rype: DNA 1-922 kIII> rences!: EMBL:X54547	parapertussis r membrane pr arapertussis quence_revisi 4659 Novotny, P.; 417, 1991 an outer-me 204; MUD:912 L:X54547; NID	tus ane uss rev / y / 91 ter ter ter / 1D:	otein P70 on 07-Apr-1994 #text_ch Charles, I.G. mbrane protein from Bor 51771; PMID:2041476 :939761; PIDN:CAA38419.	change 08-Oct-1999 ordetella parapertussis: clo 9.1; PID:g39762
	Ouery Match Best Local Matches 5	Match Local	h Simil 57; C	ch Similarity 57; Conserva	87.3%; 95.0%; vative	ap ap	Score 298.5; DB 2; Length Pred. No. 1.6e-12; 0; Mismatches 0; Indels	rth 922; Lis 3; Gaps 3;
	Oy 1 Db 564		KAPPAE KAPPAE	KPAPOPG	PQPGP PQPGP	9-4 6-4	GAKAPPAPKPAPQPGPQPGPQPGPQPPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 	QPPAGRELSAA 59 QPPAGRELSAA 621
	RESULT 2 A47675 6R outer membrane protein C; Species: Bordetella bronc C; Date: 19-pec-1993 #sequen C; Accession: A47675 R; Li, J.; Fairweather, N.F. J. Gen. Microbiol. 138, 166 A; Reference number: A77675 A; Contents: [CN7531 A; Accession: A47675 A; Status: preliminary A; Molecule type: nucleic ac A; Residues: 1-911 ALII- A; Cross-references: GB:X546 A; Note: sequence extracted	ir membras 88: Borde 119-76-7-1 110-76-7-1 110-7-7-1 1-7-7-1 1	nbrane ordete ec-199 A4767 Irweat Obiol. number CN7531 A4767 Plimin Fee: n Fee: n	ULT 2 6055 6075 6075 6075 6075 6075 6076 6076	n P.66 enchise enchise ence	8 p eptrev rev ovo 705 705 GB	in - Bordetell 18-Nov-1994 #t .; Dougan, G.; nd heterologou 14; PMID:15275 6; NID:939396; ckbone (NCBIN:	a bronchiseptica ext_change 08-Oct-1999 Charles, I.G. s expression of the protective o 10 PIDN:CAA38584.1; PID:939397 113318, NCBIP:113319)
	Query M Best Lo Matches	fatt Ca S	Simi 1;	ch Similarity 85. 51; Conservative	78.2%; 85.0%; tive		Score 267.5; DB 2; Length Pred. No. 1.5e-10; 0; Mismatches 0; Indels	th 911; .ls 9; Gaps 2;
	0у 1		KAPPAF 	KPAPQPG	PQPGP	0PG 	GÅKAPPARKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPGRELSAA	-PEAPAPQPPAGRELSAA 59

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Gaps

13;

Length 449;

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C; Species: Volvox carteri
C; Species: Volvox carteri
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A; Title: Differential targetting of closely related ECM-glycoproteins: The pherophori
A; Reference number: Z17154; MUID:97162277; PMID:9909264
A; Reference number: Z17154; MUID:97162277; PMID:9009264
A; Stetus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-599 GGDD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocyst A;Reference number: JC2299; MUID:96051989; PMID:8535973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Pneumocystis carinii
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C; Accession: JC2301
C; Accession: JC2301
BNA Res. 1, 163-168, 1994
A; Title: MSG gene cluster encoding major cell surface glycoproteins of rat:
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             A;Residues: 1-449 <ROB>
A;Cross-references: EMBL:X60376; NID:g22596; PID:g22597
                                                                                             Score 161.5; DB 2;
Pred. No. 0.00044;
4; Mismatches 17;
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Pred. No. 0.00046;
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Pred. No. 0.0006;
2; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical 47.8K protein - Pneumocystis carinii
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47.1%; Score 161; DB
Best Local Similarity 50.0%; Pred. No. 0.00
Matches 32; Conservative 1; Mismatches
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llarity 45.2%;
Conservative
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Matches 26; Conservative
                                                                                       Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-430 <WAD>
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PP 116
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                                                                                                                                              C:Species: Dordetella pertussis
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: A32560
R:Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A:Title: Molecular cloning and characterization of protective outer membrane protein P.6
A:Reference number: A32560; MUID:89264462; PMID:2542937
A:Accession: A32560
A:Molecule: 1-910 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rikaneko, T.; Nakamura, Y.; Wolk, C.D.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8. 205-213, 2001
A.Filie: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A.Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proline-rich protein - rape (fragment)
C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C; Accession: SIG748
R; Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. submitted to the EMBL Data Library, August 1991
A; Reference number: Cloning and characterization of a proline-rich gene expressed specificall A; Accession: SIG748
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A. Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-383 <KUR>
A; Cross-references: GB:BA00019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
559 GAKAPPAPKPA-----PQPGPQPGPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross-references: GB.J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A)Note: 11: Su moertain whether Met-1 or Met-3 is the initiator
C;Keywords: membrane protein
F;1-34/Domain: algual sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 203.5; DB 2;
Pred. No. 1.7e-06;
l; Mismatches 0;
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Pred. No. 0.00039;
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57.48;
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69.5%;
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                                                                                                                                   outer membrane protein P.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 41; Conserv
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Matches 27; Conserv
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20;

Length 430; 11; Indels targeted to the cell-

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Gaps

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19; Indels

Length

us-09-855-754b-16.rpr

Α.ς.

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A; Molecule rype: mRNA
A; Residues: 1.200 | <MNA
A; Cross-references: GB:Ll1439; NID:g310922; PIDN:AAA34059.1; PID:g310923
A; Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
R; de S Goldman, M.H.; Dezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A; Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A; Reference number: PQ0474; MUID:93005740; PMID:1392607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cysteine-rich extensin-like protein 1 precursor - common tobacco C;Species: Micotlana tabacum (common tobacco)
C;Date: 26-May-1994 #sequenc_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A4825.2; p00475; S24617
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. SCI. U.S.A. 90, 6829-6833, 1993
A;Tille: A tobacco gene family for flower cell wall proteins with a proline-rich doma A;Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AE004091; NID:g9946031; PIDN:AAG03586.1; GSPDB:GN
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C; Reywords: cell vall; extracellular matrix; fertilization; glycoprotein
F;1-19/Domain: signal sequence *status predicted <SIG>
F;20-209/Product: cysteine-rich extensin-like protein 1 *status experimental <MAT>
F;146/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                      P.; Hickey,
A.; Larbig,
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                                                                  4
                                                                                                                                                                                                                                                                                                                hypothetical protein PA0197 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: H83619
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, ..., Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
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                                                               4
                                                                                                                                                Length 209;
         Length 3164;
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                                                                                                                  PAPKPAPOPGPOPGPOPGPOP-POP-POP-POP-POPPORPEAPAPOPPAG
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A;Experimental source: stigma, style; strain Petit Havana SR1
                                                               11;
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45.8%; Score 156.5; DB 2;
Best Local Similarity 48.2%; Pred. No. 0.00051;
Matches 27; Conservative 4; Mismatches 16;
Score 158; DB 1;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 157; DB 2;
Pred. No. 0.00058;
4; Mismatches 17
                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain PAO1 (Senetics; A; Genetics; A; Gene: PAO197 C; Superfamily: tonB protein
   46.28;
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ilarity 50.0%;
Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-270 <STO>
A, Cross-references: GB:AE004458;
                                                            Conservative
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A; Residues: 39-209 <GOL>
   Query Match
Best Local Similarity
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Best Local Similarity
Matches 29; Conserv
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A; Status: preliminary
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Ulus protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: 130085
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim A;Reference number: A30083; MUID:88274327; PMID:2839594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
J. Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A;Reference number: A33647; MUID:90094551; PMID:2689458
A;Accession: A33647
                                                                              C; Species: Owenia fusiformis
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C; Accession: A34043; B34043
R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A; Title: Presence in invertebrate genomes of sequences characterized by the repetition
A; Reference number: A90159; MUID:90147742; PMID:2105723
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A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
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                                                            hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Volvox carteri
C;Date: 11-Apr-1990 *sequence_revision 11-Apr-1990 *text_change 21-Jul-2000
C;Accession: A33647
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C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 141;
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C;Superfamlly: varicella-zoster virus gene 22 protein
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Pred. No. 0.00031;
0; Mismatches 23
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sulfated surface glycoprotein 185 – Volvox carteri
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Local Similarity 54.0%;
nes 27; Conservative
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A; Residues: 1.141 <BAK>
A; Cross references: GB:M32217
A; Accession: B34043
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A;Residues: 59-136 <BA2>
A;Cross-references: GB:M32217
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A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
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.mmediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser); Species: suid herpesvirus 1
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Job time: 12.0562 secs
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Nucleic Acids Res. 17, 4637-4646, 1989
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A;Reference number: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0474
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S21961
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
A;Description: Cloning and characterization of a proline-rich gene expressed specificall
A;Reference number: S16748
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C;Reywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 *status experimental <MAT>
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             -- PPQPPQRPEAPAPQPP
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Pred. No. 0.00066;
5; Mismatches 16; Indels
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Pred. No. 0.0016;
2; Mismatches 19;
PPAPKPAPQPGPQPGPQPGPQPPQPPQ-
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A;Gene: APG
A;Introns: 256/1; 299/3; 387/3; 470/1
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Best Local Similarity 54.2%;
Matches 26; Conservative
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Best Local Similarity 56.0%;
Matches 28; Conservative
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A; Residues: 'MAG',1-105 <GOL>
A; Cross-references: EMBL:214014
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A; Residues: 1-196 <WUA>
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A; Molecule type: DNA
A; Residues: 1-534 <ROB>
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A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies A;Reference number: S04713; MUID:89315207; PMID:2546124 A;Accession: S04713
                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                6 PAPKPAPQPG------PQPGP--QPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAG 53
                                                                                                                                                                                                            Length 1460;
                                                                    A; Molecule type: DNA
A; Residues: 1-1460 <CHE>
C; Superfamily: herpesvirus immediate-early protein IE175
C; Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                               Score 150.5; DB 1;
Pred. No. 0.0054;
4; Mismatches 15;
                                                                                                                                                                                                  Query Match
Best Local Similarity 49.2%;
Matches 29; Conservative
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:49 ; Search time 5.72913 Seconds (without alignments) 427.133 Million cell updates/sec Мау Run on:

Title: Perfect score: Sequence:

US-09-855-754B-16 342 1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 59

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ription	P24328 bordetella	Q03035 bordetella	P14283 bordetella	P40603 brassica na	P21260 owenia fusi	volvox		5 chlamyd			9	ď	m	P48038 oryctolagus	. Q03211 nicotiana t	Q83949 orgyta pseu				Q06084 trypanosoma					~	mus	Q05860 mus musculu	O60885 homo sapien	н	P78621 emericella	Q64467 mus musculu	P22670 homo sapten	у у
SUMMARIES		ΩI	PERT_BORPA	PERT_BORBR	PERT_BORPE	APG_BRANA	YPRO_OWEFU	SSGP_VOLCA	TEGU_HSV11	GP1_CHLRE	EBN2_EBV	APG_ARATH	COLL_HSVSC	PRP2_MOUSE	PRP3_MOUSE	ACRO_RABIT	EXLP_TOBAC	TO66_NPVOP	MOZ_HUMAN	PARB_TRYBB	PAR1_TRYBB	PARC_TRYBB	WASP_HUMAN	WASP_MOUSE	MOT8_MOUSE	CSP_PLABE	CSP_PLABA	FM14_MOUSE	FMN1_MOUSE	BRD4_HUMAN	ACRO_PIG	SEPA_EMENI	G3PT_MOUSE	RFX1_HUMAN	TRX2_HUMAN
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		Match Length	922	911	910	449	141	485	3164	555	487	534	102	261	296	431	426	875	2004	129	143	145	205	220	265	339	347	1206	1468	1362	415	1790	440	979	2715
đ	Query	Match		78.2	59.5	47.2	46.2	46.2	46.2	43.7	43.4	43.4	43.0	42.4	42.4	42.1	41.8	41.4	41.1	40.6	39.8	39.8	39.8	39.6	39.5	38.9	38.9	38.9	38.9	38.7	38.6	38.6	38.5	38.5	38.2
		Score	σ			161.5	158	158	158	149.5	148.5	148.5	147	145	145	144	143	141.5	140.5	139	136	136		135.5	134	133	133	133	133	132.5	132	132	131.5	131.5	130.5
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								O10341 oravia pseu			P58840 homo sapien	
COLL_HSVS7	GDA6_WHEAT	Y091_NPVAC	SRA4_RAT	WASL_BOVIN	PCAP_MOUSE	MB11_ARATH	WASL_HUMAN	Y091_NPVOP	GDA5_WHEAT	SN24_HUMAN	ACRL_HUMAN	
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130	130	129.5	129.5	126.5	126.5	126	125.5	125	124.5	124.5	124	
34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

CINGRADA	RESULT 1 PERT_BORPA 10 PERT_BORPA 11 DA1320	recursor (Outer			<pre>RL Mol. Microbiol. 5:409-417(1991). CC -1- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS</pre>	CC MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.	-1- SUBCELLULAR LOCATION: Outer membrane.	CC -1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. CC -1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG/2+)	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf		entities requires a license or send an email to license	EMBL;	DR EMBL; A20124; CAA01746.1; DR EMBL; A19182; CAA01454.1; DR PIR; S15204; [S15204	DR PIR; S14659; S14659. DR InterPro; IPR004899; Pertact_sup.	DR InterPro; IPR003992; pertactin. DR InterPro; IPR003991; pertactin_vir. DR Pfam; PP03212; Pertactin; 1.	PRINTS; PR01482; PERTACT PRINTS; PR01484; PRTACTN	KW Outer membrane; Signal; Virulence; Repeat. 1 34 POTENTIAL. FT CHAIN 35 922 P.92	N 35 647 PERTACTIN (P.70). EP 648 922 POTENTIAL.	
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                               X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 138:1697-1705(1992).

GENCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

SUBUNIT: MONOMER.

- SUBCELLULAR LOCATION: Outer membrane.

- SUBCELLULAR LOCATION: Outer membrane.

- SUBCELLULAR LOCATION: Outer membrane.

- MISCELLANDOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                   LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
    ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                            ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                          Score 298.5; DB 1; Length 922;
Pred. No. 2.3e-11;
0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                   911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTNFAMLY.
Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X54815; CAA38584.1; -.
EMBL; A19180; CAA01453.1; -.
PIR; A47675; A47675;
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.
Pfam; PF03212; Pertactin.
                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92407514; PubMed-1527510;
                                                                                                                              95178 MW;
                                                                                                                                                          87.38;
                                                                                                                                                                          95.0%;
                                                                                                                                                                       1 Similarity 95.0
57; Conservative
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                             266
271
276
281
575
922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CN7531
                                                                                                                                                                                                                                                                                                                              PERT_BORBR
                                                                                                          DOMAIN
SEQUENCE
                                                                                                                                                          Query Match
                                                                                                                                                                          Local
                                               REPEAT
REPEAT
                                DOMAIN
                                                                             REPEAT
                                                                                               REPEAT
                                                                                                                                                                                                                                                                                             RESULT 2
PERT_BORBR
                                                                                                                                                                        Best Loca
Matches
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                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novchy P., Morrissey P., Fairweather N.F.; Molecular Cloning and characterization of protective outer membrane protein P.69 from Bordetella pertusis."; Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-96196517; PubMed-8609998;
Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;
"Structure of Bordetella pertussis virulence factor P.69 pertactin.";
Nature 381:90-92(1996).
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                          CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
   ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92407514; PubMed-1527510;
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                         ..
6
                                                                                                                                                                    DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                                                       Indels
                                                                                                                   X 3 AA REPEATS OF P-Q-P. 3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                    . 0
                                                                                                                                                                                        Pred. No. 1.4e-09;
                                                                                                     (APPROXIMATE).
                                                                                                                                                                   78.2%; Score 267.5;
85.0%; Pred. No. 1.4e
.ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89264462; PubMed-2542937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                     MW.
                                                                                                                                   93995
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO 264 AND 332
                               703
275
270
275
280
601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: MONOMER
                                                                                                                                 911 AA;
                                                                                                                                                                                  Local Similarity
tes 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRN OR OMP69A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CN2992
                                                                                                                                                                                                                                                                                                                                                PERT_BORPE
P14283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella,
                                                                                                                                 SEQUENCE
                                                                                                                                                                   Query Match
                                                                REPEAT
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                                                                                                                   DOMAIN
                                                                                                                                                                                                Matches
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FTTFTTS
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Gaps

Indels

Length 449;

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3 KAPPAPKEAPOPGPOPG------PQPGPQPGPQPPQPPQPPQPPQRPEAPAPO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90147742; PubMed-2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
"Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                          9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                              DB 1;
                                                                                                                                                                                              47.2%; Score 161.5; DB 1;
1,arity 45.2%; Pred. No. 0.0011;
Conservative 4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158; DB 1;
Pred. No. 0.00079;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem, Biophys. Res. Commun. 166:66-73(1990)
PIR; A34043; A34043.
PIR; B34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 18, Last sequence update) (NOV-1995 (Rel. 32, Last annotation update) Hypothetical proline-rich protein (Fragment). Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AA
                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nagariensis / HK10;
MEDLINE-90094551; PubMed-2689458;
                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-PRO.
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \begin{array}{c|c} \text{Hypothetical} \mid \text{protein}; & \text{DNA-binding}. \\ \text{NON\_TER} & 1 & 1 \\ \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
                                                                                                                                       48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%;
54.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                    132
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NCBI_TaxID=3067;
                                                                                 132
428
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                               Local Similarity
les 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 PP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPRO_OWEFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
NON_TER
SEQUENCE
                                                                                                            ACT_SITE
SEQUENCE
                                                                                 ACT_SITE
                                                                                                                                                                                                    Query Match
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                                                         NON_TER
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YPRO_OWEFU
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SSGP_VOLCA
                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL J. 3:111-120(1993).
TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; "Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                     LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                         CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 203.5; DB 1; Length 910;
Pred. No. 6.9e-06;
1; Mismatches 0; Indels 17
                                                                                                                                                                                                                                                                                        PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA.
                                                                                                                                                                                                 Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                   POTENTIAL
               InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Profam; PP03212; Pertactin_vir.
Profam; PP03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94004980; PubMed=8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL
                                                                                                                                    PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRIACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.5%;
69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
PIR; A32560; A32560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                    Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR CEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APG_BRANA
P40603;
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DOMAIN SEQUENCE Query Match

Matches

Best

APG_BRANA

RESULT

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REPEAT

DOMAIN REPEAT REPEAT REPEAT REPEAT

PROPEP SITE

SIGNAL

CHAIN CHAIN ö

Gaps

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23;

Plant

Length 141;

Gaps

11; Indels

46.2%; Score 158; DB 1; 64.7%; Pred. No. 0.0069; tive 3; Mismatches 11

33; Conservative

Similarity

Local

Matches

Query Match

Length 3164;

35 X 2 AA TANDEM REPEATS OF P-Q. IW; CC5D31FF4F9FE3F4 CRC64;

335857 MW;

Pfam; PF03586; Herpes_UL36; 1.
Repeat.
DOMAIN 2911 2980 3
SEQUENCE 3164 AA; 335857 MW

ETT SO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                  the cellular compartment...

J. Cell Biol. 109:3493-3501(1989).

-!- FONGTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWREN THE SACCHARIDE CHAINS
RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-!- PTW: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-88274327; Pubmed-2839594;
MCGOCCH D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       herpes simplex virus type 1.";

Gen. Virol. 69:1531-1574(1988).

-!- FUNCTION: TEGUMENT PROTEIN.

-!- FUNCTION: TEGLOMGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,

EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 158; DB 1; Length 485;
Pred. No. 0.0019;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQRPEAPAPQPP 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Sulfation; Hydroxylation.
DOMAIN 228 340 PRO-RICH.
DOMAIN 260 295 POLY-PRO.
SEQUENCE 485 AA; 50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus (type 1 / strain 17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X51616; CAA35953.1; -. PIR; A33647; A33647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.2
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10299
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P10220;
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PIR; 130085; WMBEH6. InterPro; IPR005210; Herpes_UL36.

EMBL; X14112; CAA32311.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                         "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
6AS84A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J., Goodenough U.W.;
                                                                                                                               Q9FPQ6; Q03927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91017504; PubMed-169925;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                 6 PAPKPAPQPGPQPGPQPGPQPGPQP-PQP-PQP-PQPPQRPEAPAPQPPAG 53
                                                                                                                      555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: Associates with GP2 and GP3.
-1- PIM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                             lant hydroxyproline-rich glycoproteins.";
lochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro: IPR002965; P_itch_extensn.
Interpro: IPR003862; Pistil_extensln.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
Glycoprotein; Repeat; Signal.
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21159092; Pubmed=11258910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF309494; AAG45420.1; -.
EMBL; M58496; AAA69706.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54219 MW;
                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FPQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30
259
399
455
455
553
AA;
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                                                                                                                    GP1_CHLRE
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                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-842/U066; FUDMEG=8U8/149; Baer R., Bankler A.L., Farrell P.J., Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibbon T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Virol. 65:2545-2554(1991).
-1- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: NUCLEAR, ASSOCIATED WITH THE NUCLEAR MATRIX.
                                     Gaps
                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90266473; PubMed-2161150;
Pettl L., Sample C., Kleff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus
latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91202599; PubMed-1850028; Cohen J.I., Wang F., Kleff E.; "Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
                                                                    4 APPAPK-PAPQPGPQPGPQPGPQP-----GPQPPQPPQPPQPPQRPEAPAPQPPA
                                     6
   Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
6 X·2 AA TANDEM REPEATS OF R-G.
DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 140.0, Pred, No. 0.0066;
                                     Indels
                                                                                                                                                                                                                                                                                                         Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                17;
 DB 1;
 Score 149.5; DB
Pred. No. 0.0063;
                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.4%; Score 148.5; 51.9%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION, AND PHOSPHORYLATION
                                                                                                                                                                                        487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V01555; CAA24877.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52544 MW;
 43.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 310:207-211(1984).
                                   28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Repeat.

    -!- PTM: PHOSPHORYLATED.

                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                         EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 AA;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSFAC; T01618;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF LMP-1
                                                                                                                                                                                      EBN2_EBV
P12978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECURING TRAINCY. Columbia:

RECURING TRAINCY
APG_ARATH STANDARD; PRT; 534 AA.
P40602; 093214; 09LNT8;
01-FEB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
AR ATABIGOPSIS thallana (Mouse-ear cress)
Eukaryota; ViidIdIplantae; Streptophyta; Embryophyta; Tracheophyta; SpermatOphyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Prassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. Cclumbia;
STRAIN-CV. Cclumbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNa clones (RAFLs) sequenced by the "RIKEN Arabidopsis full length cDNa clones (RAFLs) sequenced by the SSP consortium (Salk/Stenford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
--- TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER. ONLY IN MALE FERTILE PLANYS.
---- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-3702;
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EMBL; X60377; CAA42925.1; -.
EMBL; AC022472; AAF79900.1; ALT_SEQ

Gaps

PPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQP-PAGRE

'n Matches

ö q

3; Mismatches

27; Conservative

οĘ

SIGNAL

CHAIN

Best Loca Matches

à q COLL_HSVSC

RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86059475; PubMed-2999141;
Ann D.K., Carlson D.M.;
"The structure and organization of a proline-rich protein gene of
                                                                                                                                                                                                                                              Ann D.K., Carlson D.M.; "The structure and organization of a proline-rich protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQP--GPQPGPQPGPQPPQ--PPQPPQRPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0068;
2; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROLINE-RICH PROTEIN MP-2. 36E13BA7387F47D4 CRC64;
                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Proline-rich protein MP-3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                      mouse multigene family.";
J. Biol. Chem. 260:15863-15872(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 260:15863-15872(1985).
                                                                        Proline-rich protein MP-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-86059475; PubMed-2999141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seqt
01-0cT-1994 (Rel. 30, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA; 26034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M12099; AAA40004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M12100; AAA40005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.4
Best Local Similarity 50.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:97773; Prp.
Repeat; Saliva; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse multigene family
                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                13-AUG-1987
13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
PRP3_MOUSE
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewes the Swiss Institute of Bioinformatics and the EWES outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                          ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blesinger B., Trimble J.J., Desroslers R.C., Fleckenstein B.,
"The divergence between two oncogenic Herpesvirus saimiri strains in
a genomic region related to the transforming phenotype.";
Virology 176:505-514(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQ--PGPQ--PGPQPGPQPPQPPQPPQRPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                Length 534;
                                                                                                                                                                                                                                                                                                                                                                                            43.0%; Score 147; DB 1; Length 102; 56.1%; Pred. No. 0.0027; 1ive 1; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                    3 KAPPAPKPAPQPGPQPGPQPGPQPGPQ-PPQPPQPPQPPQRPEAPAPQPP 51
                                                                                                                                                                                                  S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLAGEN-LIKE,
4C2CD389E78A03C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpesvirus saimiri (subgroup C / strain 488).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                            Score 148.5; DB 1;
                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                0.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AVG-1991 (Rel. 19, Last sequence update) 01-MAY-1992 (Rel. 22, Last annotation update) Collagen-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
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                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                        Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
EMBL; AY058847; AAL24235.1; -. PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90266466; PubMed-2161148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequ
01-MAY-1992 (Rel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B34770; B34770.
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                      58007 MW;
                                                                                                                                                                                                                                                                                          43.4%;
54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 102 AA; 9893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55264; AAA72929.1; -.
                                                                                                                                                                                                                                                                                                                                27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                    534 AA;
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLL_HSVSC
P22576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRP2_MOUSE
P05142;
                                                                                                                                                                          ACT_SITE
CONFLICT
                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                    Signal.
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Gaps

4

Length 261;

23

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DOMAIN

Matches

ð d

15

PRP2_MOUSE

RESULT 12

Repeat; Saliva

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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                EXLP_TOBAC
                                                                                                                                                                                                                                                                                   RESULT 15
    8.11.11.11
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                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-New Zealand white; TISSUE-Testis;
STRAIN-New Zealand white; TISSUE-Testis;
STRAIN-New Zealand white; TISSUE-Testis;
McDardson R.T., O'Rand M.G.
"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";
Biochim. Biophys. Acta 1219:215-218(1994).
IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A STRINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                              Gaps
                                                                                                                                   44 СРРРРССРОРКРРОСРРРССРОРКРРОСРОРРССРОРКРРОСРОРРССРОРКРРОС 100
                                                                                                           23
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
1 16 BY SIMILARITY.
17 431 ACROSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
                                                                                                         GAKAPPAPKPAPQPGPQP--GPQPGPQPGPQPPQPPQ--PPQPPQRPEAPAPQPPAG
                                                                               ÷
                                               Length 296;
                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
              7F146824E8AF3269 CRC64;
                                           Score 145; DB 1;
Pred. No. 0.0074;
2; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE.
                                                                                                                                                                                                                     431 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY
                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
           29521 MW;
                                             42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U05204; AAA61630.1; -.
                                                                            Conservative
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
152
160
87
87
              296 AA;
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                                                            L Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.223;
                                                                                                                                                                                                                                               01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                ACRO_RABIT
P48038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
NON_TER
SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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                                                               Local
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                                                             Best Loc
Matches
                                                                                                                                                                                                   ACRO_RABIT
                                                                                                                                                                                      RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-1700 M. M. M. Petit Havana; TISSUE-Pistil; MEDLINE-30065740; Pubbled-192607; MEDLINE-930065740; Pubbled-192607; Medline-930065740; Pubbled-192607; Medline-1706580; M. M. H. Pezzotti M., Seurinck J., Mariani C.; Developmental expression of tobacco pistil-specific genes encoding novel expension-like proteins."; Plant cell 4:1041-1051(1992).

1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).

1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).

1- TISSUE SPECIFICITY: MOWAND AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWAND AND LEVELS GRADUALLY DECREASE AFTER AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil specific extensin-like protein precursor (PELP).
Nicotiana tabacum (Common tobacco).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBL TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                SIA495CC94017812 CRC64;
                                                                                                                                                                                                                                                                                                                  2 AKAPPAPKPAPQPGPQPGPQPGP----QPGPQPPQPPQPPQPPQRPEAPAPQPPA 52
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                                                                                                                                                                                                                     Score 144; DB 1; Length 431;
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                                                                                                                                                                                                                                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JQ1696; JQ1696.
InterPro; IPR000419; Pollen_Ole_e_I.
Pfam: PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
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                                                                                                                                                                                                                                            Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AA
                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                        46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44278 MW;
                                                                                                                                                                                                                     42.18;
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                               208
208
140
238
431 AA;
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Best Local Simi.
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Search completed: May 7, 2003, 16:48:08 Job time : 6.72913 secs

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MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-1089896;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815-4817(2000).
EMBL: AJZ50083; CAB76437.1; InterPro; IPR004899; Pertact_sup.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09K5H3 PRELIMINARY; PRT, 115 AA.
09K5H3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.9%; Score 331.5; DB 2; Best Local Similarity 98.3%; Pred. No. 3e-20; Matches 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                          013305
09JLE9
09P944
08T1Y6
0948Y6
08Y0B7
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P93797
Q9ARY7
                                                                                                                                                                                                                                                        093L98
069257
08RSU0
093L97
09UVD1
                                                                                                                                      0956M9
0953M8
0956N0
                                                                                                                                                                                                09S6N1
069259
088143
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                                                                                                                                                                                                                                                                                                                                     493
938
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203.5
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                                                                                                                              7, 2003, 16:38:52 ; Search time 30.1533 Seconds (without alignments) 403.166 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                          US-09-855-754B-16
342
1 Gakappapkpapgpgpgpgp.....porpeapapgppagkelsaa
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09a1q2
09a1q4
09a1p9
0914e2
098591
0985p9
0985h9
                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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09K5G7
09K5G9
09KJX9
09KJQ2
09K5H1
09K5H2
09K5H2
09K5H2
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Q9K5H9
Q9K5H7
Q9KJY1
Q9KJY0
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_mhc:* sp_organelle:* sp_phage:*

sp_plant:* sp_rodent:*

sp_virus:*

SPTREMBL_21:* 1: sp_archea:* 2: sp_bacteria:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

Query Match Length DB

Score

Result Š. 294.5 294.5 294.5

274 267.5 267.5 267.5 267.5 249.5

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21

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bordetella bordetella bordetella

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1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPPGPPQPPQPPQPPGR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPGPELSAA 97
                                                                                                                                                                                                                                                                                                                                         Kell D.J., Fenwick B.; "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Query Match

Best Local Similarity 91.7%; Pred. No. 3e-17;

Matches 55; Conservative 0; Mismatches 0; Indels 5,
                                                                                                                                                      01:0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0M1-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                        anino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF156773; AAF82397.1;
InterPro: IPR004899; Pertact_sup.
InterPro: IPR002965; P_rich_extensn.
Pfam: PF03212; Pertactin: 1.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 12 122 NON_TER 122 AA; 12395 MW; RED00966A40FF994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007265; AAG38441.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC19395;
MEDLINE=21117018; PubMed=11179374;
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                              STRAIN=16039;
Keil D.J., Fe
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NON_TER
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09ALQ2;
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Boursaux-Eude C., Guiso N.;

Infect. Immun. 68.4815-4817(2000).

EMBL: AJ250089; CAB7643.1;

EMBL: AJ250089; CAB7643.1;

InterPro: IPR0024899; Pertact_sup.

InterPro: IPR0024899; Prich_extensn.

Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boursaux Eude C., Guiso N.;
Boursaux Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Ppertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817.(2000).
EMBL: AJ250087; CAB7644.1;
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002965; Prich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 111;
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86.1%; Score 294.5; DB 2; Length 111;
Best Local Similarity 91.7%; Pred. No. 2.8e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 5:
                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Pred. No. 1.3e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA; 11416 MW; 5140669692808F8E CRC64;
                                                             01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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                                    PRT;
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Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                 Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.3%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 95.0%
Matches 57; Conservative
                                   PRELIMINARY;
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                                                                                                                                                                                    Bordetella
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SEQUENCE
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Q9K5G7
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Gaps

09K5H1

RESULT 6 **09K5H1**

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Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250081; CAB76435.1; ...
InterPro: IRR004899; Pertact_sup.
InterPro: IRR002965; P_rich_extensn.
Pfam; PF03212; Pertact_n.
                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAFKPAPQPGPQPGPQPGPQPPGPPQPPQPPQRPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID-518;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                     Length 215;
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                                                                         215 215
215 AA; 22327 MW; 5C21D45CF784B4AE CRC64;
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Last annotation update)
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Last annotation update)
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85.0%; Pred. No. 3.9e-15;
tive 0; Mismatches 0;
                                                                                                                                 80.1%; Score 274; DB 2; I
ilarity 86.7%; Pred. No. 2.1e-15;
Conservative 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TEMBLE). 15, Created)
01-OCT-2000 (TEMBLE). 15, Last seq
01-JUN-2002 (TEMBLE). 21, Last ann
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MEDLINE-21117018; PubMed-11179374;
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                         PRINTS; PR01432; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin (P.68) (Fragment).
     Pfam; PF03212; Pertactin; 1.
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Matches 51; Conservative
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                                                                                                                                                 Local Similarity
nes 52; Conserv
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Q9ALP9;
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SERUBLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
PPolymorphism of Repeated Regions of Pertactin in Bordetella pertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4015-4817(2000).
EMBL; AJ550085; CAB76439.1;
INTERPRO 1PR004899; Pertact_sup.
Pfam: PP031212; Pertactin; 1.
MON TER
                                                                                                                             170 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRDPPGRDPPARQPPAGRELSAA 225
                                                                             Gaps
                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GAKAPPAPKPAPQPGPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 74
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                                        DB 2; Length 252;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                  Query Match 86.1%; Score 294.5; DB 2; Length : Best Local Similarity 91.7%; Pred. No. 5.3e-17; Matches 55; Conservative 0; Mismatches 0; Indels
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26107 MW; 368C142508D77057 CRC64;
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Last annotation update)
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86.7%; Pred. No. 1.2e-15;
tive 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
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Infect. Immun. 6:1917-1921(2001).
EMBL; AY007263; AG38439.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact. Sup.
InterPro; IPR002965; P_rich_extensn.
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MEDLINE-21117018; PubMed-11179374;
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                                                                                                                                                                                                                                            PRELIMINARY;
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 252 AA;
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 SEQUENCE
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SEQUENCE FROM N.A.
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                                      NCBI_TaxID=518;
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Q9ALP3
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Q9K5H9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (ANG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AJJ45927; CAB82515.1; InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.
Mooi F.R.;
                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%; Score 267.5; DB 2; Length 911; 85.0%; Pred. No. 2.1e-14; Live 0; Mismatches 0; Indels 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                  20826 MW; 9F3AC6E4128942E6.CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              ch 78.2%; Score 267.5; DB 2; 1 Similarity 85.0%; Pred. No. 6.4e-15; 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA
                                            Infect. Immun. 69:1917-1921(2001).
EMBL; AY007271, AAG38447.1;
InterPro; IPR004992; pertactin.
InterPro; IPR004899; Pertact sup.
InterPro; IPR02965; Prich_extensn.
Pfam; PF03121; Pertactin; IPRNTS; PR03121; PERRACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               200 AA;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9L4E2
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Q9L4E2
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Q9K5G1
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MEDLINE-20359389; PubMed-10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Broussis, Borderella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
Infect. Immun. 68:4491:
InterPro, IPR004899; Pertact.sup.
InterPro, IPR002865; P.rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Pred. No. 2e-13;
1; Mismatches 3; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL; AVO07277; AAG38453.1; InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertact_sup.
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                                                                                                                                                                                                                                                                                                           107 AA; 11073 MW; A0A339BFF0EABBC6 CRC64;
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231 AA; 23930 MW; 5FB281B95E74678C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     Query Match 73.0%; Score 249.5; DB 2; Best Local Similarity 81.7%; Pred. No. 1.1e-13; Matches 49; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA.
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PRINTS; PR01217; PRICHEXTENSN.
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Best Local Similarity 78.0%;
Matches 46; Conservative 1
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Q9K5H9;
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                            Pertactin (Frigment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%; Score 247; DB 2; Length 115; 80.0%; Pred. No. 1.8e-13; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156771; ARF82395.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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115 AA; 11693 MW; FA3A76596F7097EB CRC64;
                                01-OCT-2000 ($rEMBLrel. 15, Created)
01-OCT-2000 ($rEMBLrel. 15, Last sequence update)
01-JUN-2002 ($rEMBLrel. 21, Last annotation update)
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Job time: 30.1533 secs
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PRINTS; PR01217; PRICHEXTENSN.
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nes 48; Conservative
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Keil D.J., Fenwick B.;
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                                                                                                                                                                                                                      NCBI_TaxID=518;
                                                                                                                                                                                              Bordetella.
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infects Immun. 68:4815-4817(2000).
EMBL; AJZ5077; CAB76431.1;
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
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Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250079; CAB76433.1;
InterPro; IPR004699; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 247; DB 2; Length 104;
Pred. No. 1.7e-13;
0; Mismatches 0; Indels 12; Gaps
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                                                                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 A.A.
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                                                                              Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 72.2%;
1 Similarity 80.0%;
48; Conservative
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Best Local Similarity
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Q9K5H7;
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Q9K5H7
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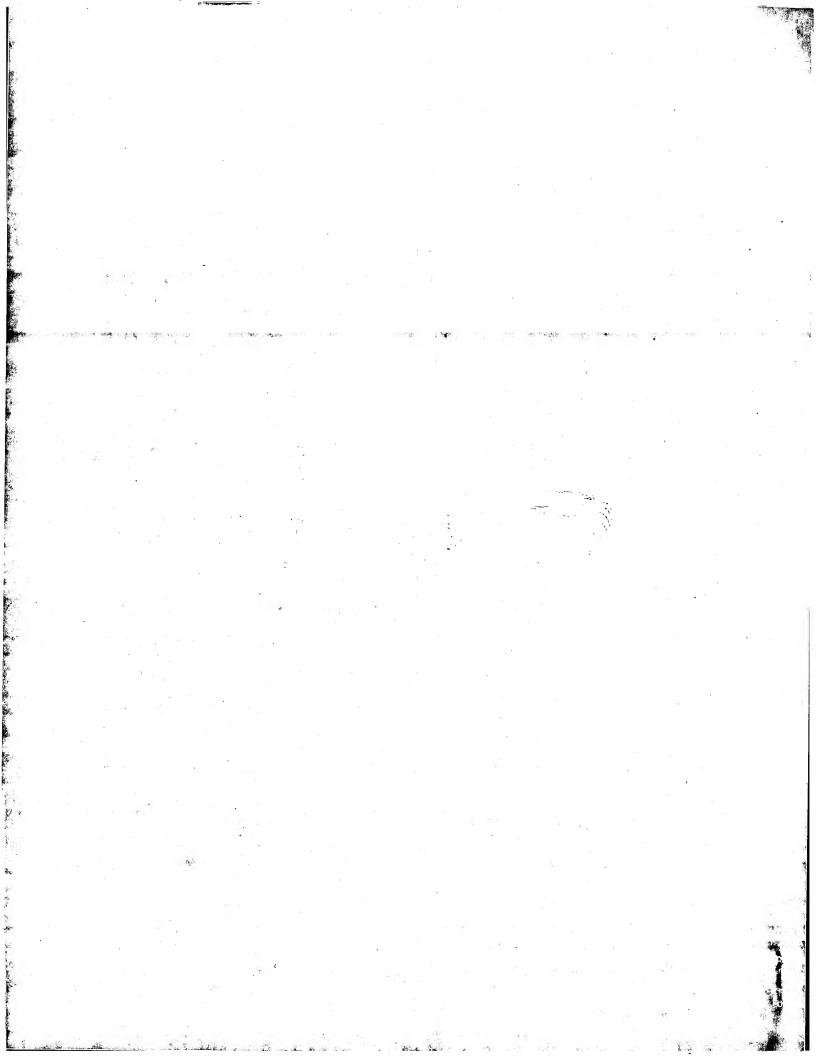
PRELIMINARY;

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Gaps

12;



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7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754B-17 298 1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 52 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Genesseq_101002:* 1: \SIDS2/gcddata/genesseq/genesseqp-embl/AA1980.DAT:* 2: \SIDS2/gcddata/genesseq/geneseqp-embl/AA1981.DAT:* 3: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 4: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 5: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 5: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 7: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 7: \SIDS2/gcddata/geneseqy-embl/AA1981.DAT:* 8: \SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 9: \SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 10: \SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:* 11: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 12: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 13: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 14: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 15: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 16: \SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* 17: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 18: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 19: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 20: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 21: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 22: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:* 23: \SIDS2/gcgdata/geneseqy-geneseqp-embl/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	B. bronchiseptica	Pertactin antiqen	prn proteins. Bor	Bordetella bronch1	B. bronchiseptica	Bordetella paraper	Bordetella paraper
	ID		AAE16197	AAE16195	AAE16194	AAR14320	AAR26503	AAE16183	AAE16198	AAR25578	AAE16185
	DB	23	23	23	23	12	13	23	23	13	23
	Query e Match Length DB I	53	26	9	52	911	911	911	58	922	922
dР	Query Match	96.5	94.6	91.9	6.06	6.06	6.06	6.06	9.68	9.68	89.6
	Score	287.5	282	274	271	271	271	271	267	267	267
	Result No.	П	7	е	4	Ŋ	9	7	œ	6	10

Pertactin antigen B. bronchiseptica Bordetella pertuss Novel human diagno Human polypeptide Herbicidally activ Sugar beet chitina Streptococcus pneu	NOVEL ILLINIAL INGORES SYNTHEIGHTE SUGARCEAR PROJECT NOVEL HUMAN diagn
AAR14321 AAE16199 AAE16200 AAE16201 AAE16201 AAE16201 AAE16201 AAE16202 AAE16203 AAE16203 AAE17146 AAE1737 AAE1737 AAE1737 AAE1737 AAE1737 AAE1737 AAE09876 AAE09877 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876 AAE09876	4305 4360
AAR1432 AAE1619 AAE1620 AAE1620 AAE1620 AAE1620 AAE1714 AAR173 AAR173 AAR020207 AAR0932	AAR8764 AAE1430 ABG0436
2152218	17 23 22
922 49 49 40 40 40 40 40 40 40 40 40 40 40 40 40	324 329 356
<i></i> ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	نججز
250 250 250 250 250 250 250 250 250 250	125 124.5 123.5
111111111111111111111111111111111111111	1444 1646

ALIGNMENTS

AAE16196 standard; peptide; 53 AA. 26-MAR-2002 (first entry) AAE16196; RESULT 1 **AAE16196** PX SX X X X X X X Y Y

B. bronchiseptica strain II-4 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica. WO200190143-A2. 29-NOV-2001.

Guiso-maclouf N, Boursaux-eude 25-MAY-2000; 2000US-206969P. (INSP) INST PASTEUR.

23-MAY: 2001; 2001WO-EP06457.

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WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodical fullds, such as human or other animal body fluids, including human sera, antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
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Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AA;
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Gaps
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 Score 287.5; DB 23; Length 53; Pred. No. 1.6e-15;
                           0; Indels
                        0; Mismatches
96.5%;
98.1%;
                        52; Conservative
             Best Local Similarity
  Query Match
                        Matches
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA õ g

AAE16197 standard; peptide; 56 AAE16197; RESULT 2

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B. bronchiseptica strain II-5 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. 26-MAR-2002 (first entry)

Bordetella bronchiseptica. WO200190143-A2.

29-NOV-2001

25-MAY-2000; 2000US-206969P

23-MAY-2001; 2001WO-EP06457

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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Gaps
 Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQ----RPEAPAPQPPAGRELSAA
                                                                                                                                      Length 56,
                                                                                               Indels
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                                                                   Score 282; DB pred. No. 4.3e-1; Mismatches
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Best Local Similarity 91.1%;
Matches 51; Conservative
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AAE16195 standard; peptide; 60 RESULT 3

AAE16195;

(first entry) 26-MAR-2002

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B. bronchiseptica strain II-3 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Boursaux-eude C; Guiso-maclouf N,

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

60 AA; Sequence

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1 GAKAPPAPKPAPQPGPQPGPQPG-----PQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                Indels
                                ö
91.9%; Score 274; DB 23;
86.7%; Pred. No. 1.8e-14;
ive 0; Mismatches 0;
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26-MAR-2002

AAE16194;

RESULT 4 **AAE16194** 29-NOV-2001

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Pichia microcrganisms are transformed for the expression of pertactin antigans. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPARKPAPQPGPQPGPQPGPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia microcrganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
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Pred. No. 2.3e-13;
0; Mismatches 0;
                        Location/Qualifiers
266..270
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Best Local Similarity 96.2%;
Matches 51; Conservative (
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Bordetella bronchiseptica
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N-PSDB; AAQ14319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used to detect Bordetella, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                  B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on 90.9%; Score 271; DB 23; Similarity 96.2%; Pred. No. 2.8e-14; 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR14320 standard; Protein; 911 AA.
                                            AAE16194 standard; peptide; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Fig 1c; 47pp; English.
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                  Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-097639/13.
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Gaps

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22

20-JAN-1992

AAR14320;

AAR14320

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51;

Sequence

Query Match Local Best Loca Matches

Key Protein

Region Region

Peptide Peptide

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal calls, as well as biological fluids, such as human or other animal colls, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 271; DB 23; Length 911;
Pred. No. 2.3e-13;
0; Mismatches 0; Indels
           /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 28; 47pp; English.
                                                                                                                                                                                                                                  Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE16198 standard; peptide; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.9%;
96.2%;
                                                                                                                    23-MAY-2001; 2001WO-EP06457
                                                                                                                                                         25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000; 2000US-206969P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.9
Best Local Similarity 96.2
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                   WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 AA;
                                                                                                                                                                                                                                                                                      N-PSDB; AAD26440
                                          WO200190143-A2.
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                                                                                                                                                                                             (INSP ) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                 29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE16198;
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AAE16198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against arrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 271; DB 13; Length 911;
Pred. No. 2.3e-13;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
                                                                                                                                                                  260..262
/label- RGD_tripeptide
                                                                                                                                                                                                     701..703
/label= RGD_tripeptide
                                                                                           266..279
/label= Repeat_region
                                                                                                                                                   /label= Repeat_region
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE16183 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 28pp; English.
                                                        35..632
/label- P.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.9%;
96.2%;
                                                                                                                                                                                                                                                                                                                                       92WO-GB00561
                                                                                                                                                                                                                                                                                                                                                                          91GB-0006568
                                                                                                                                                                                                                                                                                                                                                                                                             (WELL ) WELLCOME FOUND LID.
Bordetalla bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica
                                                                                                                               570..589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA;
                                                                                                                                                                                                                                                                                                                                   27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                             WO9217587-A
                                                                                                                                                                                                                                                                                                15-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                               Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Loca Matches

ò 셤 RESULT 7 AAE16183 Region Region

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Gaps

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WPI; 1992-250033/30. N-PSDB; AAQ26509.

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                                                                                                                                           Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                 pertactin in Bordetella species, useful in immunogenic compositions for
treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                  present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                        760..262
/note= "motif associated with cell-cell adhesion"
266..285
/note= "contains 5 direct, tandem repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "contains 9 direct repeats of Pro-Gln-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "motif associated with cell-cell adhesion"
                                                       οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                    polymorphisms of the repeated regions
                                                                                                                                                                                                                                                                                                                                                      Length 58;
                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                     Score 267; DB 23;
Pred. No. 6.1e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR25578 standard; Protein; 922 AA
Boursaux-eude C;
                                                                                                      Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35..643
/label- P70 .
                                                                                                                                                                                                                                                                                                                                                     89.6%;
87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91WO-GB02302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "c
575..612
/note= "c
712..714
                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella parapertussis.
                                                    Polypeptides containing
pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                        WPI; 2002-097639/13
                                                                                                                                                                                                                                                                                                                          58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1991;
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                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR25578;
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                            A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70.000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 922;
                                              Acellular vaccine for immunisation against whooping cough
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
89.6%; Score 267; DB 13;
Best Local Similarity 87.9%; Pred. No. 4.7e-13;
Matches 51; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
254..304
564..621
/note= "Pertactin region I"
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16185 standard; Protein; 922 AA.
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                                                                                                                  Claim 1; Fig 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; AAD26442.
                                                                                                                                                                                                                                                                                                                                                                                           922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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90GB-0007416. 91WO-GB00487

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Pichia microorganisms are transformed for the expression of
                                                                                                                         Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                       Disclosure; Fig 1C; 38pp; English
                                                        (WELL ) WELLCOME FOUNDATION LTD.
                                                                           Clare JJ, Romanos MA;
                                                                                            WPI; 1991-325214/44.
N-PSDB; AAQ14320.
                 28-MAR-1991;
                                     02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001.
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    AAE16193;
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                                    Outer membrane protein) or their fragments. Pertactin (PRN) is used as and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the Bordetella in a materials such as human sera, antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
                                                                                                                                                                                                              ?
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                             ;
                                                                                                                                                                                    Similarity 87.9%; Score 267; DB 23; Length 922; Similarity 87.9%; Pred. No. 4.7e-13; Conservative 0; Mismatches 1; Indels
                            present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                         Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
           Page 34; 47pp; English.
                                                                                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          586..588
/label= --
                                                                                                                                                                                                                                                                                             AAR14321 standard; Protein; 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= repeat
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781..285
7abel= re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,3..577
| Tabel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589..591
/label= re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                276..280
'label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583..585
/label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79..581
label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592..594
'label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95..597
'label- re
                                                                                                                                                                                                                                                                                                                                                                                            Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .600
                                                                                                                                                                                                                                                                                                                                                      Pertactin antigen P.70.
                                                                                                                                                                 922 AA;
                                                                                                                                                                                                                                                                                                                                   20-JAN-1992
          Disclosure;
                                                                                                                                                                                  Query Match
Best Local Simi
Matches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9115571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-0CT-1991
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                AAR14321;
                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Peptide
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B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQP-----PQPPQPPQR-PEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                  8
                                                                                 The 46 Xs represent amino acids missing in the specification
                                                                                                                                                          Score 258; DB 12; Length 922;
Pred. No. 2.3e-12;
0; Mismatches 0; Indels (
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                           AAE16193 standard; peptide; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                    Query Match
Best Local Similarity 86.4%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                       922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN;
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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical and tassue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Courter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques in affinity chromatographic columns. Pertactin is useful as antiquens and infinity chromatographic columns. Pertactin is useful as antiquens and introduces to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bronchiseptica strain II-7 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Length 49;
                                                                                                                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                              Score 250.5; DB 23; Leus-
Pred. No. 9.5e-13; Orients O; Indels
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                                                                                                                                                                                                                                                                         84.18;
90.68;
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                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                        49 AA;
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                                                                                                                                                                                                                                                                                                                  48;
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                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-8 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                          Gaps
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        Length 48;
       Score 244; DB 23;
Pred. No. 2.9e-12;
                      Pred. No. 2.96
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                    AAE16200 standard; peptide; 52
   81.9%;
llarity 88.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica
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Ouery Match
Best Local Similarity
Matches 47; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                     AAE16200;
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ID AAE1
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B. bronchiseptica strain II-9 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunoganic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                               Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                           Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                       23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                         25-MAY-2000; 2000US-206969P
                           26-MAR-2002 (first entry)
                                                                                              Bordetella bronchiseptica
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                                                                                                                 WO200190143-A2
                                                                                                                                   29-NOV-2001.
         AAE16201;
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burlfying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

54 AA; Sequence

6; Gaps Length 54; 1; Indels Score 235; DB 23; Pred. No. 1.5e-11; 1; Mismatches 1; 78.9%; 85.7%; 48; Conservative Query Match Best Local Similarity Matches 48; Conserva

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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQP---PQ-RPEAPAPQPPAGRELSAA

ò g Search completed: May 7, 2003, 16:47:07 Job time: 28.0187 secs

Sequence Sequence Sequence

Sequence Seq

Sequence:

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Searched:

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US-08-457-273B-42

US-08-556-419-21

US-09-535-008-61

US-09-535-008-67

US-09-535-008-67

US-09-535-008-75

US-09-535-008-77

US-08-731-01-12
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298
1 GAKAPPAPKPAPQPGPQPGP......pgrpeapapqPPAGRELSAA
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-453-265-16
US-09-02E-87-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
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RESULT 1 US-460-269C-4 Sequence 4, Application US/08460269C Sequence 4, Application US/08460269C Sequence 6.197548 Sequence 6.197548 SET APPLICANTION: TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: STREET: 2200 Clarendon Blvd., Suite 1400	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,269C FILLING DATE: 02-Jun-1995 ATTORNEY,AGENT INFORMATION: NAME: LEDOVIE, Richard M. REGISTRATION NUMBER: 37,067 REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTER: LENGTH: 911 amino acids TYPE: amino acid TYPE: amino acid MOLECULE TYPE: protein SEQUENCE TYPE: protein SEGUENCE DESCRIPTION: SEQ ID NO: 4:	Query Match Query Match Best Local Similarity 96.2%; Pred. No. 1.3e-16; Matches 51; Conservative 0; Mismatches 0; Indels 2; Matches 1; Conservative 0; Mismatches 2; QY 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52

5202236 3, Appli 1, Appli 1, Appli 2, Appli 2, Appli 5, Appl

Appl Appli Appli Appli Appli Appli

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568 GAKAPPAPKPA------PQPGPQPPQPPQPP-QPEAPAPQPPAGRELSAA 609
                                                                                                                                                                                                                                                                                                                                                        Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/237,716
FILING DATE: US-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        Score 207; DB 4;
Pred. No. 4.7e-11;
1; Mismatches 0
                                                                     REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-UN-1991
ATTORNEY/AGENT INFORMATION:
                       NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               TELEPHONE: (703) 243-6333
                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08237716
Patent No. 5589384
                                                                                                                                      (703) 243-6410
                                                                                                                                                                                                         LENGTH: 910 amino acids
  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             69.5%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-616-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wilson, Mary J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                   FELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-237-716-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                              APPLICANT: CLARE, JEFEREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 267; DB 4; Length 922;
Pred. No. 3e-16;
                                                                                                                                                                                                    ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Millen, White, Zelano & Branigan, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/460,269C
BILING DATE: 02-10n-1995
ATONEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
RESISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Inhear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-460-269C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
Sequence 6, Application US/08460269C
Patent No. 6197548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.6%;
Best Local Similarity 87.9%;
Matches 51; Conservative
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                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-460-269C-2
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                                                                                                 APPLICATT: MANGH, KATHY J.:ANDERSON, DAVID M.:STRAUSBERG, SUSAN L.:MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 APPAPKPAPQPG-----PQPGPQPGPQPPQPPQRPEAPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 APPAPAFAPAPALAPAPPNPNPQSPSPPSPPSPPTPPFTPPS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 122; DB 6;
Pred. No. 0.00044;
2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09095443
Patent No. 6342593
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Peles, Eior
TITLE OF INVENTION: DIACNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: FASTSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/049,477
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICÁTION DATA:
APPLICATION NUMBER: 60/049
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.98;
51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INE: (213) 489-1600
: (213) 955-0440
67+3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.19
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                  Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 334
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                                                                                                                                                             PROTEIN
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Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
TTLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCE: 16
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                 /label= P69 BB05 epitope of Bordetella pertussis sequence
                                                                                                                                                                                                                                                                                  Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 24;
                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Onterio

COUNTRY: Canada
ZIP: M5G 1N7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RD-Ease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                             Score 134; DB 1;
Pred. No. 5 1e-06;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 125; DB 4;
Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                        /label- LTB sequence
                                                                                                                  /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFENCE/DOCKET NUMBER: 1038-660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416, 595-1155
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 aming acids
                                                                                                                                                                                                                                                                                                                                                                                     5 PGPEIAPQPGPQPPQPP--QPEAPAPEP 32
                                                                                                                                                                                                                                                                                                                                                              14 PGPQPGPQPGPQPPQPPQRPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PQPGPQPPQPPQP--QPEAPAPQPP 23
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 76.7%;
Matches 23; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
NAME/KEY: Region LOCATION: 1..2 OTHER INFORMATION:
                                                                                               LOCATION: 4.7
OTHER INFORMATION:
                                                                                                                                                                              COCATION: 10.31
CTHER INFORMATION:
CTHER INFORMATION:
US-08-237-716-11
                                                                            NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                           NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-750-624-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-750-624-11
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Gaps

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5, Application US/08453265
5693757
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5202236-37
;Patent No. 5202236
                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                             Gaps
                                                                                                                                          Score 121.5; DB 4; Length 1274;
Pred. No. 0.0016;
1; Mismatches 11; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.8%; Score 121.5; DB 1; Length 3119;
Best Local Similarity 48.0%; Pred. No. 0.0035;
Matches 24; Conservative 3; Mismatches 12; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 QPGPQPGPQPPQPPQPPQRPEAPAPQPP-----AGRELSA 51
                                                                                                                                                                                                                   1 GAKAP-----GPQPPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
CONDURRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.25
SUFWARE: PatentIn Release #1.0, Version #1.25
SUFRENT APPLICATION DATA: WORREY APPLICATION NUMBER: US/08/246,982A
FILING DATE: MAY 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REDEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
TELEFRAXION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
                                                                                                                                      Query Match 40.8%;
Best Local Similarity 39.7%;
Matches 31; Conservative
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                                     625 QAPGLLPPQSPYPYAPOP 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                31 Q----PPQRPEAPAPQP 43
                        TYPE: amino acid
STRANDEDNESS: single
                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-246-982A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Wa:
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                 US-09-095-443-2
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RESULT 9 US-08-453-265-16

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Gaps
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Pred. No. 0.0035;
3; Mismatches 12; Indels 11;
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

Query Match

40.6%; Score 121; DB 6; Length 331;
Best Local Similarity 47.7%; Pred. No. 0.00053;
Matches 21; Conservative 2; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 QPGPQPGPQPGPQPPQPPQRPEAPAPQPP------AGRELSA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUSAN L.; MCCANDLISS, RUSS; WEI, TERN; FILPULA, DAVID
TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
; PROTEIN
                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOKNET ALGERY STEVEN R.
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-MG11987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.08;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-453-265-16
                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 331
5202236-37
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us-09-855-754b-17.rai

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1 GAKAPPAFKPAPQPGPQPGPQPGPQPPQP------PPQRPEAPAPQPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 2; Length 380;
0.0011;
ches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09227420
Patent No. 5990087
GENERAL INFORMATION:
APPLICANT: 1al, Preeti
APPLICANT: (uegler, Karl J.
APPLICANT: (corley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,587
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SUSTEMENT PERSENSON OF WINDOWS VERSION 2.0 SURRENT APPLICATION DATA: US/09/227,420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB
Pred. No. 0.001
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORIES / AGENT INFORMATION:
MAMBE: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0471 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0471 US
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: B111/10/25, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAEEEO for Windo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.6%;
Best Local Similarity 43.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
COMPUTER READMBLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                              Sequence 8, Application US/08460269C
Patent No. 6197548
GENERAL INPORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                   GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Gueglar, Karl J.
APPLICANT: Grolley, Neil C.
TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 4;
Pred. No. 9.1e-05;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6410
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-460-269C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PQPGPQPPQPPQP--QPEAPAPQP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 PQPGPQPPQPPQRPEAPAPQP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09026587
Patent No. 5912128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.6%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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US-09-026-587-4
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Floppy disk

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1 GAKAPPAPKPAPQPGPGP-----QPG-PQPPQPPQPPQRPEAPAPQPPAG 46
                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                   4 Embarcadero Center, Suite 3400
                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 494-6771
TELEEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID 0. 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                (415) 494-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 330 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                   ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-642-255-32
                                                   California
                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May Job time: 9.68375 secs
                                                                          USA
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                                                                                                                                                                                                                                  FILING DATE
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                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                              Length 380;
                                                                                                                                                                                                                                                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: CAPPELLO, Tranco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPEAPAQP
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Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                               Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bjornvad, Mads E.
APPLICANT: Bjornvad, Mariko
APPLICANT: Batakeyama, Mariko
APPLICANT: Schulein, Maritin
APPLICANT: Schulein, Maritin
APPLICANT: Schulein, Maritin
TITLE OF INVENTION: Endo-Beta-1, 4-Glucanas,
TITLE OF INVENTION: Saccharchtrix
TITLE OF INVENTION: Saccharchtrix
TITLE OF INVENTION: Saccharchtrix
CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 0812/97
EARLIER FILING DATE: 1997-07-11
EARLIER FILING DATE: 1997-07-11
EARLIER FILING DATE: 1997-07-13
                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharothrix australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09109841
Patent No. 6207436
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                  Query Match 39.6%;
Best Local Similarity 43.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.4%;
Best Local Similarity 44.2%;
Matches 19; Conservative (
                                                                  INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                             TOPOLOGY: Innear IMMEDIATE SOURCE:
                                                                                                                                                                                MEDIAL
LIBRARY: General 624964
                                                                                                                                                                                                               ; CLONE: (US-09-227-420-4
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-109-841-2
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TYPE: PRT
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Gaps

Length 330;

DB 1;

Score 113.5; I Pred. No. 0.00; 0; Mismatches

single

7, 2003, 16:57:18

FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HC

Thu May

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2 US-10-023-523-43

US-09-823-240-10

US-09-976-740-47

US-10-023-529-47

US-10-023-523-47

US-10-023-523-47

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-926-4761-34988

US-09-864-761-34988

US-09-864-761-34988

US-09-864-967

US-09-864-967

US-09-765-212-160

US-09-765-212-160

US-09-769-5238-61

US-09-298-5238-61

US-09-298-5238-61

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US-09-298-5238-61
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  117.5
114
114
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112.5
  7, 2003, 16:53:34 ; Search time 15.5911 Seconds (without alignments) 306.927 Million cell updates/sec
                                                                                                                               1 GAKAPPAPKPAPQPGPQPGP.........PQRPEAPAPQPPAGRELSAA
          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                 OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                             US-09-855-754B-17
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Мау

Run on:

298

Perfect score:

Sequence:

Scoring table:

Sequence 10, Appl Sequence 47, Appl Sequence 47, Appl Sequence 125, Appl Sequence 2, Appl Sequence 1002, Ap Sequence 1002, Ap Sequence 1002, Ap Sequence 34988, A Sequence 3644, A Sequence 3644, A Sequence 66, Appl Sequence 67, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 61, Appl

ALIGNMENTS

Sequence 7, Appli Sequence 10936, P Sequence 4, Appli Sequence 56, Appl Sequence 5, Appl

US-09-904-987-7 US-09-815-242-10936

110.5

Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

349150 seqs, 92025710 residues

Searched:

US-09-866-562-56 US-09-770-689A-5 US-09-824-574-4

APPLICANT: GUISO-MACLOUF, NICOLINE
APPLICANT: GUISO-MACLOUF, NICOLINE
TITLE OF INVENTION: PEGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS,
AND BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE DE INVENTION: BRONDETELLA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLE DATE: 2000-09-16
PRIOR FILLE DATE: 2000-05-25
SOFTWARE: PALECTION NUMBER: 50/206,969
PRIOR FILLE DATE: 2000-05-25
SOFTWARE: PALECTION VOINGER: 20. US-05-855-754-16
Sequence 16, Application US/09855754
Sequence 16, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED ö 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGRELSAA 52 Ouery Match

Ouery Match

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 52; Conservative 0; Mismatches 0; Indels ; ORGANISM: Bordetella bronchiseptica US-09-855-7,54-17 Sequence 17, Aprilication US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOUESAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE -09-855-754-17 SEQ ID NO 17 LENGTH: 52 TYPE: PRT ð 9 sequence 43, Appl Sequence 43, Appl

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Gaps

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCD_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			٠		SUMMARIES	
Result	,	& Query				
o :	Score	Match	Match Length DB	BB :	ID	Description
-	298	100.0	52	6	US-09-855-754-17	Sequence 17, Appl
7	284.5	95.5	59	6	US-09-855-754-16	Sequence 16, Appl
က	282	94.6	26	σ	US-09-855-754-18	18,
4	271	6.06	52	σ	US-09-855-754-15	Sequence 15, Appl
S	271	90.9	911	σ	US-09-855-754-4	4, A
9	267	89.6	58	σ	US-09-855-754-19	19,
7	267	89.6	922	6	US-09-855-754-6	. 9
8	250.5	84.1	49	φ	US-09-855-754-14	14
6	244	81.9	48	6	US-09-855-754-20	20,
10	236	79.2	52	6	US-09-855-754-21	21,
11	235	78.9	54	σ	US-09-855-754-22	Sequence 22, Appl
12	207	69.5	42	σ	US-09-855-754-23	Sequence 23, Appl
13	207	69.5	910	σ	US-09-855-754-5	5, A
14	186.5	62.6		σ	US-09-855-754-24	Sequence 24, Appl
15	130.5	43.8		σ	US-10-171-384-3	Sequence 3, Appli
16	121.5	40.8	1274	<u>о</u>	US-10-020-215-2	Sequence 2, Appli
17	121	40.6		10	US-09-823-240-2	'n
18	118.5	39.8	538	σ	US-09-976-740-43	Sequence 43, Appl

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CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 51; Conserv
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Matches 51; Conserv
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                                                                                                                                                   SEQ ID NO 15
LENGIH: 52
                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIESEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 30495-00500
CURRENT APPLICATION NUMBER: 102/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCTELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIX COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 0409-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPG-----PQPPQPPQPPQRPEAPAPQPPAGRELSAA 52
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 284.5; DB 9; Length 59;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 282; DB 9; Length 56;
Pred. No. 1.6e-13;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09855754 Publication No. US2020192237A1 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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91.1%;
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ilarity 88.1%;
Conservative
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Matches 52; Conserv
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Best Local Similarity
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US-09-855-754-15
                                                                                                                                                                                                                                                                SEQ ID NO 16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND STRICES, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 52;
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                                                                                                                                                                                                                                                                                                             90.9%; Score 271; DB 9;
illarity 96.2%; Pred. No. 8.3e-13;
Conservative 0; Mismatches 0
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96.2%; Pred. No. 9e-12;
ive 0; Mismatches 0
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTING VOT: 2.1
                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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APPLICANT: BOURGAUX-EUDE, CAROLINE
APPLICANT: BOURGAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERRACTINI IN BORDETELLA PERUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN FILLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN FILLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN GILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOUTHWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                               Length 49;
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                                                            DB 9;
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88.7%; Pred. No. 5.4e-11;
                                                         Score 250.5; DB
Pred. No. 2e-11;
0; Mismatches
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Live 1; Mismatches
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US-09-855-754-20
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US-09-855-754-21
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APPLICANT: BOURSAUX: EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                ; Sequence 20, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
                                                         84.1%;
90.6%;
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Best Local Similarity 88.73
Matches 47; Conservative
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Best Local Similarity 88.99
Matches 48; Conservative
                                                                                                           Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
                                                       Query Match
Best Local Similarity
Matches 48; Conserv
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US-09-855-754-20
       US-09-855-754-14
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 06/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOSTWARE: PATENTING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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Publication No. US20020192237A1

GENERAL INFORMATION:
APPLICANT: BOURSATION:
APPLICANT: BUGISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEAT

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTILE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTILE OF INVENTION: IMMUNOGENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10

PRIOR PLILING DATE: 2000-05-25
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Pred. No. 1.7e-11;
0; Mismatches 1; Indels
                                                                                                                                                                             Length 58;
                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                        Score 267; DB 9;
Pred. No. 1.7e-12;
0; Mismatches 1
                                                                                                 ORGANISM: Bordetella bronchiseptica
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; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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Best Local Similarity 87.9%;
Matches 51; Conservative
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l Similarity 87.9%;
51; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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SOFTWARE: Patentin Ver.
SEQ ID NO 14
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Best Local Similarity
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LENGTH: 922
                                                                         TYPE: PRT
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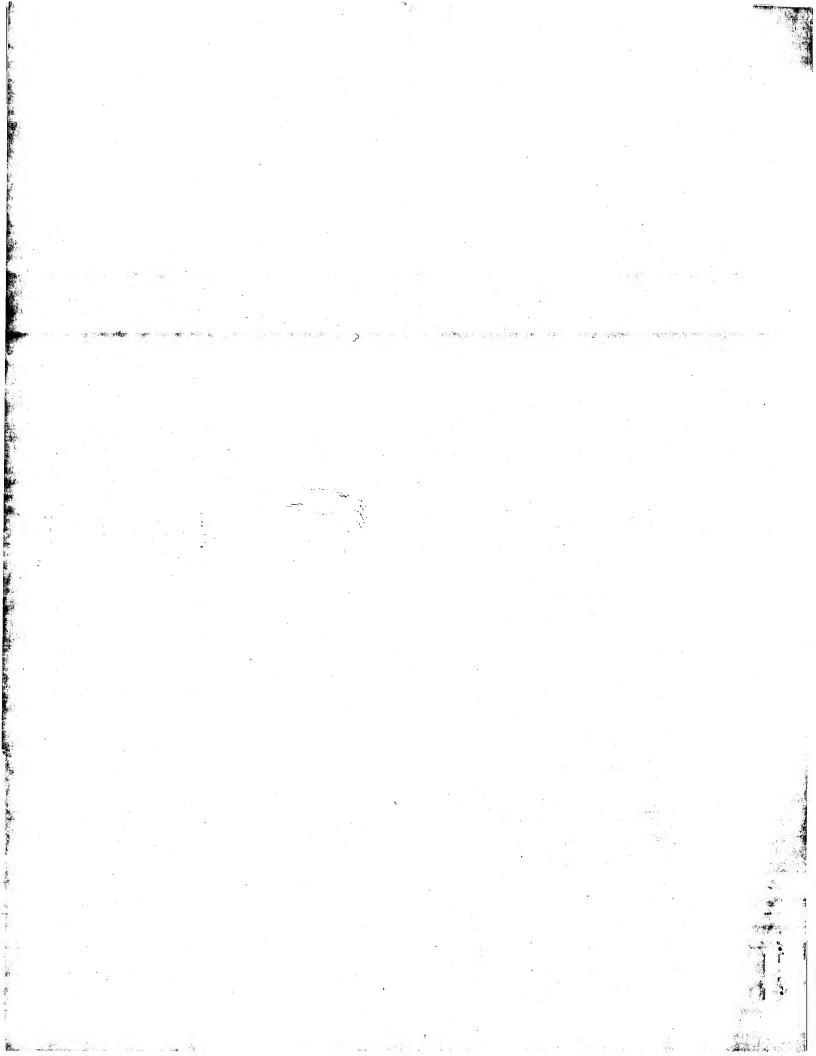
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754-24
                                                                                                                          APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09855754
Publication No. US20020192237A1
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                                                       Sequence 5, Application US/09855754
Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                         2001-09-10
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US-09-855-754-5
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78.8%;
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 78.8
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2000-05
                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
                                                                                                   GENERAL INFORMATION:
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US-09-855-754-24
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LENGTH: 910
                                  US-09-855-754-5
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARABETRUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 30495-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PREPARTICINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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2.5e-10;
ches 1;
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Pred. No. 1.6e-08;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
                                                                                                                                                        Sequence 22, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09855754
Publication No. US20020192237A1
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 85.7%;
Matches 48; Conservative
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Best Local Similarity 78.8%;
Matches 41; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 54
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                                                                                                                                 US-09-855-754-22
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                                                                TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND 1
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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APPLICANT: GUISSO-MACICUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PE
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETE
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOST
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 207; DB 9; Le
Pred. No. 2.1e-07;
1; Mismatches 0;
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Best Local Similarity 73.1%; Pred. No. 3.9e-07;
Matches 38; Conservative 1; Mismatches 0;
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Sequence 3, Application US/10171384

Publication No. US20030031680A1
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May 7, 2003, 16:41:02 ; Search time 9.7446 Seconds (without alignments) 513.008 Million cell updates/sec
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298
1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA 52
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	68K outer membrane	pertactin - Bordet	outer membrane pro	hypothetical 47.8K	cysteine-rich exte	proline-rich prote	hydroxyproline-ric	cysteine-rich exte	hypothetical prote		pherophorin-S - Vo	sulfated surface q	nuclear protein EB	hypothetical proli			chitinase (EC 3.2.	proline-rich prote	T20H2.9 protein -	protein-tyrosine-p	hypothetical prote	proline-rich prote			4	hypothetical prote	proline-rich prote	_	_
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SUMMARIES		! ! !																												
SUMM	Ω	A47675	S15204	A32560	JC2301	A48232	S16748	T07907	B48232	н83619	AE2295	T10798	A33647	S42442	A34043	WMBEH6	S21961	S51939	T17737	A86335	T14355	T24470	T17531	T10340	T48814	T17908	T02632	T17547	T17636	T17815
	DB	7	7	~	~	~	~	~	7	7	~	~	7	7	~	7	~	7	~	~	7	7	7	~	7	7	~	~	7	7
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Gaps

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1 GÄKAPPAPÄPAPQPGPGPGPGP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52

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Ouery Match 89.6%; Score 267; DB 2; Length 922; Best Local Similarity 87.9%; Pred. No. 3.6e-11; Matches 51; Conservative 0; Mismatches 1; Indels

30 125 41.9 549 2 T17525 31 125 41.9 929 2 C96623 32 124 4.6 41.8 33.2 T31611 34 124 5 41.8 348 1 OZZOMB 35 124 5 41.8 348 1 OZZOMB 36 124 6 41.6 431 2 547538 37 124 41.6 426 2 B34770 38 123.5 41.1 227 2 C29149 40 122.5 41.1 227 2 C29149 41 122.5 41.1 426 2 J01696 42 122 40.9 415 1 A34170 44 121.5 40.8 240 2 A24264 45 121.5 40.8 240 2 A24264	proline-rich prote hypothetical prote hypothetical prote circumsporozoite p proline-rich prote proline-rich prote proline-rich prote proline-rich prote proline-rich prote proline-rich prote
RESULT 1 A47675 68K outer membrane protein P.68 pertactin - Bordetella bronchiss C; Species: Bordetella bronchiseptica C; Date: 19-pec-1993 #sequence_revision 18-Nov-1994 #text_change C; Accession: A47675; B; Li, J; Fälrweather, N.F.; Novotny, P.; Dougan, G.; Charles, J; Gen. Microbiol, 138, 1697-1705, 1992 A; Title: Cloning, nucleotide sequence and heterologous expression: A47675; MulD:92407314; PMID:1527510 A; Reference number: A47675; MulD:92407314; PMID:1527510 A; Recession: A47675; MulD:92407314; PMID:1527510 A; Residues: 1-911 - (LI1) A; Residues: 1-911 - (LI1) A; Residues: 1-911 - (LI1) A; Conserreferences; GB:X54815; GB:S46416; NID:g39396; PIDN:CAA3 A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NC Query Match Best Local Similarity 96.2%; Pred: No. 1.9e-11; Matches 559 GARAPPARPARPORPORPORPORPORPORPORPORPAGREESAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	- Bordetella bronchiseptica -Nov-1994 #text_change 08-Oct-1999 Dougan, G.; Charles, I.G. heterologous expression of the protective o; PMID:1527510 NID:g39396; PIDN:CAA38584.1; PID:g39397 Done (NCBIN:113318, NCBIP:113319) 71; DB 2; Length 911; o. 1.9e-11; atches 0; Indels 2; Gaps 2; PPOR-PEAPAPOPPAGRELSAA 52
RESULT 2 S15204 Pertactin Bordetella parapertussis N.Alternate names: outer membrane.protein P70 C.Species: Bordetella parapertussis C.Date: O'Apr-1994 #sequence_revision O7-Apr-19 C.Accession: S15204; S14659 R.Li, L.J.; Dougan, G.; Novotny, P.; Charles, I. Mol. Microblol. 5, 409-417, 1991 A.Title: P.70 pertactin, an outer-membrane prote A.Reference number: S15204; MUID:91251771; PMID: A.Accession: S15204 A.Molecule type: DNA A.Residues: 1-922 cLIL> A.Cross-references: EMBL:X54547; NID:939761; PID C.Genetics: A.Gene: pro	P70 -Apr-1994 #text_change 08-Oct-1999 les, I.G. e protein from Bordetella parapertussis: clo ; PMID:2041476 61; PIDN:CAA38419.1; PID:g39762

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Gaps

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proline-rich protein - rape (fragment)
C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Species: 13-Jan-1995 #text_change 09-Sep-1997
C; Accession: S16748
R; Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991
A; Reference number: S16748
A; Reference number: S16748
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-449 - ROB>
A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
                                                    R; de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A; Title: Developmental expression of tobacco pistil-specific genes encoding novel e
A; Reference number: P00474; MUID: 93005740; PMID: 1392607
A; Accession: P00475
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 39-209 <GGL>
A; Residues: 39-209 <GGL>
A; Experimental source: ELMBL: Z14020; NID: 919918; PID: 919919
A; Experimental source: stigma, style; strain Petit Havana SR1
C; Superfamily: gluttelin
C; Reywords: cell wall: extracellular matrix; fertilization; glycoprotein
F; 1-19/Domain: slpmal sequence #status predicted <SIG>
F; 1-19/Pomain: slpmal sequence #status protein 1 #status experimental <MAT>
F; 146/Blnding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
C;Accession: T07907
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F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-446/Product: hydroxyproline-rich glycoprotein GAS28 #status predicted
                          3:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
Pezzotti, M.; Seurinck, J.; Mariani,.C.
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A) Reference number: 216207
A) Reference number: 216207
A) Raccession: T07907
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
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llarity 53.3%; Pred. No. 0.0062;
Conservative 4; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPAPKPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 145; DB 2;
Pred. No. 0.0013;
2; Mismatches 15
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Pred. No. 0.0046;
3; Mismatches 14
                             GB:L13439; NID:g310922;
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50.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 50.9
Matches 27; Conservative
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Matches 23; Conservative
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Accession: A332560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989
Proc. Natl. Acad. Scl. U.S.A. 86, 3554-3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.6
A; Reference number: A32560; MUID:89264462; PMID:2542937
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Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:D31909; GB:D1741; NID:g559718; PIDN:BAA06706.1; PID:d1007278; PJ
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May.1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48232; pQ0475; S24617
                                                                                                                                                      outer membrane protein P.69 precursor – Bordetella pertussis.
C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
A, Residues: 1-910 < CCHA>
A, Residues: 1-910 < CCHA>
A, Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A, Note: it is uncertain whether Met-1 or Met-3 is the initiator
A; Notes: it is uncertain whether Met-1 or met-3 is the initiator
C; Neywords: membrane protein
F; Neywords: squance #status predicted <SIG>
F; 35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQPPQRGPEAPAPQPPAGRELSAA 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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Pred. No. 0.0021;
5; Mismatches 11; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 47.8K protein - Pneumocystis carinii N;Alternate names: ORF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 48.8%;
1.Similarity 40.9%;
27; Conservative
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Best Local, Similarity
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46 67 **AMAT**

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A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 (; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AE2295 FX aneko, T.; Wakazaki, N.; Shimpo, S.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 206-213, 2001
A; Itile: Complete (Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MuID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Volvox carteri
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T10798
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
R; Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
A; Title: Differential targetting of closely related ECM-glycoproteins: The pherophori
A; Reference number: Z17154; MUID: 97162277; PMID: 9009264
A; Accession: T10798
A; Molecule type: nRNA
A; Molecule type: nRNA
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Datesslon: A33647
C;Accesslon: A33647
S:Ertl, H; Mengele, R.; Menzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of the cellu
A;Reference number: A33647; MUID:90094551; PMID:2689458
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                                                                                                                                                         hypothetical protein all3916 [imported] - Nostoc sp. (strain PCC 7120)
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A;Cross-references: EMBL: V07752; NID:g1655698; PIDN:CAA69032.1; A;Experimental source: strain HK 10; sub_species Nagariensis A;Note: in contrast to the other pherophorins, pherophorin-S is C;Keywords; extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 599;
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Pred. No. 0.0069;
1; Mismatches 1
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Pred. No. 0.0097;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <KUR>
A;Cross-references: GB:BA000019; PIDN:B
A;Experimental source: strain PCC 7120
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55.0%;
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Matches 22; Conserv
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Best Local Simi
Matches 22;
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A;Gene: all3916
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A.; Larbig, K.; Lim,
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A;Accession: H83619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-270 <STO>
                                                                                                                                                                                                                            C; Species: Nicotiana tabacum (common tobacco)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C; Accession: B48232; PQ0474; S24616
R; Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A; Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A; Reference number: A48232; MUID:93342083; PMID:8341705
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A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Developmental expression of tobacco pistil-specific genes encoding Reference number: P00474; MUID:93005740; PMID:1392607
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k, J.; Mariani, C.
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C;Superfamily: cell wall; extracellular matrix; fertilization
C;Reywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 #status
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Pred. No. 0.0035;
3; Mismatches 15; Indels
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A; Residues: 1-196 GWIA>
A; Cross-references: GB:L13440; NID:g310924; PIDN:AAA34060.
R; de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, Plant Cell 4, 1041-1051, 1992
                                                                                                                                                                                                              common
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Best Local Similarity 55.0%;
Matches 22; Conservative
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RiMcGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P.J. Gen. Virol. 69, 1531-1574, 1988
A:Titler The complete DNA sequence of the long unique region in the genome of herpes A:Reference number: A30083; MUID:88274327; PMID:2839594
A:Accession: I30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-3164 <MCG>
A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C;Genetics:
                                                                                                                                                                                                                                                                                                                                          Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000 Accession: 130085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3164;
                          Length 141;
                                                                      Indels
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                  Score 134; DB 2; L
Pred. No. 0.005;
); Mismatches 20;
                                                                                                                                                5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.5%; Score 132.5; DE Best Local Similarity 62.8%; Pred. No. 0.07; Matches 27; Conservative 3; Mismatches
                                            Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                        protein - human herpesvirus 1 (strain 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7, 2003, 16:55:26
               Query Match
Best Local Similarity 53.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                     Species: human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May Job time: 10.7445 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: UL36
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;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2, Accession: $42447; MUID:85063846; PMID:6209719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
roc. Natl. Acad. Sci. U.S.A. 83, 5056-5100, 1986
;Title: Nucleotide sequences of mRMAs encoding Epstein-Barr virus nuclear proteins; a
;Reference number: 842440; MUID:86259739; PMID:3460083
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: human herpesvirus 4, Epstein-Barr virus
Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A;Residues: 1-88,'PPP',89-487 <DAM>
A;Residues: 1-88,'PPP',89-487 <DAM>
A;Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                               Gaps
                                                                           A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
                                                                                                                                                                                                               ö
                                                                                                                                                          Length 485;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                      5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPP 44
                                                                                                                                                          Score 136; DB 2;
Pred. No. 0.0096;
                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubmitted to the EMBL Data Library, March 1988 Reference number: S32973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S42442; S32988; S42447
                                                                                                                                                       45.6%;
55.0%;
                                                                                                                                                  Query Match
Best Local Similarity 55.0%
Matches 22; Conservative
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-487 <FAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-487 <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear protein EBNA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
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Accession: S42442

q à

Residues:

3

Gaps

R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M. Blochem. Blophys. Res. Commun. 166, 66-73, 1990 A;Title: Presence in invertebrate genomes of sequences characterized by the repetition A;Reference number: A90159; MUID:90147742; PMID:2105723

A;Residues: 1-141 <BAK> A;Cross-references: GB:M32217

A; Accession: B34043

Molecule type: DNA

A; Accession: A34043

A; Cross-references: GB:M32217 A; Molecule type: DNA A; Residues: 59-136 <BA2>

hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)

5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR 47

Species: Owenia fusiformis :Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000 :Accession: A34043; B34043

ö

Gaps

Indels

Length 487;

Score 135; DB 2; I Pred. No. 0.011;); Mismatches 20;

45.3%; 53.5%;

Best Local Similarity 53.59 Matches 23; Conservative

δ g homo sapien arabidopsis homo sapien

mus musculu

sapien sapien saplen saplen

homo homo homo

homo sapien mus musculu

rattus norv

mus musculu

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchiseptica.";
J. Gen. Microbiol. 138:1697-1705(1992).
J. Gen. Microbiol. 138:1697-1705(1992).
J. FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
-1- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Outer membrane.
-i- DISBASE: MAY CONTRIBUTE TO THE DISBASE STATE OF WHOOPING COUGH.
-i- MISCELLANDOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CN7531,
MEDIANE-92407514; PubMed-1527510;
MIDIANE-92407514; PubMed-1527510;
MIDIANE-92407514; PubMed-1527510;
MIDIANE-92407514; PubMed-1527510;
MIDIANE-92407514; Novotno, P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERTACTIN (P.68).
POTENTIAL.
CELL ATACHMENT SITE (INVOLVED IN
ADHESION TO VARIOUS EUKARYOTIC CELL
                                 099244 P42859 n
P42859 n
P46937 P
P70315 n
P51111 n
P10323 P
                                                                                                                                                                               014514
P42858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                      003035;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54815; CAA38584.1; --
EMBL; A47675; A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; Pertactin.
InterPro; IPR003991; pertactin.
IPR0312; Pertactin.
IPR0312; PR01484; PRTACTNFAMIX.
Outer membrane; Signal; Virulence; Repeat.
INTERPROPERTACTION I
                                                                                                                                                                                                                                                                                                                                         911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 35-44
                                                                                                                                                                                                                                                    ALIGNMENTS
               WASP_HUMAN
MB11_ARATH
Z219_HUMAN
HD_MOUSE
YAP1_HUMAN
                                                                                                                                                          CDNC_HUMAN
BAI1_HUMAN
HD_HUMAN
                                                                                                                                           ACRO_HUMAN
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722
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                                                                                                                                                                                                                                                                                                                                         PERT_BORBR
116
113.5
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PERT_BORBR
arabidopsis
orgyia pseu
homo sapien
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bordetella
bordetella
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                                                                                                                7, 2003, 16:31:49 ; Search time 5.0494 Seconds (without alignments) 427.133 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA
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Q92794
P06915
P23093
P48038
P22576
Q03211
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P22670
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Q05859
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Q64467
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             GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERT_BORBR
PERT_BORPA
PERT_BORPE
APG_BRANA
SSGP_VOLCA
EBN2_EBV
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Y066_NPVOP
MOZ_HUMAN
CSP_PLABE
CSP_PLABA
ACRO_RABIT
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EXLP_TOBAC
ACRO_PIG
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PRP3_MOUSE
MOT8_MOUSE
G3PT_MOUSE
SEPA_EMENI
PARB_TRYBB
RFX1_HUMAN
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CAPU_DROME
PAR1_TRYBB
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GP1_CHLRE
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FM14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
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271 267 267 267 267 140.5 135 135 137 137 139 139 129.5 129.5 124.5 124.5 124.5

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120 120 118.5 118.5

116.5 116.5 116.5 116.5 116

Minimum DB seq Maximum DB seq

Database :

Perfect score:

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Sequence:

Scoring table:

Searched:

ADHESION TO VARIOUS EUKARYOTIC CELL

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       FTGAIN-CN2591;
MEDLINE-9123171; PubMed-2041476;
MEDLINE-91231771; PubMed-2041476;
MEDLINE-91231771; PubMed-2041476;
MEDLINE-91231771; PubMed-2041476;
P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coll.";
Mol. Microbiol. 5:409-417(1991).
MOL. Microbiol. 5:409-417(1991).
MOL. MICROBION: AGGLOTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Outer membrane. DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CELL ATTACHMENT SITE (POTENTIAL).
3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                   5
                                                                                                                                                      22
                                                                                          Score 271; DB 1; Length 911;
Pred. No. 1.6e-10;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95)
                                              3 (APPROXIMATE).
7 x 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERTACTIN (P.70).
POTENTIAL.
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                                                                                                        Pred. No. 1.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004899; Pertact_sup. InterPro; IPR003992; pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
                                                                                             90.9%;
96.2%;
                                                                      93995
                                                                                                                    51; Conservative
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S15204; S15204
PIR; S14659; S14659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONCENTRATIONS
                                                                       911 AA;
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=519;
                                                                                                                                                                                                                          PERT_BORPA
P24328;
                                                                                                                                                                                                                                                                                                                              Bordetella
                                                                       SEQUENCE
                                                                                              Query Match
                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                    REPEAT
REPEAT
                                                            DOMAIN
              DOMAIN
                                                                                                                                                                                                    RESULT 2
PERT_BORPA
                           REPEAT
                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetalla pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBGELLUTAR LOCATION: Outer membrane.
-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                                                                                                3 AA APPROXIMATE REPEATS OF P-Q-P
                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQP----GPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 52
LINES).
4 x 5 aa tandem Repeats of G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                      Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-TEN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRN OR OMFOSA.
                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                     3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                 Score 267; DB 1;
Pred. No. 2.8e-10;
0; Mismatches 1.
                                                                                                                     4 (APPROXIMATE)
9 X 3 AA APPROX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04560; AAA22980.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 264 AND 332.
MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                     95178 MW;
                                                                                                                                                                                                                      89.6%;
                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                      290
270
275
280
285
603
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                                                                                                                                                                     922 AA;
                                                                                                                                                                                                                                               Similarity
                      266
266
271
271
281
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CN2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERT_BORPE
P14283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella.
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us-09-855-754b-17.rsp

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NON_TER
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Matches
                                                                                                                                                                                                                                                                                                      RESULT 5
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          STTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATURATION.
-!- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                            POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.5%; Score 207; DB 1; Length 910; 78.8%; Pred. No. 1.2e-06; Live 1; Mismatches 0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                         X 3 AA TANDEM REPEATS OF P-Q-P. A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                           PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                       (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                         (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA.
                                                                                                                                   Outer membrane; Signal; Virulence; Repeat.
                InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94004980; PubMed-8401599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001087; Lipase_GDSL
                                                                      Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                            93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60376; CAA42924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 78.8%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus (Rape).
PIR; A32560; A32560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S16748; S16748.
                                                                                                                                                                                                                                                                                                                                                                                                                            910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                        266
2266
271
276
276
281
286
579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APG_BRANA
P40603;
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                         CHAIN
PROPEP
                                                                                                                                                       SIGNAL
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                 9
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                                                                                                                           47.1%; Score 140.5; DB 1; Length 449; 50.9%; Pred. No. 0.0079; tive 3; Mismatches 14; Indels 9;
                                                                                                                                                                                                       46
                                                                                                                                                                                                                      45.6%; Score 136; DB 1; Length 485; 55.0%; Pred. No. 0.016;
                                                                                                                                                                                             3 KAPPAPKFA-----PQPGPQPGPQPGPQPPQPPQP-PQRPEAPAPQPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                           9EFB6A3AB28EEA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50436 MW; A52216400A031421 CRC64;
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                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                  485 AA.
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1; Mismatches
                                                        BY SIMILARITY.
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28 340 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                 1/32 1.32 B)
4.28 4.28 P(
449 AA; 48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 AA;
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; |A33647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein, Su
DOMAIN 228
DOMAIN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                           Volvox carteri.
                                                                                                                           Query Match
Best Local Simi
Matches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A33647
                                                                                                                                                                                                                                                                                                                           SSGP_VOLCA
P21997;
                                                     ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EBN2_EBV
ID EBN2_EBV
AC P12978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Gaps

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Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bresence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurlne."
Blochem. Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                      Length 141;
                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                58 POLY-PRO.
116 H-T-H MOTIF (POTENTIAL).
1141
15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2941 PQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPG 2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID-10299;
                                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 PAPKPAPQPGPQPGPQP-PQP-PQPPQRPEAPAPQPPAG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 132.5; DB 1;
Pred. No. 0.098;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134; DB 1;
Pred. No. 0.0086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Large tegument protein (Virion protein UL36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą.
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                          \begin{array}{c} \operatorname{Hypothetical\ protein;\ DNA-binding.} \\ \operatorname{NON\_TER} & 1 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; I30085; WMBEH6.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                  45.0%;
ilarity 53.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14112; CAA32311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Query Match

Best Local Similarity 62.00,

Best Local Similarity 62.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                             141 AA;
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEGU_HSV11
                                                                                                                                                                                                                                                   DNA_BIND
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149; MEDLINE-84270667; PubMed-6087149; Baer R. Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Harfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G., "Na sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91202599; PubMed-1850028; Cohen J.I., Wang F., Kleff E.; Cohen J.I., Wang F., Kleff E.; Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation."; J. Virol. 65:2545-2554(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90266473; PubMed=2161150;
Petti L., Sample C., Kieff E.;
Subuculear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V01555; CAA24877.1; ALT_INIT.
TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Owenidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 X 2 AA TANDEM REPEATS OF R-G. DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.3%; Score 135; DB 1; Length 487; 53.5%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.018;
0; Mismatches 20; Indels
                                                                                                    Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNa viruses, no RNa stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PPAPKPAPQPGPQPGPQPPQPPQPPQRPEAPAPQPPAGR 47
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPRO_OWEFU STANDARD; PRT; 141 AA. P21260; P21261; A. P21260; P21261; Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-WAY-1995 (Rel. 32, Last annotation update) Hypothetical proline-rich protein (Fragment). Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 AA; 52544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: PHOSPHORYLATED.
                                                              EBNA-2 nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                   NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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DOMAIN

Matches

ò q YPRO_OWEFU

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of

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Gaps

ä;

O9LNT8;

0932.14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBDAIT: Associates with GP2 and GP3.
-1- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                     "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding cell wall hydroxyproline rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-! FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
                                                                                                                                                                       Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                       Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                        OFFQ6; Q03927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91017504; PubMed-1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 130.5; DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 130...,
Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 APPAPK-PAPQPGPQPGPQPGPQP-----PQPPQPPQRPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (POS 6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                      PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF309494; AAG45420.1; -. BMBL; MS8496; AAA69706.1; ALT_SEQ. GycosuiteDB; O9FP06; -. InterPro; IPR002965; P_rich_extensn. InterPro; IPR003862; Pistil_extensin. BRINTS; PR01217; PRICHEXTENSIN. PRINTS; PR01218; PSTLEXTENSIN.
                            PRT;
                                                                                                                                                                                                                                                       MEDLINE-21159092; PubMed-11258910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54219 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.1%;
                                                                                                                                                          Chlamydomonas reinhardtii.
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                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259
299
399
455
455
855
AA;
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                                                                                                                                                                                                         NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
SIGNAL
                            CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
CARBOHYD
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             GP1_CHLRE
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RESULT 9
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534 AA.

PRT;

STANDARD;

APG_ARATH

RESULT 10 APG_ARATH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin. C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,
Dunn P., Etqi P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Coldsmith A.D., Haas B., Hansen N.F., Hudhes B., Hulzar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Langin-Hoopef S., Lee A., Lee J.M., Lee J.M., Karai J. H., Li Y.-P.,
Lin Ki, Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Militscher J., Miranda M., Nguyen M., Nterman W.C., Osborne B.I.,
Ran G., Peterson J., Pham P.K., Rizzo M., Soney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome I of the plant Arabidopsis
              01-FEB-1995 (Rel. 31, Greated)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter:specific proline rich protein APG precursor.
APG OR ATIG20130 OR T20H2.9.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; wagnoliophyta; eudioctyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huizar L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATURATION.
-1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
-1- CAUTION: Ref. 2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN—cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the SSP consortium (salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-1-TISSUE SPECIFCITY: FOUND IN SPOROHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-1-DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                             MEDLINE-94004980; PubMed-8401599;
Roberts M.R.; Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Darpet J., Scott R.;
Roberts M.R.; Scott R.;
Rametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC022472; AAF79900.1; ALT_SEQ
EMBL; AY058847; AAL24235.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Columbia;
MEDLINE-21015719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60377; CAA42925.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                           NCBI_TaxID=3702;
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                                                                                                                                                                                   ä
                                         ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 806-875 FROM N.A.
MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ahrens C.H., Rohrmann G.F.; The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                    083949; Q65364; O10323; Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
                                                                                                                                                      Score 130; DB 1; Length 534; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene essential for Orgyia pseudotsugata baculovirus DNA replication.";
                                                                                   S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                             43
                                                                                                                                                                                                            3 KAPPAPKPAPQPGPQPGPQPPQ--PPQPPQRPEAPAPQP
                                                                                                                                                                     Pred. No. 0.039
2; Mismatches
 PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97271300; PubMed-9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seudosugata.";
. Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 91 PC
875 AA; 98603 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U75930; AAC59070.1; -.
                                                                                                                                                      43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U39145; AAB04047.1; -. EMBL; D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                               325
58007 1
                                                                                                                                                                                24; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
DOMAIN 86 9
                                                                                                                           534 AA;
                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pseudosugata.
                                                                                                                                                                                                                                                                                                           YOGG NPVOP
PROSITE; Signal.
                                         CHAIN
ACT_SITE
                                                                     ACT_SITE
CONFLICT
                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                        Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Machine Postory (1) Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; The translocation t(8;16)(pl1;pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).

I. FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.

I. SUBCELLUTAR LOCATION: Nuclear.

I. DISEASE: PARTICIPATES IN A T(8;16)(P11;P13) CHROMOSOMAL TRANSLOCATION THAT PRODUCES A MOX-CEP CHIMAERA OBSERVED IN THE M4/AB SUBTYPE OF ACUTE MYELOID LEUKEMIA.

I. SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocation; Zinc-finger; Repeat;
        Length
                                                             Indels
                                                                                                                                                103 PPQPPPDQPQQPQQPPQQPPQQPPQQPPQQPPQQP-PQPP 145
                                                                                                                     44
                                                                                                               5 PPAPKP----APQPGPQPGPQPPQPPQPPQRPEAPAPQPP
Score 129.5; DB 1;
Pred. No. 0.059;
1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                 2004 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR00217; MOZ_SAS.
InterPro; IPR0019465; Znf_PHD.
Pfam; PF00628; PHD; 2.
Pfam; PF00628; NAZ_SAS; 1.
SWART; SM00526; H15; 1.
SWART; SM00249; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-96376968; Pubmed-8782817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01359; ZF_PHD_1; 1. PROSITE; PS50016; ZF_PHD_2; 2. Proto-oncogene; Chromosomal tra
43.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U47742; AAC50662.1;
Genew; HGNC:13013; ZNF220.
MIM; 601408; -.
                                                          26; Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1150
1242
1302
1414
Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear prote
                                                                                                                                                                                                                                                                                                                 MOZ_HUMAN
Q92794;
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Matches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACRO_RABIT
P48038;
                                      CSP_PLABA
P23093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACRO_RABIT
                               CSP_PLABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                      RESULT 14
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                         BREAKPOINT FOR TRANSLOCATION TO FORM MOZ-CBP.
                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIRCUMSPOROZOITE PROTEIN.

13 X B AA TANDEM REPEATS.

16 X AA TANDEM REPEATS.

F E8068A6D11D9551B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 339;
                                                                 Length 2004;
                                                                                                                                                                                                                              Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%; Score 124.5; DB 1; Length 58.1%; Pred. No. 0.061; tive 1; Mismatches 11; Indels
                                               9FFBBAC3792854BA CRC64;
                                                                                     13; Indels
                                                                                                                  1652 PPPPPQQPQP-PPPQPQPAPQPPPPQQQPQQQPQPQPPPPP 1695
                                                                                                      5 PPAPKPAPQPGPQPGPQPPQPPQPPQ-----RPEAPAPQPP 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 PAP----KPAPQPGPQPGPQPGPQPPQPPQRPEAPAPQP 43
                                                                 Score 125; DB 1;
                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                       339 AA
                                                                            Pred. No. 0.2;
                                                                                    2; Mismatches
          GLN/PRO-RICH.
MET-RICH.
                                                                                                                                                                                                                       Circumsporozoite protein precursor (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A25083; OZZQMB.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                               2004 AA; 225054 MW;
                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00090; tsp_1; 1.
PRINTS, PR0130; CRMSPRZOITE.
SWART; SW00209; TSD1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 238
339 AA; 37138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; Sporozoite; Repeat;
                                                                 41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M14135; AAA29577.1; -.
                                                                                    24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339
196
238
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                       VERTEBRATE HOST)
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
1593
1643
1897
1546
                                                                                                                                                                                                                                                  NCBI_TaxID=5821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A25083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                       CSP_PLABE
P06915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
                                               SEQUENCE
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                                                                Query Match
                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
DOMAIN
DOMAIN
DOMAIN
SITE
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Matches
                                                                                     Matches
                                                                                                                                                              CSP_PLABE
                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATE HOST).

-1- MISCELLEANEDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE |THE SURFACE ANTIGEN OF THE ORGANISM.

-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
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                                                                                                                                                                              Eukaryota; Alyeolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_raxID=5823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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13 X 8 AA REPEATS.

17 X 2 AA REPEATS OF P-Q.

0EC240EE35681AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 PAPPOGNÄNPQPQPRPQPQPQPQPQPQPQPQPPPQ-PQPQP
                                        01-NOV_1991 (Rel. 20, Created)
01-NOV_1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.062;
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01-FEB-1996 (Rel. 31, Last sequence update)
101-FUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.8%; Score 124.5;
                                                                                                                          Circumsporozolite protein precursor (CS).
Plasmodium berghei (strain Anka).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X17666; CAA35608.1;
PIR, S07873; OZZOBK.
INTERPLO: IPRO003067; Cremsprzoite.
INTERPLO: IPRO0084; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.7 AA; 37776 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
STANDARD;
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                                                                                                                                                                                                          CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                         SEQUENCE FROM N.A.
STARIN-New Zealand white; TISSUE-Testis;
STARIN-New Zealand white; TISSUE-Testis;
MEDLINE-94368861; Pubmed-e086468;
Richardson R.T., O'Rand MG;
"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
preproacrosin-related cDNA.";
Blochim. Blophys. Acta 1219:215-218(1994).
I- FUNCTION: ACROSIN IS THE MAJOR PROTEACE OF MANMALIAN SPERMATOZOA.
II SA SERINE PROTEACE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
IS A SERINE PROTEACE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.8%; Score 124.5; DB 1; Length 431;
43.6%; Pred. No. 0.072;
Live 0; Mismatches 20; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROSIN LIGHT CHAIN (BY SIMILARITY)
ACROSIN HEAVY CHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCHAC. . ) (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AKAPPAPKPAPQPGPQ------PGPQPGPQPPQPPQPPQRPEAPAPQPPA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C015A4E0BC0C668 CRC64;
                                                                                                                                                                                                                                                       DISULTINE BONDS.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; SO1.223; --
InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 43.6 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA;
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ACT_SITE
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Search completed: May 7, 2003, 16:48:09 Job time: 6.0494 secs

Run on:

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Oi3305 pneumocysti
Q9sbml volvox cart
Q9p944 pneumocysti
Q9rcx9 streptomyce
             09k5g1 bordetella
09alp7 bordetella
09alp5 bordetella
09alp6 bordetella
09ax8 bordetella
09s6m9 bordetella
09s6m9 bordetella
09s6n1 bordetella
09s6n1 bordetella
09s7s bordetella
06925 bordetella
06927 bordetella
069198 bordetella
069198 bordetella
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008194 nicotiana t
093197 bordetella
096vjl pneumocysti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE_20359389; PubMed=10899896;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertusis, abrdetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250085; CAB76439.1; -.
InterPro; IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQR-PEAPAPQPPAGRELSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNI-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 287.5; DB 2;
Pred. No. 1.8e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                             069257
QBRSU0
Q9UVD1
Q9UR16
Q01823
Q96V14
Q91LE9
Q081197
Q931L97
Q8W158
Q13305
                                                                                                                                                                                                                                                                                                                Q9SBM1
Q9P944
                                     Q9ALQ0
Q9ALP5
                                                             Q9AIX8
Q9S6M9
                                                                                                                                     088143
093L98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.1%;
Matches 52; Conservative
                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; |PF03212; Pertactin; 1.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE
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186.5
149.5
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145.5
145.5
145.5
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09AL04
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bordetella
                                                                   7, 2003, 16:38:52; Search time 26.5758 Seconds (without alignments) 403.166 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                 298
1 GAKAPPARKPAPQPGPQPGP......PQRPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09alq4
09k5g9
09k1x9
09k1x9
09k5h3
09k5h5
09k5h7
09k5h9
09k5h9
09k5h9
09k5h9
09k5h9
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                                                                                                                             671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09ALQ4
09K5G9
09KJX9
09K5H3
09K5H3
09K5H3
09L4E2
09K2H7
09K5H7
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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sp_organelle:*
                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                      US-09-855-754B-17
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Match Length
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Perfect score:
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22

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1 GAKAPPAPKPAPQPGPGPGPGPGPGPPQPPQPPQPPGRPAPAPAPAPGPPGRELSAA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQ----RPEAPAPQPPAGRELSAA 52
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                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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EMBL; AVO07265; AAG38441...
InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR00265; P.rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 282; DB 2; Length 12
Pred. No. 5.7e-17;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156773; AAF82397.1;
InterPro; IPR004699; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Ffam; PF03212; Pertactin; 1.
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122 Aa; 12395 MW; BED00966A40FF994 CRC64;
                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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MEDLINE-21117018; PubMed-11179374;
Register K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01217; PRICHEXTENSN.
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.1%;
Matches 51; Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                             NCBI_TaxID=518;
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NON_TER
SEQUENCE
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NON_TER
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                                                                                                        RESULT 4
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250087; CAB764411;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 96.5%; Score 287.5; DB 2; Length 215; Best Local Similarity 98.1%; Pred. No. 3.2e-17; Matches 52; Conservative 0; Mismatches 0; Indels 1
                                                                                                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.6%; Score 282; DB 2; Length 111; 91.1%; Pred. No. 5.3e-17; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            Register K.B.,
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL, AY007263, AAG38439.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact.
InterPro; IPR004899; Pertact.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5C21D45CF784B4AE CRC64;
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                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
     215 AA.
     PRT;
                                                                                                                                                                                                                                            STRAIN=S010328;
MEDLINE=21117018; PubMed=11179374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
22327 MW;
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PRINTS; PRO1217; PRICHEXTENSN.
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PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03212; Pertactin; 1.
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                          Pertactin (Fragment).
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                       NCBI_TaxID=518;
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
09ALQ4
09ALQ4;
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InterPro; IPR002965; P_rich_extensn.
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SEQUENCE FROM N.A.
STRAIN=B14;
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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NCBI_TaxID=518;
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SEQUENCE
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MEDLINE-20359389; PubMed=10899896;
MEDLINE-20359389; PubMed=10899896;
MEDLINE-20359389; PubMed=1080 N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immuu. 68.4815.4817 (2000).
EMBL; AJ250083; CAB76437.1; ...
Interpro; IPR004899; Pertact_sup.
Interpro; IPR004899; P_ICA_extensn.
Pfam; PF03212; Pertactin; IPROPERTENSN.
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250081; CAR76445.1; -.
InterPro: IPR004899; Pertact_sup.
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                          DB 2; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368C142508D77057 CRC64;
                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 274; DB 2;
Pred. No. 2.5e-16;
0; Mismatches 0
                                    Score 282; DB 2;
Pred. No. 1e-16;
1; Mismatches
                                                                                                                                                                                                                                                                   115 AA
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26107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.9%;
86.7%;
                                        94.6%;
91.1%;
                                  Query Match
Best Local Similarity 91.1
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 86.7 ies 52; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella.
SEQUENCE
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Q9K5H5;
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Q9K5H5
                                                                                                                                                                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Prcteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001). EMBL; ANOU271; AA538447.1; ... InterPro; IPRO04899; Pertactin. InterPro; IPRO04899; Pertact.sup. InterPro; IPRO02965; P.rich_extensn.
                                                                107 107
107 AA; 11036 MW; 1AC13209D0238107 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                 Query Match 90.9%; Score 271; DB 2; 1
Best Local Similarity 96.2%; Pred, No. 4.2e-16;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 271; DB 2,
Pred. No. 7e-16;
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MEDLINE-21117018; Pubmed-11179374;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
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96.2%;
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PRELIMINARY;
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                                                                                                                           SEQUENCE FROM N.A.
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Bordetella.
NCBI_TaxID=518;
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertusis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815.4817(2000).
EMBL; A.7550089; CAB76443.1; ---
InterPro; IPR004899; Pertact_sup.
InterPro; IPR0049955; P. InterPro; IPR005955; P. InterPro;
                                                                  "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ245927; CAB82512, 1.

InterPro; IPR003992; pertactin.

InterPro; IPR003991; pertactin.vir.

InterPro; IPR004899; Pertact.sup.

Pfam; PF03212; Pertact.sup.

PROM PF03212; Pertact.sup.

PRINTS; PR01484; PRRACTINEMLY.

SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
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Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.,
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 911;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.9%; Score 271; DB 2; I 96.2%; Pred. No. 2.3e-15; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.6%; Score 267; DB 2;
87.9%; Pred. No. 9.3e-16;
1ve 0; Mismatches 1
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Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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Matches
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Boursaux-Ende C., Guiso N., "Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
                           Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250077; CAB76431.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                 Score 250.5; DB 2; Length 104;
Pred. No. 2.1e-14;
0; Mismatches 0; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TV-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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llarity 90.6%; Pred. No. 2.1e-14;
Conservative 0; Mismatches 0;
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MEDLINE=20359389; PubMed=10899896;
MEDLINE-20359389; PubMed-10899896;
                                                                                                                                                                           InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
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Best Local Similarity 90.6%;
Matches 48; Conservative
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SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=518;
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                                                                                                        Kell D.J., Fenwick B., "Warlability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ell D.J., Fenwick B.; variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.1%; Score 250.5; DB 2; Length 115; llarity 90.6%; Pred. No. 2.2e-14; Conservative 0; Mismatches 0; Indels 5
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR156772; AR462396.1;
InterPro; IRR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                      115 115
115 AA; 11693 MW; FA3A76596F7097EB CRC64;
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115 AA; 11705 MW; EIABD4D347D20652 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 2.2e-14;
0; Mismatches 0;
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INTERPRO; IPRO0A899; Pertact_sup.
INTERPRO; IPRO02965; P_rich_extensn.
Pfam; PF03212; PertactIn; 1.
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Best Local Similarity 90.6%;
Matches 48; Conservative
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PRN.
                                                                                                                                                                                 amino acid repeats.
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                                                                 SEQUENCE FROM N.A.
                   NCBI_TaxID-518;
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SEQUENCE
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Kell D.J.,
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SEQUENCE
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Q9AHP0
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Gaps
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Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                      Genetic and Phenotypic Heterogeneity in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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84.1%; Score 250.5; DB 2;
Best Local Similarity 90.6%; Pred. No. 3.5e-14;
Matches 48; Conservative 0; Mismatches 0;
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Interpro; IPN004899; Pertact_sup.
Interpro; IPN002965; P.1ch_extensn.
Pfam; PF03212; Pertactin; I.
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Job time: 27.5758 secs
                                                                                                                                       STRAIN-MBORD(31;
MEDLINE-21117018; PubMed-11179374;
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PRINTS; PR01317; PRICHEXTENSN.
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Peptide 683 derive

Human polypeptide Human polypeptide Human polypeptide Drosophila melanog

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Herbicidally activ Bioadhesive precur Sequence of a bioa

Drosophila melanog Human low density Rabbit low density

Arabidopsis thalia

Streptococcus pneu Ser-Pro-Pro-Pro Drosophila melanog

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Database

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    B. bronchiseptica strain II-5 pertactin outer membrane protein region II.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
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                                                                                                                                                                                                                                                                                                                      ABG27250
AAR28150
AAG49660
AAG42036
ABG21919
AABB3838
AAAB3194
AAG22949
AABB4403
AABB2406
AABB2807
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130.5
130.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
133.5
133
132.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16197
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
Bordetella paraper
Bordetella paraper
Pertactin antigen
B. bronchiseptica
Pertactin antigen
prin proteins. Bor
                                                                                                    7, 2003, 16:31:28; Search time 29.0971 Seconds (without alignments) 256.453 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
| SIDSZ/gcgdata/geneseqg-emb1/AA1991.DAT:*
| SIDSZ/gcgdata/geneseqg-emb1/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                  US-09-855-754B-18
322
I GARAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
           5.1.4_p5_4578
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
           GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR25578
AAE16185
AAR14321
AAE16196
AAE16194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16195
AAE16198
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AAR26503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE16197
                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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60
60
922
922
922
922
923
911
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96.3
94.1
94.1
991.3
90.5
88.5
                                                                                                         May
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310 303 303 303 294 291.5 285 285

45067800

Score

Result S ï

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fourter membrane protein) or their fragments. Pertactin present invention or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens an impaint issue and human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                               present invention relates to Bordetella bronchiseptica pertactin
Claim 26; Fig 1c; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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ö
                             Gaps
                             ö
  Length 56;
                             Indels
100.0%; Score 322; DB 23;
100.0%; Pred. No. 1.2e-17;
ive 0; Mismatches 0;
                             ö,
 Query Match
Best Local Similarity 100.
Matches 56; Conservative
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56 ŏ g

RESULT

AAE16195

AAE16195 standard; peptide; 60 AAE16195;

26-MAR-2002 (first entry)

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B. bronchiseptica strain II-3 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fullds, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                        B. bronchiseptica strain II-6 pertactin outer membrane protein region
                                                                                                                   Gaps
                                                                                                                                                                    1 GAKAPPAPKPA----PQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPGRELSAA 56
 B. bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                    Length 60;
                                                                                                                   Indels
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 sequence is
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0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.1%; Score 303; DB 23; 94.8%; Pred. No. 3.2e-16;
                                                                                  Score 310; DB 23;
                                                                                                  Pred. No. 9.9e-17;
0; Mismatches
Bordetella in a material. The present sequer pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boursaux-eude C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                   AAE16198 standard; peptide; 58
                                                                                  96.38;
                                                                                                  93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica.
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.8 Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 AA;
                                                  60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISNI ( dSNI)
                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                      AAE16198;
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                                                    Sequence
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                                                                                  Query Match
                                                                                                     Best Local
                                                                                                                   Matches
                                                                                                                                                                                                                                     RESULT 3
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 8.888
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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;

therapy; antiblotic; antibacterial; p.70.

Bordetella parapertussis.

254..304 /note= "Pertactin region I" 564..621 /note= "Pertactin region II"

Location/Qualifiers 254..304

Key Region Region

Bordetella parapertussis pertactin outer membrane protein, p.70.

AAE16185 standard; Protein; 922 AA.

26-MAR-2002 (first entry)

AAE16185;

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RESULT 5
AAE16185
                                               A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kv. Antigenic fragments of the protein will be useful in developing an accillular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                         Location/Qualifiers
35..643
/label- P70
260..262
/note- motif associated with cell-cell adhesion
266..285
/note- "contains 5 direct. tandom recorded."
                                                                                                                                                                                                                                                                                                                                                      575.612
//note="contains 9 direct repeats of Pro-Gln-Pro"
712.714
/note="motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acellular vaccine for immunisation against whooping cough -comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                           Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 303; DB 13; Length 922;
Pred. No. 2.3e-15;
0; Mismatches 1; Indels
                                                                                                                                            Bordetella parapertussis P95 antigen precursor.
                                            AAR25578 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.1%;
Best Local Similarity 94.8%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90GB-0027901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-GB02302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WELL ) WELLCOME FOUND LID.
                                                                                                           (first entry)
                                                                                                                                                                                                           Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-250033/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ26509.
                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1990;
                                                                                                           08-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9211292-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                             AAR25578;
                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                         Region
             RESULT 4
AAR25578
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Suiso_maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

N-PSDB; AAD26442

(INSP') INST PASTEUR

23-MAY-2001; 2001WO-EP06457 25-MAY-2000; 2000US-206969P

WO200190143-A2. 29-NOV-2001. Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

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                                                                        Couter membrane protein or their fragments. Pertactin (PRN) is used as an used to detect Bordetella antiques in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques of in affinity chromatographic columns. Pertactin is useful as antiques an implicitly antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiques can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                     The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 303; DB 23;
Pred. No. 2.3e-15;
0; Mismatches 1;
Disclosure; Page 34; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR14321 standard; Protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%;
94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.8°
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR14321;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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g ð

(first entry)

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B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
                         AAE16196 standard; peptide; 53 AA
                                                       26-MAR-2002
                                         AAE16196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16194
                  AAE16196
            RESULT
                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                 Pichla microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 294; DB 12; Length 922; Pred. No. 1.1e-14; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
                            Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1C; 38pp; English
                                                                                276..280
/label= ren
                                                                                               281.285
                                                                                                                                          583..585
/label= rc
                                                                                                                                                                                                                                                                                                                              (WELL ) WELLCOME FOUNDATION LTD
                                                                                                                                                                                             repeat
                                                                                                                                                                                                                                              610..612
/label= repeat
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Best Local Similarity 93.2%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                               90GB-0007416.
                                                                                                                                                                                                                                                                                                91WO-GB00487
                                                                                                                                                                     586..588
/label= re
20-JAN-1992 (first entry)
                                                                                                                                         79..581
Tabel= re
                                                                                                                                                                                                  592..594
/label=_re
                                                                                                                                                                                                                595..597
/label= re
                                                                 266..270
/label= r
                                                                                                                           75..577
Tabel- re
                                                                                                                                                                                     591
                                                                                                                                                                                                                               98..600
                                           Bordetella parapertussis.
                                                                                ..275
                                                                                                                                                                                                                                        label-
             Pertactin antigen P.70.
                                                                                                                                                                                     189..5
                                                                                                                                                                                                                                                                                                                                             Clare JJ, Romanos MA;
                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-325214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 AA;
                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ14320
                                                                                                                                                                                                                                                                                                 28-MAR-1991;
                                                                                                                                                                                                                                                                                                                02-APR-1990;
                                                                                                                                                                                                                                                                                   17-0CT-1991.
                                                                                                                                                                                                                                                                    W09115571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                           Key
Peptide
                                                                                                                                                                                                                 Pept1de
                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                               Peptide
                                                                                Peptide
                                                                                              Peptide
                                                                                                             Peptide
                                                                                                                            Peptide
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal calls, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.5%; Score 291.5; DB 2 Best Local Similarity 94.6%; Pred. No. 2.1e-15; Matches 53; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                                                                                                                                                          23-MAY-2001; 2001WO-EP06457
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                                                                                                   Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                          (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guiso-maclouf N,
                                                                                                                                                       WO200190143-A2.
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQP---PQPPQPPQRPPGRPAPAPGPPAGRELSAA 56

564

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28-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                     17-0CT-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR26503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Protein
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                                                                                                                                           Peptide
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(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 285; DB 23;
Pred. No. 6.4e-15;
0; Mismatches 0
therapy; antiblotic; antibacterial; region II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR14320 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                     Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Fig 1c; 47pp; English.
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/label= repeat
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574..576
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578..580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat
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illarity 92.9%;
Conservative
                                                                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                         25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica.
                                                         Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271..275
/label- re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570..572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing
pertactin in Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pertactin antigen P.68
                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                  Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AA;
                                                                                                         40200190143-A2
                                                                                                                                                               29-NOV-2001
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Peptide
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pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertusais P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQRPGREAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 285; DB 12; Length 911;
Pred. No. 5e-14;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia microorganisms are transformed for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Repeat_region
260.262
/label= RGD_tripeptide
701.703
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               581..583
/label= repeat
584..586
/label= repeat
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                                                                                                                                                                                                                                                                                                                                                                        (WELL !) WELLCOME FOUNDATION LTD
/label= repeat
                                                                                                                          repeat
                                                                                                                                                               /label= repeat
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92.9%;
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/label= P.68
                                                                                                                                                                                                                                                                                           91WO-GB00487
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                                                                                                587..589
/label= re
599..601
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266..279
/label= Re
570..589
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                                                                                                                                                                                                                                                                                                                                                                                                                 Clare JJ, Romanos MA;
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N-PSDB; AAQ14319.
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of

/label- RGD_tripeptide

27-MAR-1992; 27-MAR-1991;

Charles IG;

PYNXNX X BYN X BYN

WO9217587-A 15-0CT-1992

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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
                                                                                                                                pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides containing polymorphisms of the repeated regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Length 911;
                                                                                                                                                                                                                               The present invention relates to Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285; DB 23
Pred. No. 5e-14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                         Disclosure; Page 28; 47pp; English.
  ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
  Boursaux-eude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . AAE16193 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.5%;
Best Local Similarity 92.9%;
Matches 52; Conservative
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                                                                                                                           Bordetella
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                                       WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 AA;
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16193;
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88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.68 antigen is formed by alternative cleavage of this protein.
P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRPQPPQRDPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                                                                      DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence given is the P.94 antigen from B. bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 285; DB 13; Length 911;
Pred. No. 5e-14;
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/note= "Pertactin region I"
759..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE16183 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.5%;
92.9%;
                                                                                                                                                                 91GB-0006568
                                                                                                                       92WO-GB00561
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                                                                                                                                                                                                                                                                                        WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entire P.94 sequence
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Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      911 AA;
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26-MAR-2002

AAE16183;

RESULT 11 AAE16183

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Sequence Query Match Pertactin;

Key Region Region

29-NOV-2001

ij,

Gaps

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vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, alycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bronchiseptica strain II-7 pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56
                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                  Length 49;
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                                                                                                                                                                                                                                                                DB 23;
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                                                                                                                                                                                                                                                              Score 264.5; DB
Pred. No. 2e-13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16199 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Fig 1c; 47pp; English.
                                                                                                                                                                                                                                                              82.1%;
87.5%;
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Matches 49; Conserv
                                                                                                                                                                                                                           49 AA;
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48 AA;

sequence

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                                                                                                                                                                                                                                                                   	exttt{B.} bronchiseptica strain II-	exttt{B} pertactin outer membrane protein region II.
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                                                                                                                                                                                                                                                                                                  Pertactin; P_R^{(N)}; outer membrane protein; vaccine; Bordetella infection; therapy; antibotic; antibacterial; region II.
                               Gaps
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                                                                              1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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   Length 48;
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                                 Indels
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Pred. No. 7.7e-13;
0; Mismatches 2;
Score 258; DB 23;
Pred. No. 6.1e-13;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guiso-maclouf N, Boursaux-eude
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                                                                                                                                                                       AAE16200 standard; peptide; 52
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80.1%;
85.7%;
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86.0%;
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                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica
                               Conservative
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Best Local Similarity
Matches 49; Conserv
               Similarity
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                               48;
Query Match
Best Local S
Matches 48
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AAE16201
ID AAE16:
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AAE16200
ID AAE16
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 4jycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological filuids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

    B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
                                                                                                                                                                                                                                                                                                                                                                                                                          Guiso-maclouf N, Boursaux-eude C;
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                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                           Bordetella bronchiseptica,
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Gaps 1 GAKAPPAPRPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56 5 Indels Score 256; DB 23; Pred. No. 9.4e-13; 0; Mismatches 5; 49; Conservative Query Match Best Local Similarity Matches 49; Conserv ò

79.5%; 87.5%;

54 AA;

Sequence

Length 54;

Search completed: May 7, 2003, 16:47:07 Job time: 29.0971 secs

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Sequence

-09-535-008-63

App

US-09-026-587-4 US-09-227-420-4

5352575-5 5470718-4 ALIGNMENTS

Sequence 6 Sequence 5 Sequence 7 Sequence 7 Sequence 6 Sequence 6 Sequence 7 Sequence 2 Sequence 2 Sequence 4 Sequence 4 Sequence 4 Sequence 4 Sequence 4

US-09-535-008-61 US-09-535-008-67 US-09-535-008-72 US-09-535-008-72 US-09-535-008-69 US-09-535-008-69 US-09-535-008-73 US-09-535-008-73 US-09-535-008-73 US-09-535-008-73 US-09-535-008-73 US-09-179-588-66

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CITY: ARLINGTON STATE: VA
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Patent No. 5
Patent No. 5
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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
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                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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3-08-453-265-16
3-09-095-443-2
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5-09-041-886-28
5-09-041-886-29
5-09-041-886-30
5-09-041-886-31
5-08-246-982A-6
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-08-556-419-21
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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322
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Match
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337.7.7
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Maximum DB
                                                                                                                                                                                                                                                Sequence:
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                                                                                                                               Run on:
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Gaps
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                                                                                         APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
CORPATER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET UNBER: 37,067
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan,
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 303; DB 4;
Pred. No. 4.7e-19;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 243-6333 INFORMATION FOR SEQ ID NO: 6:
RESULT 1
US-08-460-269C-6
Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.18;
                                                                                                                                                                  SEQUENCES: 17
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Best Local Similarity 94.8
Matches 55; Conservative
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US-07-609-716-65

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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPQPPQRQPEAPAPQPPAGRELSAA 56
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STREET: 1100 No. 5589384th Glebe Road, 8th Floor
CTTY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       Score 210; DB 4;
Pred. No. 4.1e-11;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                               NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UN-1992
APPLICATION NUMBER: G 1253.4
FILING DATE: 11-UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LIPSCOMBE, Martin J
APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, lan G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & Vanderhye, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08237716
Patent No. 5589384
                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                            65.2%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wilson, Mary J
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.2
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECUMANE: 703-62-
TELEPHONE: 703-616-4100
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TOPOLOGY: linear
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Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
TILLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEARS
                                                                                                                     APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.5%; Score 285; DB 4; Length 911; 92.9%; Pred. No. 1.6e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                   Sequence 4, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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Best Local Similarity 92.99
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                         ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22201
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                                   US-08-460-269C-4
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APPLICANT: Kandil, Ali
APPLICANT: James, Olive A
APPLICANT: James, Olive A
APPLICANT: Klein, Michel H

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GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Luyao, Mabel P.
APPLICANT: Luyao, Mabel P.
APPLICANT: Gusella, James F.
APPLICANT: Gusella, James F.
                                       Length 334;
                                                                                                                                               2 AKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA 49
                                                                                                                                                                                    20 APAPPNPNPQSPPSPPSPPTPPTPPSPPSPPSPPPSPPS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750 CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.4%; Score 127; DB 4; L. 79.3%; Pred. No. 2.1e-05;
                                    Score 134; DB 6;
Pred. No. 5.4e-05;
1; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 PQPGPQPPQPPQPPQRQPEAPAPQPP 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-FEB-1997
CLASSIFTCAPION: 424
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOOKET NUMBER: 1038-660
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 16, Aprilication US/08246982A; Patent No. 5686288
                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08750624 Patent No. 6290971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                    41.6%;
ilarity 47.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.39
Matches | 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                              Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-750-624-11
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                                                                                                                                                                                                                                                                                     /label- P69 BB05 epitope of Bordetella
pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 134; DB 6; Length 33
Pred. No. 5.4e-05;
1; Mismatches 24; Indels
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; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TILLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
; PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 АКАРРАРКРАРОРСРОРСРОРСРОРОРОРРОРРОРРОРОВ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 136; DB 1;
Pred. No. 4.7e-06;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 PGPQPGPQPGPQPPQPPQPPQRQPEAPAPQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PGPEIAPQPGPQPPQP-----QPEAPAPEP 32
                                                         /label- LTB sequence
                                                                                                                                                                       /label- hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 39
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 83,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 70.6%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.9%;
Matches 23; Conservative
                                       LOCATION: 1..2
OTHER INFORMATION:
                                                                                                                                      LOCATION: 4.7
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                          LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
   Region
                                                                                                             NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:37:
LENGTH: 331
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5202236-3
                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                               US-08-237-716-11
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5202236-3
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1 GAKAP-----PAPKPAPQPGPQPGPQP----GPQPPQPPQPPQ----PP 36
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                                                                                                                                                                                                                                                                                         Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Plowman, Gregory
APPLICANT: Peles, Elor
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 122.5; DB Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                             13 QPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPA----
                                                                                                                                                                                                                                                                                         Score 123.5; DB
Pred. No. 0.0031
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUNEAU APPLICATION DATA:
APPLICATION NUMBER: US/09/095,443
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
APPLICAD DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-095-443-2; Sequence 2, Application US/09095443; Patent No. 6342593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEAX: (212) --
TELEX: 67-3510
TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,32
REFERENCE/DOCKET NUMBER: 2
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.0%;
Best Local Similarity 41.0%;
Matches 32; Conservative 3
                                                                                                                                                                                                                                                                                                   38.48;
51.98;
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-095-443-2
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   Matches
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Patent No. 5693757
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GRELSA 55
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAX-1995
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/246,982A
FILING DATE: MAY 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 QPGPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.0031;
                                     Sterne, Kessler, Goldstein & Fox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
                                                                   1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET UNMBER: 06(
TELECOMMUNICATION:
TELECHONE: (202) 371-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.4%;
Best Local Similarity 51.9%;
Matches 27; Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                     CITY: Washington STATE: D.C.
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                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-246-982A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz TITLE De INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: PolyPeptides and Methods of Use NUMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESSE: ADDRESSE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC compatible
COMPUTER: The PC compatible
OPERATION SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGEPT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.7%; Score 121.5; DB 4;
48.2%; Pred. No. 0.00092;
tive 2; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/041,886
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09041886 Patent No. 6235372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/OCKET NUMBER: P:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 535-901
TELERAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 43/0 CCTV: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 513 amino acids
amino acid
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amino acid
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Best Local Similarity 48.29
Matches 27; Conservative
United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-041-886-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                 POLYNUCLEOTIDE VACCINE PROTECTIVE AGAINST MALARIA, METHODS OF PROTECT DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Folice LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.7%; Score 121.5; DB 3; Best Local Similarity 51.1%; Pred. No. 0.00087; Matches 24; Conservative 3; Mismatches 19;
                                                                                                                                                                                                                  APPLICANT: HOffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Bedegah, Martha
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PR
TITLE OF INVENTION: AGAINST MALARIA, METHODS
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE
CORRESPONDENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: ADDRESSE:
ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: Bldg. 1, T-12 8901 Wisconsin Ave.
CITY: Bethesda
STATE: Maryland
COUNTRY: ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spewack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/CDCKET NUMBER: 24,743
REFERENCE/CDCKET NUMBER: N.C. 75,851
FELECOMUNICATION INFORMATION:
TELEPHONE: (202) 295-6759
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRI.
ZIP: 20889-560b
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--venteR: IBM PC compatible
--venteR: PC-DOS/MS-DOS
                                                                                                                            RESULT 11
US-08-155-888-2
; Sequence 2, Application US/08155888
; Patent No. 6066623
                                           | | |::| |||||
625 QAPGLLPPQSPYPYAPQP 642
                 37 QR----QPEAP---APQP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 478 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-155-888-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Diego
California
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                                                                                                                                          5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                                                                                                                                    5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                                                                    7;
                                                         Score 121.5; DB 4; Length 530;
Pred. No. 0.00095;
2; Mismatches 20; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 121.5; DB 4; Length 552; Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Proapoptotic Peptides, Dependen TITLE OF INVENTION: Polypeptides and Methods of Use UNMBER OF SEQUENCES: 72 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.7%; Sco...
48.2%; Pred. No. o...
... 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   Sequence 30, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
                                                           Query Match 37.7%;
Best Local Similarity 48.2%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 48.29
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
; MOLECULE TYPE: peptide US-09-041-886-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                 US-09-041-886-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-041-886-30
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US-09-041-886-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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5 PPAPKPAPQPGPQPGPQ-----PGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 589;
                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 121.5; DB
Pred. No. 0.001;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 7, 2003, 16:57:20 Job time: 11.3447 secs
Campbell & Flores LLP
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.7%;
Best Local Similarity 48.2%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (619) 535-9001
                                                        STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-041-886-31
                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
        STREET: 45.
                                                                                                                                                                                                                                                                    FILING DATE:
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us-09-855-754b-7.rsp

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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1t J. 3:41-49(1993).
TISSUE SPECIFICITY: ENHANCED EXPRESSION IN MALE FLOWERS.
ACCOMULATES IN THE GLUMES AND IN ANTHER WALLS, PALEAS AND LEMMAS OF MATURE FLORETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT TASSEL GROWTH UP UNTIL MATURE POLLEN IS PRODUCED IN THE ANTHERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. BEIO; TISSUE-Tassel;
MEDILINE-94004997; Pubmed-8401606;
Wilght S.Y., Suner M.-M., Bell P.J., Vaudin M., Greenland A.J.;
"Isolation and characterization of male flower cDNAs from malze.";
Plant J. 3:41-49(1993).
                                                                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                    PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                           DB 1; Length 911;
                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                    1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                  (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                         ch 85.5%; Score 232.5; DB 1
1 Similarity 90.2%; Pred. No. 5.9e-16;
46; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                      p32439;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                    Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
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EMBL; A19180; CAA01453.1; -.
PIR; A47675; A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                LINES)
                                                    Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                      93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X67324; CAA47738.1; -. PIR; S25103; S25103.
MalzeDB; 78601; -.
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MFS18 protein precursor. MFS18
                                                                                                          911
712
911
262
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                                                                                                                                                                       701
266
266
271
276
570
911 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                             MF18_MAIZE
                                                                                                                                                                                                                            DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                       Local
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CHAIN
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SITE
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DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 23:125-131(1994).

-I- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-I- SUBDUIT: HE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.

-I- SUBCELLUIAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.

-I- PIM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-Lung;
MEDLINE-95130669; PubMed-7829060;
MEDLINE-95130069; PubMed-7829060;
Mydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoelastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mėtazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                      X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.2%; Score 74; DB 1; Length 860; 43.6%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                      AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                       7661ECC596E0D778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein; Repeat; Signal; Connective tissue
                                                                                                                                                                                                                                                                                                                                                                                  Score 78; DB 1;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
10-CT-1996 (Rel. 34, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 GDAPAGGAVPGGAVPGGAVPG----GFGPLLDGW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFS18 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
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                                                                                             1-3.
8 x 4.
2-1.
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PRINTS; PR01500; TROPOELASTIN.
                                                                                                                                                                                                                                                                                                                                     12535 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71955 MW;
                                                                                                                                                                                                                                                                                                                                                                                28.78;
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                                                                                                                                                                                                                                                                                                                                                                                                         44.18;
                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 44.1'
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                              113
128 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 7
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P54320;
                                                                                                                                                                                                                                                              REPEAT
REPEAT
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SEQUENCE
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                                                                                                                                             REPEAT
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"Sequence analysis upstream of the gene encoding the precursor to the major merozoite surface antigens of Plasmodium yoelii."; MOI. Blochem. Parasitol. 39:285-288(1990).
             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
METOZOITE SUTFACE protein 1 precursor (Merozoite surface antigens)
(PMMSA) (230 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 85:602-606(1988).
                                                                                                                                                                                                                                                                                                                   MEDLINE-88124889; PubMed-2448778;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
Tiph 3', portion of the gene for a plasmodium yoeli1 merozoite surf
antigen encodes the epitope recognized by a protective monoclonal
antibody.";
                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5862;
                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90205979; PubMed=2320061;
                                                                                                                                                                                                                                                                                           SEQUENCE OF 1093-1772 FROM N.A. STRAIN-17XL;
                                                                                                               Plasmodium berghei yoelii.
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                                                                                                                                                                                                            Lewis A.P.;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEN custation the the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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 Gaps
                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Cytoplasmic antigen) (74.6 kDa
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93050041; Pubmed-1426134;
Eckert V., Sanchez L., Cochrane A.H., Enea V.;
"Plasmodium cynonogi: the hsp 70 gene.";
Exp. Parasitol. 75:323-28(1992).
-1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN THE ASEXUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 x 4 AA TANDEM REPEATS OF G-G-M-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.
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8
                                                                                                                                                                                                                                                                                                                                                                                                                       BLOOD STAGE FORMS.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 686;
                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5828;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FF31F448FFCBF286 CRC64;
                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                            2 RATIRRGDAPAGGAVPG----GAVPG----GAVPGGFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.5; DB Pred. No. 5.2; 4; Mismatches
                                                                                                                                               686 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            653 GGMPGGMNFPGGMPGGA-PAGSGPTVE 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GDAPAG----GAVPGGAVPGGAVPGGFGPLLD 35
                                                                                                                                                                                                                                                           Plasmodium cynomolgi (strain Berok)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P08109; ICKR.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70. 1.
PRINTS; PR00301; HEATSHOCK70.
Probom; PD000089; Hsp70. 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
ATP-binding; Heat shock; Repeat.
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..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M90978; AAA29625.1; -. PIR; A49242; A49242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Conservative
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                             HS70_PLACB
Q05746;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GIDIRVAGSSVD 1379
(Potential).

-I- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SCHFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TIRRGDAPA-----GGAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL
                                                                                                                                                                                                                                                                                                                                Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1772;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> V (IN REF. 2).
9A6291658EB0F45D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DB 1;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1330 TTLAADAPATPEGAVPGAVPGAVPGAVPGAVPGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197230 MW;
                                                                                                                                                                                                                                                   EMBL; J03612; AAA29762.1; -. EMBL; J04668; AAA29702.1; -. PIR; A28121. A28121. PIR; A45532; A45532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.18;
                                                                                                                                                                                                                                                                                                                                                       GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1629
1680
1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1772 AA;
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PRT; 1772 AA

STANDARD;

MSP1_PLAYO
ID MSP1_PLAYO

RESULT 7

RESULT 8 CUT2_CAEEL

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                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                        Gaps
                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                               12 X 4 AA REPEAT OF A-A-P-[AVI].
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67.5; DB 1; Length 231;
Pred. No. 3.8;
1; Mismatches 13; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                           A48C9C5498D8E797 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GAAPAGGAYQSGPAFGGAAPAGGAYQSGPAFGGAAPAVGGAY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDAPAGGAVPGGAVPGGAVP-----GGFGPLLDGWY 38
            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Cuticiin 2 precursor.
231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BR3A_HUMAN STANDARD; PRT; 423 AA 01851; 015318; 014986; 01-JUL-1993 (Rel. 26. Created) 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                   POTENTIAL.
CUTICLIN 2.
POLY-GLY.
POLY-PRO.
PRT;
                                                                                   SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-95021520; Pubmed-7935621;
                                                                                                                                                                                                                                                                                                                                                                                                           20833 MW;
                                                                                                                                                                                                                                                             EMBL; X74838; CAA52832.1; -. PIR; S37108; S37108.
                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                llarity 40.5%;
Conservative
STANDARD;
                                                                                                                                                                                                                                                                          Cuticle; Signal; Repeat.
                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                   218
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BR3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A COLIUMR R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K., Thell T., Moroy T., DePinho R.A., Alt F.W., A croce C.M., Israel M.A., Thell T., Moroy T., DePinho R.A., Alt F.W., The Core C.M., Israel M.A., Thell T., Moroy T., DePinho R.A., Alt F.W., The Core Commandian nervous system.

In Uncleic Acids Res. 20:4919-4925(1992).

I FUNCIONIS ROBABLE TRANSCRIPTION FACTOR WHICH MAY PLAY A ROLE IN THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A SUBSET OF THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

I SUBSCRIPTION: NO. OF SEMS TO BE SPECIFIC TO THE RETINA.

SUBSCRIPTION OF SEMS TO BE SPECIFIC TO THE RETINA.

I TISSUE SERCIFICITY: BRAIN. SEEMS TO BE SPECIFIC TO THE RETINA.

THE DEPUNDANTAL STAGE: EXPRESSION PEAKS EARLY IN EMBRYOGENESIS

(DAY 13.5) AND IS UNDEFECTABLE 14 DAYS AFTER BIRTH.

C. -- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Retina;
MEDLINE-95348789; PubMed-7623109;
MEDLINE-95348789; PubMed-7623109;
Miang M., Zhou, L.-J., Macke J.P., Yoshioka T., Hendry S.H., Eddy R.L., Shows T.B., Nathans J.;
Shows T.B., Nathans J.;
"The Brn-3 family of POU-domain factors: primary structure, binding specificity, and expression in subsets of retinal ganglion cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLING-94052142; PubMed-8234287; Abargava A.K., Ll Z., Weissman S.M.; Blifferential expression of four members of the POU family of proteins in activated and phorbol 12-myristate 13-acetate-treated
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (OCT-T1)
(Homeobox/POU|domain protein RDC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 90:10260-10264(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASS-4 SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93027214; PubMed-1357630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U10063; AAA57161.1; -.
EMBL; U10062; AAA57161.1; JOINED.
EMBL; [L20433] AAA6565.1; -.
EMBL; X64624; CAA45907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          somatosensory neurons.";
J. Neurosci. 15:4762-4785(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU_domain; 1.
SMART; SM00399; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001356; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 85-423 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:9218; POU4F1.
                                                                                                                                   POU4F1 OR BRN3A OR RDC1.
                                                                                                                                                                          (Human)
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; TO1876;
TRANSFAC; TO4463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jurkat T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rISSUE=Placenta;
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P10037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
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NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                      Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OST-PTP)
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPO_RAT
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 286-401 FROW N.A.

STRAIN-T6 / TW1; TISSUE-Testis;

MEDLINE-90221898; Pubmed=1970171;

MEDLINE-90221898; Pubmed=1970171;

Goldsborough A., Ashworth A., Willison K.;

"Cloning and sequencing of Poul-boxes expressed in mouse testis.";

"Cloning and sequencing of Poul-boxes expressed in mouse testis.";

"L'EUNCLION: PROBABLE TRANSCRIPTION FACTOR WHICH MAY PLAY A ROLE IN THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A SUBSET OF THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

"THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS."

"THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM AND SECRIFICITY: BRAIN; PERIPHERAL SENSORY NERVOUS SYSTEM AND RETINA. IN THE ADULT NERVOUS SYSTEM BRN-3.0 PREDOMINATES IN THE MEDIAL HABBRULA, SUPERFICIAL GRAY OF THE SUPERIOR COLLICULUS, RED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
MEDLINE-9415319; PubMed-8162704;
MEDLINE-94215319; PubMed-8162704;
Theil T., Zechner U., Klett C., Adolph S., Moeroey T.;
Thronosomal localization and sequences of the murine Brn-3 family of developmental control genes."; 71(1994).
Cytogenet. Cell Genet. 66:267-271(1994).
                                                                                                                                                                                                                                                                                                                                     Gaps
SMART; SM00352; POU; 1.
PROSITE; PS00025; HOMEOBOX_1; 1.
PROSITE; PS00465; POU_2; 1.
PROSITE; PS00465; POU_2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UNM-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (BRN-3.0).
POUGFI OR BRN3A OR BRN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                             Score 67; DB 1; Length 423;
                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                        A -> R (IN REF. 3).

AER -> GS (IN REF. 3).

AQR -> PS (IN REF. 3).

B3AE4732E1309F34 CRC64;
                                                                                                                                                -> R (IN REF. 1).
AG -> ARR (IN REF. 3).
                                                                                                                                                                                          GP -> AA (IN REF. 3).
GP -> PR (IN REF. 3).
GP -> AA (IN REF. 3).
                                                                                                                                                                      MISSING (IN REF. 2).
MISSING (IN REF. 3).
                                                                                                                                         TS -> H (IN REF. 3)
                                                                                                                                                                                                                        G -> A (IN REF. 3).
A -> S (IN REF. 2).
MISSING (IN REF. 3)
                                                                                                                                                                                                                                                                                                        24.6%; Score v,; ___
56.0%; Pred. No. 7.4;
+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              421 AA.
                                                                            POU-IV BOX.
                                                                                      POLY-HIS.
GLY-RICH.
                                                                                                           ALA-RICH.
                                                                                                                              HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                153 GGCPGGGGGGGGGG--GGGGP 175
                                                                                                                                                                                                                                                                                                                                                   8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                      42939 MW;
                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                     123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           BR3A_MOUSE
                                                                                                                             DNA_BIND
CONFLICT
                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                      Local
                                                                                                      DOMAIN
                                                                         DOMAIN
                                                                                    DOMAIN
                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
BR3A_MOUSE
g
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NUCLEUS, MESENCEPHALIC NUCLEUS OF THE TRIGEMINAL GANGLION, NUCLEUS AMBIGUUS, INFERIOR OLIVARY NUCLEUS, AND PERIPHERAL SENSORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Osteotesticular protein tyrosine phosphatase precursor (EC 3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of a hormonally regulated protein tyrosine phosphatase associated with bone and testicular differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Osteosarcoma;
MEDLINE-95704080; PubMed=7527035;
Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,
                                                                          -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42781 MW; 34EC99D789EBE939 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                  -!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1711 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 65.5; E
58.3%; Pred. No. 10;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POU-IV BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-HIS.
GLY-RICH.
ALA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POU.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S09237; S09237.
HSSP; P10037; 1AU7.
MGD; MGI:102525; Pou4f1.
InterPrc; IPR001356; Homeobox.
InterPrc; IPR000327; POU_domain.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00157; Pou; 1.
PRINTS; PR00028; Pou; 1.
PR10Dom; PD000010; Homeobox; 1.
ProDom; PD000589; Pou_domain; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 DAPAGGAVP-GGAVPGGAVPGGFG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX.1; 1.
PROSITE; PS00045; POU.1; 1.
PROSITE; PS00465; POU.2; 1.
PROSITE; PS50071; HOMEOBOX.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S69350; AAB30577.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                              CLASS-4 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 AA;
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89 1711 AA;
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                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                           CARBOHYD
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                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local
                                          CARBOHYD
                                                                              CARBOHYD
                                                                                             CARBOHYD
                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P03439;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
HEMA_IAME2
       ö
                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
HOL. Chem. 269:30659-30667(1994).
FUNCTION: MAY FUNCTION IN SIGNALING PATHWAYS DURING BONE
REMODELING, AS WELL AS SERVE A BROADER ROLE IN CELL INTERACTIONS
ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS. OPTIMAL PH FOR
                                                                                                                     TYPOSITION TO THE FOURTH PROBLEM FILES THE PROBLEM FOR THE TRANSPLANCE THE TRA
                                                                    PHOSPHATASE ACTIVITY IS 5.6.
ASSOCIATED WITH DIFFERENTIATION IN BONE AND TESTIS.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY PARATHYROID HORMONE AND CYCLIC AMP ANALOGS.
PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS. SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 9.
FIBROTEIN-TYROSINE PHOSPHATASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSTEOTESTICULAR PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2PP; 2.
Hydrolase; Transmembrane; Repeat; Signal; Glycoprotein.
SIGNAL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR000340; DS_phosphatase.
InterPro: IPR003961; FN_III.
InterPro: IPR003962; FnIII_repeat.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00041; fn3; 7, Pfam; Pfam; PF00102; x_phosphatase; 1. PR.NYTS; PR.0014; FNTYPEIII. PRINTS; PR00700; PRTYPHPHAASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00060; FN3; 6.
SMART; SM00194; PTPc; 1.
SMART; SM00012; PTPc_DSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L36884; AAA63911.1; -. HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1096
                                                                                                                                                                                                                                                                                                                                        EPITHELIUM.
                                                                                                                                                                                                                                                                                                                                                                                              SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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-1- FUNCTION! HERAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INBECTION.

-1- SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMACGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Sledgh M.J., Both G.W., Brownlee G.G., Bender V.J., Moss B.A.;
Sledgh M.J., Both G.W., Brownlee G.G., Bender V.J., Moss B.A.;
The haemaggluthnin gene of influenza A virus: nucleotide sequence
analysis of cloned DNA copies.";
(In) Laver G., Air G. (eds.);
Structure and variation in influenza virus, pp.69-79, Elsevier,
                                                                                    POTENTIAL)
                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä;
                                                        POTENTIAL)
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                                                                                                                                                                                                                                                                                                                         (POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDG-WYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-GCT-2001 (Rel. 40, Last annotation update)
Hemagglutinin precursor [Contains: Hemagglutinin HAl chain;
Hemagglutinin HA2 chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 38.5%; Pred. No. 37;
20; Conservative 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Memphis/102/72).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
NCBL_TaxID=11439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P03437; 2VIU.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
Probom; P0000225; Hemagglutn; 1.
Broelope protein; Hemagglutin; 3ignal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                         0F04D2D1A47A18A0
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HEMAGGLUTININ HAZ
                                                                                                                                                                                       (GLCNAC.
                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 65.5; 38.5%; Pred. No. 37
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                      187292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V01089; CAA24273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)

01-NOV-1995 01-NOV-1995 HS71_CANAL P41797;

Heat shock protein SSA1. SSA1 OR HSP70. Candida albicans (Yeast).

655 AA.

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RESULT 14
HS71_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   :::| | | | | | | ::
280 KSSIMRSDAPIGTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNV 339
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snutch T.P., Heschl M.F.P., Balllie D.L.; "The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                              POTENTIAL)
                                                          (POTENTIAL)
                                   POTENTIAL)
                                                                                                                                                            51;
                                                                         (POTENTIAL)
                                                                                                                               Score 64.5; DB 1; Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 64:241-255(1988).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 640;
                                                                                                                                                     10; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBLES PROCESS: HSP70; 1.
PROSITE: PS00297; HSP70_1; 1.
PROSITE: PS00329; HSP70_2; 1.
PROSITE: PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SROUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                   1D9313AB3C380CD7 CRC64;
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                                              (GLCNAC.
                                                                         (GLCNAC.
                                                                                                                  23.7%; Sco. 20.2%; Pred. No. 1., 20.2%; Pred. No. 1., ...
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Last annotation update)
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Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peloderinae; Caenorhabditis
  N-LINKED
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                                                                                                                                                                                                                                                                    340 PEKRIRGLFGAIAGFIENGWEGMIDGWYG 368
                                                                                                                                                                                                                                         24 -----GAVPG----GFGPLLDGWYG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88297155; PubMed-2841196;
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                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
                                                                                                   63264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                             Heat shock 70 kDa protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M18540; AAA28078.1; -. PIR; JT0285; HHKW7A.
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Pfam; PF00012; HSP70; 1.
                                                                                                                                   West Local Similarics
Watches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         HSP-1 OR HSP70A.
Caenorhabditis elegans.
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                                                                                                566 AA;
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Matches 14; Conserv
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HSSP; P19120; 1HPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabdītidae;
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01-FEB-1994
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                                                                                                   Cassone A.C., la Valle R.L., Crisanti A.C., Muller H.M., Bromuro C.B.; Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                            Excles P., Sentandreu M., Florza M.V., Sentandreu R.;
"Cloning of a DNA fragment encoding part of a 70-kDa heat shock protein of Candida albicans.";
FEMS Microbiol. Lett. 128:95-100(1995).
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
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A -> G (IN REF. 2).
634743E4D6DAD9D5 CRC64;
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2; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00301; HEATSHCKTO.
ProDom; PD000089; Hsp70, 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS001395; HSP70_2; 1.
PROSITE; PS001395; HSP70_2; 1.
Heat shock; ATP-binding; Multigene family; Acetylation.
INIT_MET 0 0 BY SIMILARITY
MOD_RES 1 1 1 ACETYLATION (BY SIMILARITY
CONFLICT 175 175 A -> G (IN REF. 2).
SEQUENCE 655 AA; 70192 MW; 634743E4D6DAD9D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GDAPAG-GAVPG-GAVPGGRAVPGGFGPLLDGWYGVDVSDSTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64.5;
                                                                                                                                                                                SEQUENCE OF 1-243 FROM N.A. MEDLINE=95262895; PubMed=7744244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOSE, F19120; 355C.
COMPLUYEAST-2DPAGE; P41797;
INTERPRO; IPRO01023; HSP70.
Pfam; PF00012; HSP70; 1.
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                                              SEQUENCE FROM N.A.
STRAIN=ATCC 20955;
Cassone A.C., la V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
NCBI_TaxID=5476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
ALTERNATIVE PRODUCTS: Various isoforms are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NOTHAL LIGAMENT, WHICH MOTE EXPAND RAPIDLY AND RECOVER COMPLETELY.
-1- SUBBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER INTO AN EXTENSIBLE 3D NETWORK.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                   SEQUENCE OF 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-92241859; PubMed-1572637; Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.; "Elements of the rat tropoelastin gene associated with alternative
                                                            MEDIINE-91104868; PubMed-1702999; Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.; Pierce R.A., Deak S.B., Stolle C.A., Boyd C.D.; Biecrogeneity of rat tropoelastin mRNA revealed by cDNA cloning."; Biochemistry 29:9677-9683(1990).
                                                                                                                                                               SEQUENCE OF 781-864 FROM N.A.
MEDLINE-88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 864;
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MISSING (IN CERTAIN ISOFORMS).
MISSING (IN CERTAIN ISOFORMS).
MISSING (IN CERTAIN ISOFORMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64.5; |
Pred. No. 25;
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1 Similarity 43.6%;
17; Conservative
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308
809
864 AA;
                               NCBI_TaxID=10116;
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557 GLGPGVGGVPGGVGG-LPGGVGP--GGVTGIGTGPGT 592 Search completed: May 7, 2003, 16:48:02 Job time: 10.9523 secs 셤

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Gaps

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2; Mismatches 17; Indels

8 GDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDST 46

Local Similarity

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Bordetella paraper
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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AAR25578
AAE16185
AAR14321
AAE16189
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AAE16192
AAE16187
AAR14320
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Gapop 10.0 , Gapext 0.5
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	11	204	· .		45	233	AAE17153 AAE17154		
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	181	204	ا. حزا		4.4	233	AAE17157		Pembe monocional a
	22	204.5	منا منا	2.2	4 7 7 7	7 7 3 3	AAE17158 AAE17159		PeM71 monoclonal a
	23	160.	۱.0۱.	•	59	23	AAE17147		Bordetella pertuss
	25	159.	טו-ט		36	23.2	AAE17141 AAE17170		Bordetella pertuss Maltose binding or
	26	155.	יטי	•	26	23	AAE17152		Bordetella pertuss
	27 28	15.	יזוי טוי	•	3.4	23	AAE17150		Bordetella pertuss
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AC X	AAE:	AAE16186,							
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DE	В. К	bronchi	hisep	septica s	train	I-1	pertactin o	outer membrane protein region	rotein region I.
X X	Pert	tactin		C	uter mer	membrane	protein.	vaccine. Bordetella	olla infoction.
KW	the	therapy;	antibi	, t	; ant	antibacter	ial; regi		
SO S	Bord	ordetel]	la bit	bronchis	septica				
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X F	23 - N	-MAY - 2(2001;	2001WO-EP0645	-EP06	157.			
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r d	Pol ₃	Polypeptides pertactin in	ides	contai	aining p	polyr spec	lymorphisms of	the repe	ated regions of
TA,	trea	ating	infe	ections		sed by	Bordetella	and in d	ds -
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "contains 5 direct, tandem repeats" 575..612
/note= "contains 9 direct repeats of Pro-Gln-Pro" 712..714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "motif associated with cell-cell adhesion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acellular vaccine for immunisation against whooping cough comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whooping cough; P70 antigen; P95 precursor protein; vaccination.
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                        Length 51;
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                                                                                                                                                                                                                                                                                       100.0%; Score 272; DB 23;
100.0%; Pred. No. 2.3e-24;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella parapertussis P95 antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR25578 standard; Protein; 922 AA
Claim 26; Fig 1b; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35..643 //label= P70
260..262 //note= "motil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella parapertussis.
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Matches 51; Conservative
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N-PSDB; AAQ26509.
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Claim 1; Fig 1; 20pp; English.

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin artibody is useful for treating Bordetella infections and used to detect Bordetella autigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRN; outer membrane protein; vaccine; Bordetella infection;
                            recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb claff fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol. wt. 95,177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol. wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                         Length 922;
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100.0%; Pred. No. 4.2e-23;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; antibiotic; antibacterial; p.70.
                 cosmid library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 51; Conservative
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N-PSDB; AAD26442.
                                                                                                                                                                                                                                                                        922 AA;
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Gaps

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Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
                       WPI; 1991-325214/44.
N-PSDB; AAQ14320.
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AAE16189
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used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative of perfernination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.
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                                                                                                                                                                                                Length 922
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                                                                                                                                                                                         100.0%; Score 272; DB 23;
100.0%; Pred. No. 4.2e-23;
ive 0; Mismatches 0;
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/label= re
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Best Local Similarity 100.
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella parapertussis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clare JJ, Romanos MA;
                                                                                                                                                            922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JAN-1992
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                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     AAR14321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pept1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pept1de
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                                                                                                                                                                                                                                                                                                                                                                   AAR1432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                          Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. bronchiseptica strain prnl pertactin outer membrane protein region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                             The 46 Xs represent amino acids missing in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 QRATIRRGDAPAGGAVPGGXXPGGAVPGFFGPLLDGWYGVDVSDSTVDLAQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                            Score 263; DB 12; Length 9
Pred. No. 4.5e-22;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ORATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suiso-macloug N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pig 1b; 47pp; English
Disclosure; Fig 1C; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16189 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                            96.78;
96.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2001; 2001WO-EP06457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps

5;

Indels

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Pred. No. 1.4e-19; 3; Mismatches 1

1 ORATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ

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Length 910;

DB 23;

Score 241.5;

88.8%; 83.9%;

Query Match 88.8 Best Local Similarity 83.9 Matches 47; Conservative

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used in adfinity characterial antigens in biological preparations or in burlfying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fulids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. pertussis pertactin outer membrane protein, p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                protein; vaccine; Bordetella infection;
antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                Gaps
                                                                                                                                                         51
                                                                                                                                                                    5,
                                                                                                                                                   QRATIRRGDAPAGGAVPGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                               Bordetella pertussis pertactin outer membrane protein, p.69.
                                                                                                Length
                                                                                          Score 241.5; DB 23; Length
Pred. No. 8.2e-21;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
254..309
/note= "Pertactin region I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                           Pertactin; PRN: outer membrane protein; v
therapy; antibiotic; antibacterial; p.69.
                                                                                                                                                                                                                                                      AAE16184 standard; Protein; 910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 31; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guiso-maclouf N, Boursaux-eude C;
                                                                                           88.8%;
83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Po
568..609
/note= "Po
                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella pertussis.
                                                                          (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-097639/13.
                                                             56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-097639/
N-PSDB; AAD26441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200190143-A2.
                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001.
                                                             Sequence
                                                                                                                                                                                                                                                                                      AAE16184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                          AAE1618
                                                                                                                                                                                                                               RESULT
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of waccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polio and infections caused by Haemophilus Influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present
                                                                                                                                                                                                                       Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides derived from Bordetella pertussis pertactin, usefu
a vaccine against infections caused by Bordetella strains, and othe
infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 241.5; DB 23;
Pred. No. 1.4e-19;
3; Mismatches 1;
                                                                                                                                                                                         Bordetella pertussis pertactin (Prn1) protein.
                                                                                                                                                                                                                                                                                                                                                      /note= "Conserved region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is B. pertussis prnl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 35-38; 52pp; English.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
597..604
                                                                                         AAE17146 standard; Protein; 910 AA.
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83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2001; 2001WO-NL00493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000EP-0202309
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.97
Matches 47; Conservative
                                                                                                                                                                                                                                                                                      Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-139897/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 AA;
                                                                                                                                                                                                                                                           immune response.
                                                                                                                                                                                                                                                                                                                                                                                   WO200200695-A2.
                                                                                                                                                          18-APR-2002
                                                                                                                                                                                                                                          diphtheria;
                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
                                                                                                                           AAE17146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mooi FR;
                                                                                                                                                                                                                                                                                                                      Key
Region
                                                             RESULT 7
                                                                          AAE17146
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Gaps

2:

Length 910;

RESULT 8

910 AA;

Sequence

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WO200190143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.

    bronchiseptica strain prn4 pertactin outer membrane protein region I.

                                                                                                                                                                                                                                                                                                                      Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

    B. bronchiseptica strain I-2 pertactin outer membrane protein region I.

                                                                                           Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QRATIRRGDAPAGGAVPGGAVPGGFGPVLDGWYGVDVSGSSVELAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 241; DB 23; Length 5
Pred. No. 8.6e-21;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                         Suiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16187 standard; peptide; 46 AA.
AAE16192 standard; peptide; 51 AA
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 88.6%;
l Similarity 88.2%;
45; Conservative
                                                                                                                                                                                                    23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                          25-MAY-2000; 2000US-206969P
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                             Bordetella bronchiseptica
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                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                               4PI; 2002-097639/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AA;
                                                                                                                                                    WO200190143-A2.
                                              6-MAR-2002
                                                                                                                                                                            29-NOV-2001
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                     AAE16192;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipgens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                  Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions itreating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.5%; Score 232.5; DB 23; Length 46; 90.2%; Pred. No. 7.4e-20; 1ve 0; Mismatches 0; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin; Pichia; B. pertussis; B. parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                  3uiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR14320 standard; Protein; 911
                                                                                                                                                                                                                                                                                                                                                       Claim 26; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266..270
/label= repeat
271..275
/label= repeat
570..572
/label= repeat
574..576
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584..586
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23-MAY-2001; 2001WO-EP06457
                                               25-MAY 2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella bronchiseptica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.2
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertactin antigen P.68.
                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                  WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR14320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR14320
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ï

/label= repeat 587..589 /label= repeat

599..601 /label- repeat

Pept1de Peptide

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outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                             The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of pighets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                     DNA encoding a Bordetella broncmiseptica process. compoblaining vaccines for preventing respiratory diseases, particatrophic rhinitis in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             85.5%; Score 232.5; DB 1
90.2%; Pred. No. 1.5e-18;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; antibiotic; antibacterial; p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16183 standard; Protein; 911
                                                                                                                                                                                                                                               Claim 1; Fig 1; 28pp; English.
                                                         91GB-0006568
                             92WO-GB00561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2001; 2001WO-EP06457.
                                                                                   (WELL ) WELLCOME FOUND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000; 2000US-206969P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                         WPI; 1992-366258/44.
N-PSDB; AAQ34566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-097639/13.
N-PSDB; AAD26440.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pertactin; PRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200190143-A2
                           27-MAR-1992;
                                                         27-MAR-1991;
15-0CT-1992,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                Charles IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                  Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchiseptica; P.68; outer membrane protein; piglet; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                            Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
1.5e-18;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 232.5;
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atrophic rhinitis; alternative cleavage

Bordetalla bronchiseptica

Protein

Region Region

AAR26503 standard; Protein; 911 AA.

RESULT 11

g ð

12-MAR-1993 (first entry)

AAR26503;

Ouery Match Best Local Similarity 90.2%; Matches 46; Conservative

911 AA;

Sequence

(1989).

Disclosure; Fig 1B; 38pp; English

(WELL) WELLCOME FOUNDATION LID

Romanos MA;

clare JJ,

NAME OF THE PROPERTY OF THE PR

WPI; 1991-325214/44.

N-PSDB; AAQ14319

90GB-0007416 91WO-GB00487

28-MAR-1991; 32-APR-1990;

W09115571-A 17-0CT-1991 'label= RGD_tripeptide 701..703 /label- RGD_tripeptide

W09217587-A.

Peptide

Pept1de

..262

570.589 /label- Repeat_region 266..279 /label- Repeat_region Location/Qualifiers 35..632 /label= P.68

ä

Gaps

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials Thus the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vacchne. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mathbf{for}
                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. bronchiseptica strain I-3 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outer membrane protein; vaccine; Bordetella infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRATIRRGDAPAGGAVPGGAVPGGFGPLLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 5e-18;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 232.5; I
Pred. No. 1.5e-
0; Mismatches
                                                                                                                                 Disclosure; Page 28; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16188 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.5%;
90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.7 nes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigens can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertactin; PRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200190143-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE16188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiques can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal belis, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. bronchiseptica strain prn3 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                     1 ORATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 228.5; DB 23; Length 56;
Pred. No. 2.6e-19;
3; Mismatches 3; Indels 5
                                                                                                                                                                       Length
                                                                                                                                                                                                    Indels
                                                                                                                                                                   DB 23;
                                                                                                                                                                                                      ..
..
                                                                                                                                                                  Score 228.5; DB 2:
Pred. No. 2.6e-19;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 1b; 47pp; English
                                                                                                                                                                                                                                                                                                                                                  AAE16191 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
80.4%;
                                                                                                                                                                   84.0%;
80.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR_2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica,
                                                                                                                                                                                 Local Similarity 80.4
nes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097639/13
                                                                                                                                    56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200190143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2001.
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                 AAE16191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                   Query Match
                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                  AAE1619
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when the in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B, bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                        B. bronchiseptica strain prn2 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                           Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.
1 QRATIRRGDAPAGGAVPGGAV-----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                  AAE16190 standard; peptide; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000; 2000US-206969P.
                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR
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Indels 10; Gaps
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                                                                               83.1%; Score 226; DB 23; Length 61; 73.8%; Pred. No. 5.5e-19; 1ve 3; Mismatches 3; Indels
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Best Local Similarity
Matches 45; Conserv
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Search completed: May 7, 2003, 16:47:02 Job time: 37.4991 secs

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CITY: ...
STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN
FEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STRÈET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 272; DB 4;
; Pred. No. 4e-25;
0; Mismatches 0;
                                                                         US-08-453-848-15
US-08-453-848-21
US-09-169-027-21
US-09-224-629C-31
US-08-224-629C-31
US-08-562-311-4
US-08-562-311-4
US-09-276-406-6
US-09-702-572-6
US-09-542-051-33
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-542-051-45
US-08-542-051-18
US-08-397-633A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 51, Conservative
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NUMBER OF
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178.054 Million cell updates/sec
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272
1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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                       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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. /cgn2_6/ptodata1/laa/5A_COMB.pep:*
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: /cgn2_6/ptodata71/laa/PCTUS_COMB.pep:*
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-08-342-930-2
-08-556-978B-60
-09-247-806-9
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-08-556-978B-61
-09-247-806-10
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-08-529-190B-1
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-08-845-998-8
-09-206-537-8
-09-430-854-8
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Gaps

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Indels

DB 4; Length 922;

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Gaps
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APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 QRATIRRGDALAGGAVPGGAVPGGFCPGFCPGFCFPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                         Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94.5; DB 2; Length 745; Pred. No. 0.0012; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    Score 231.5; DB 4;
Pred. No. 3.3e-20;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: BIRCH, STEWART, KOLASCH & BIRCH 8110 GATEHOUSE RD. SUITE 500E
APPLICATION NUMBER: US/08/460,269C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GGAGPGGAGPGGAGPGGAGP---GGYG 271
                                                                                                 REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GDAPAGGAVPGGAVPGGFGPLLDGWYG 39
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/09/010,928B
22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                           NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09010928B Patent No. 5994099 GENERAL INFORMATION:
                                                                                                                                                                        243-6410
                                                                                                                                                                                                                                          LENGTH: 910 amino acids
                                        ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerald M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NOTICE TO REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.7%;
Best Local Similarity 65.6%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                           85.1%;
82.1%;
                                                                                                                                                                     TELEFAX: (703) 243-6
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.13
Best Local Similarity 82.13
Matches 46; Conservative
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LENGTH: 745 amino acid
                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Ge
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRG:
COUNTRY: UNI
ZIP: 22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                                                  US-08-460-269C-2
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                 ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 QRAIIRRGDAPA-----GGAVPGGAVPGFFGPLLDGWYGVDVSDSTVDLAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Brani,
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 232.5; DB 4
Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lebovitz, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08460269C
Patent No. 6197348
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                           Sequence 4, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy dish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 911 amino acids
                                                                                                               APPLICANT: CLARE, JEFFREY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.5%;
90.2%;
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.5%;
Best Local Similarity 90.2%;
Matches 46; Conservative
                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
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US-08-460-269C-2
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Gaps
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APPLICANT: Leats, Randolph V
APPLICANT: HAYSALI, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                             Length 907;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 2;
Pred. No. 0.0035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: BIRCH, STEWART, KOLASCH & BIRCH $110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                Score 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VIRGINIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-804-227C-14; Sequence 14, Application US/08804227C; Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                     163 GGAGPGGAGPGGAGPGGAGP 187
                                                                                                                                                                                                                                                                                                             8 GDAPAGGAVPGGAVPGGEGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
  NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 2997
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
                                                                                                                                                                                                                             32.7%;
72.0%;
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                                                                                                                                                                                                                                                                      Conservative
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MOLECÜLE TYPE: protein

US-09-010-928B-9
                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                               Best Local Similarity
Matches 18; Conserve
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Best Local Similarity
Matches 15; Conserv
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CITY: FA
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        Sequence 2, Application US/09010928B
Patent No. 5994099
GENERAL INVENTION:
GENERAL INVENTION:
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEWIS, Randolph V
APPLICANT: LEWIS, Randolph V
APPLICANT: LEWIS, Randolph V
APPLICANT: LEWIS, Randolph V
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: RALLS CHURCH
STREET: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94.5; DB 2; Length 870;
Pred. No. 0.0014;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUNG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
CITY: FALLS CHURCH
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APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                          CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UNITED STATES OF AMERICA ZIP: 22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 870 amino acids amino acid
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Best Local Similarity 65.6
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-928B-2
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US-09-010-928B-2
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RESULT 6

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Query Match 25.0%; Score 68; DB 2; Length 4550; Best Local Similarity 48.5%; Pred. No. 15; Matches 16; Conservative 1; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 2
Pred. No. 15;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1576 AAGRVSGGVRSGRAVPGGVGVLFTGQGAQWVGM 1608
                                                                                                                                                                                                                                                                                                                                                                                   12 AGGAVPGGAVPGGFGPLLDG----WYGV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AGGAVPGGAVPGGFGPLLDG----WYGV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                 X-8231
                                         REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08804198
Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION UNMBER: 36,470
REFERENCE/POCKET NUMBER: P91.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,470
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Best Local Similarity 48.5%;
Matches 16; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-804-227C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-804-198-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-804-198-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhatoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                     APPLICANT: DeHOff, Bradley S.
APPLICANT: Kulbicos, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
AILLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1571 AAGRVSGGVRSGRAVPGGVGVLFTGQGAQWVGM 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0%; Score 68; DB
Best Local Similarity 48.5%; Pred. No. 15;
Matches 16; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AGGAVPGGAVPGGFGPLLDG----WYGV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: February 21, 1997
CLASSTRICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRALION NUMBER: 35,784
REFRENCE/DOCKET NUMBER: x-8231
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTK: ...
ZIP: 46285
COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4545 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
SY: unknown
                                                                                                                                                                                                                                                     RY: USA
46285
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                                                                                                                                                                                                                               STATE: I)
COUNTRY:
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Length 420;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Van Baren, Nicolas
APPLICANT: Coulte, Pierre G.
APPLICANT: Coulte, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 67; DB 4;
56.0%; Pred. No. 1.3;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Van Amsterdam, John R. REGISTRATION NUMBER: 40,212 REFERENCE/DOCKET NUMBER: L0461/7008 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    L0461/7008
                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/206,537
                                                                                                PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 GGGPGGGGGGGGG--GGGGP 172
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
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; Sequence 8, Application US/09430854
; Patent No. 6271019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : (617)720-3500
(617)720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                 : 420 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-206-537-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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STREET: boc
rav: Boston
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US-09-206-537-8
Sequence 8, Application US/09206537
Sequence 8, Application US/09206537
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulte, Plorte 6.
APPLICANT: Coulte, Plorte 6.
APPLICANT: Bosnet, Charles
APPLICANT: Bosnet, Charles
APPLICANT: Boon, Thierry
TILLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-FOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS: ADDRESS:
ADDRESSEE: ADDRESS: ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTARTION UNBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/845,998
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           US-08-845-998-8

Sequence 8, Application US/08845998

Patent No. 5879892

GENERAL INFORMATION:
APPLICANT: Van Beren, Nicolas
APPLICANT: Coulie, Pierre G.
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 420 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-845-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                         Boston
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02210
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Search completed: May 7, 2003, 16:56:57 Job time: 11.5185 secs
       TITLE OF INVENTION:
                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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                                                                                            STREET:
                                                                                                            CITY: F
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                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hyasahi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              5
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                                                                                                                                           Length 420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 GATEHOUSE RD. SUITE 500E CITY: FALLS CHURCH
                                                                                                                                                                            0; Mismatches
                                                                                                                                           Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               150 GGGPGGGGPGGGPGGG--GGGGP 172
                                                                                                                                                                                                            8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MITPHY JI., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 14
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                        Query Match
Best Local Similarity 56.0%;
Matches 14; Conservative
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                                  : 420 amino acids amino acid
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LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| |||: |||:||
PGGYGPGGSGPGGYGP 16
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INFORMATION FOR SEQ ID NO:
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                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-430-854-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22042
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA
                  SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                     US-09-010-928B-7
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OLMSTED, ELIZABETH A.

MAURO, LAURA J. DAVIS, ALAN R. DIXON, JACK E.

APPLICANT: APPLICANT: APPLICANT:

APPLICANT

Sequence 2, Application US/08342930 Patent No. 5821084 GENERAL INFORMATION:

RESULT 15 US-08-342-930-2

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Gaps

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OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QRATIRRGDAPAGGAVPGGAVPGGRGPLLDG-WYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%; Score 65.5;
38.5%; Pred. No. 9.1
                                                                             E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 813-5600
(415) 494-0792
                                                                                                                                                                      ZID: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 38.5 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                            CORRESPONDENCE ADDRESS:
                                         NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                    Palo Alto
                                                                                                                                                            USA
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7, 2003, 16:53:34; Search time 15.2913 Seconds (without alignments) 306.927 Million cell updates/sec
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1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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2: /cgn2_b/ptodata/2/pubpaa/PENEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/RES06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/graz_c/ptodata/2/pubpaa/USO3_name.pep:*
/cgnz_6/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
/cgnz_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:*
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Description	Sequence 7, Appli Sequence 6, Appli Sequence 10, Appli Sequence 13, Appli Sequence 8, Appli Sequence 9, Appli Sequence 12, Appli Sequence 11, Appli Sequence 13, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 9, Appli
SUMMARIES	US-09-855-754-7 US-09-855-754-5 US-09-855-754-10 US-09-855-754-10 US-09-855-754-18 US-09-855-754-18 US-09-855-754-14 US-09-855-754-11 US-09-855-754-11 US-09-812-382-6 US-09-812-382-8 US-09-812-382-8 US-09-813-314-6 US-09-813-969A-60 US-09-813-184-60 US-09-817-969A-9 US-09-817-969A-9 US-09-817-969A-9 US-09-817-969A-9 US-09-817-96A-9 US-09-817-96A-9 US-09-817-96A-9 US-09-817-96A-9 US-09-817-96A-9
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Score	22 23 23 24 2 27 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Result No.	12 c 4 8 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Sequence 10, Appl Sequence 14, Appl Sequence 14, Appl Sequence 18, Appl	Sequence 13, Appl Sequence 58, Appl Sequence 13, Appl Sequence 58, Appl Sequence 37, Appl	, 4 4 'N N N	Sequence 6, Appliance 12, Appliance 12, Appliance 15, Appliance 15, Appliance 24, Appliance 21, Appl	Sequence 21, Appl Sequence 95, Appl Sequence 91, Appl Sequence 2, Appli Sequence 13, Appl
10 US-09-861-597-10 9 US-10-235-674-14 10 US-09-263-689-14 9 US-09-8820-843-18	10 US-09-817-9684-13 10 US-09-841-321A-13 10 US-09-841-321A-13 10 US-09-841-321A-58 10 US-09-877-965A-37 10 US-09-877-965A-37	10 US-09-837-969A-34 10 US-09-841-321A-34 9 US-09-883-343A-31 10 US-09-888-260-25 10 US-09-864-761-35807 10 US-09-782-980-15	10 0S-09-909-743-6 10 0S-09-901-216-12 10 0S-09-891-216-12 10 0S-09-881-752A-24 10 0S-09-881-752A-24 10 0S-09-881-305A-21 10 0S-08-817-965A-21	10 US-09-815-837-95 10 US-09-815-837-95 10 US-10-185-991-2 9 US-09-992-238-13
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Database :

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GGISO-MACLOUE, NICOLE
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERTION: BONDETELLA PARAPERTUSSIS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT PAPLICATION NUMBER: 05/09/855,754
CURRENT PALING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VAR. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICAMT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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100.0%; Score 272; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRGANISM: Bordetella bronchiseptica
US-09-855-754-7
                             Sequence 7, Application US/09855754
Publication No. US20020192237A1
                                                                                 GENERAL INFORMATION:
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-09-855-754-7
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US-09-855-754-13
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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRARAERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERBENC: 03495-0236-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOS
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Pred. No. 5.5e-21;
; Mismatches 0;
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Pred. No. 1.6e-18;
3; Mismatches 0
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100.0%; Score 272; Di
Best Local Similarity 100.0%; Pred. No. 5.5
Matches 5j; Conservative 0; Mismatches
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                                                                                                                               CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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Publication No. US20020192237A1
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TITLE OF INVENTION: POLYPEPTIDES CY
TITLE OF INVENTION: BORDETELLA PAI
TITLE OF INVENTION: LAMOUNCERIC CY
FILE REFERENCE: 03495-0206-00000
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85.78;
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Best Local Similarity 85.7
Matches 48; Conservative
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                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver.
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SOFTWARE: Patentin Ver.
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TITLE OF INVENTION: POLYPEPTIOES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIOES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

THE REPERENCE: 03495-0306-00000

CURRENT APPLICATION NUMBER: 2001-09-10
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Pred. No. 5.7e-19;
3; Mismatches 1;
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Pred. No. 5.9e-19;
3; Mismatches 3;
CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
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CURRENT APPLICATION NUMBER: US/09/855,754
                           CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-13
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PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 88.2%;
Matches 45; Conservative
                                                                               PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFWARE: Patentin Ver. 2.1
SEQ ID NO LOUR LENGTH: 56
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
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Gaps

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PREPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CIRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SSOFTMARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERFOCTINI IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                     1 QRATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                 Length 56;
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                                                   DB 9;
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73.8%; Pred. No. 2.7e-17;
Live 3; Mismatches 3;
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Pred. No. 1.3e-17;
3; Mismatches 3;
                                              Score 228.5; DB 9
Pred. No. 1.3e-17;
2; Mismatches 4
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US-09-855-754-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOURSAUX-EUDE, CAROLINE
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80.4%;
                                              84.0%;
80.4%;
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Best Local Similarity 80.43
Matches 45; Conservative
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Best Local Similarity 73.8
Matches 45; Conservative
                                                                                           Conservative
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                                              Query Match
Best Local Similarity
Matches 45; Conserv
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US-09-855-754-12
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    US-09-855-754-9
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LENGTH: 56
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LENGTH: 61
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUCSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: U5/09/085,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REITITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA PITTLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT PILING DATE: 2010-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                        Length 46;
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Pred. No. 7.9e-17;
----heq 0;
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                                                                                                                                                                                           0; Mismatches
                                                                                                                                                     Score 232.5;
Pred. No. 4.2
                                                               ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-8
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ORGANISM: Bordetella bronchiseptica
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US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09855754 Publication No. US20020192237A1
                                                                                                                                                     85.5%;
90.2%;
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90.2%;
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SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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Matches 46; Conservative
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Best Local Similarity
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LENGTH: 56
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                                       LENGTH:
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Gaps

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Gaps

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APPLICANT: UTIY, Dan
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
TITLE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
CURRENT APPLICATION NUMBER: US/09/841,321A
FRIOR PELING DATE: 2001-04-30
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 60/087155
PRIOR APPLICATION NUMBER: US 60/076297
PRIOR FILING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
      IIILE OF INVENTION: Injectable Implants For Tissue Augmentation and Restoration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 111;
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                                     CURRENT APPLICATION NUMBER: US/09/837,969A
CURRENT PELING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/258,723
PRIOR FILING DATE: 1999-02-26
PRIOR FLING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: US 60/087155
PRIOR PELING DATE: 1998-05-29
PRIOR PELING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 60
SEQ ID NO 60
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Pred. No. 1.5;
1; Mismatches
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Pred. No. 1.
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Sequence 60, Application US/09841321A

Patent No. US20020116069A1

GENERAL INFORMATION:
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ilarity 58.6%;
Conservative
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 58.6%;
Matches 17; Conservative
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                            FILE REFERENCE: BERL-020/03US
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
LOCATION: (1)..(111)
CTHER INFORMATION: Synthetic
US-09-837-969A-60
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; LOCATION: (1)..(111)

; OTHER INFORMATION: Synthetic

US-09-841-321A-60
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Best Local Similarity
Matches 17; Conserv
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US-09-837-969A-9
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                          Gaps
    -- PGGAVPGGFGPLLDGWYGVDVSDSTVDLA 50
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Sequence 6, Application US/09812382

Sequence 10. Sequence 10. Sequence 10. Sequence 5. Sequence 6. Application US/009812382

SEREAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chilkoti, Ashutosh

TITLE OF INVENTION: Fusion Peptides Isolatable by Phase Transition
FILE REFERENCE: 4176-101

CURRENT APPLICATION NUMBER: US/09/812,382

CURRENT FILING DATE: 2001-03-20

PRIOR APPLICATION NUMBER: US 60/190,659

PRIOR FILING DATE: 2000-03-20

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chilkoti, Ashutosh
TITLE OF INVENTION: Fusion Peptides Isolatable by Phase Transition
FILE REFERENCE: 4176-101
CURRENT APPLICATION NUMBER: US/09/812,382
CURRENT FILING DATE: 2001-03-20
PRIOR PLLING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-20
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Pred. No. 0.99;
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Pred. No. 0.14
0; Mismatches
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US-09-837-969A-60
Sequence 60, Application US/09837969A
Patent No. US20020038150A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 GAGVPGAGVPGGGVPGGCVPGGGVP 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GDAPAGGAVPGGAVPGGFGP 32
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63.6%;
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Best Local Similarity 60.09
Matches 15; Conservative
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Best Local Similarity 63.6
Matches 14; Conservative
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; ORGANISM: ELP[V5A2G3-90]
US-09-812-382-6
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US-09-812-382-3
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                                                                                                                      61 0 61
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

 protein search, using sw model OM protein 7, 2003, 16:41:02; Search time 9.55707 Seconds (without alignments) 513.008 Million cell updates/sec May Run on:

Title:

Perfect score:

US-09-855-754B-7 272 1 QRATIRRGDAPAGGAVPGGA......PLLDGWYGVDVSDSTVDLAQ Sequence:

51

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	pertactin - Bordet	ne	outer membrane pro	probable serine-th	ATP-dependent RNA	MFS18 protein - ma	elastin precursor	major merozoite su	dnaK-type molecula	major merozoite su	heat shock protein	glycine-rich prote	hypothetical prote	hypothetical prote	O)	hypothetical prote		_	sporozoite surface	glycine-rich cell	octamer binding tr	proteinase do (EC	hypothetical prote	elastin - bovine (hypothetical prote		protein-tyrosine-p	conserved hypothet	
SUMMARIES	a	S15204	A47675	A32560	T35389	T45677	S25103	EAMS	A28121	A49242 -	A45532	PC7036	JQ1063	T24865	T29167	T03166	A85217	T04441	S37108	A45560	T09262	159234	AG3328	T30743	145885	C95291	T49890	A55148	B75476	001
	DB	7	~	~	7	7	7	-	ď	~	7	~	~	7	N	~	~	7	~	~	~	7	7	~	~	~	7	-	7	c
	Length	922	911	910	783	646	128	860	680	989	1772	641	112	422	405	1300	179	277	231	907	97	420	524	361	16	136	185	1711	310	•
ď	Query Match	100.0	85.5	85.1	30.5	29.8	28.7		25.9	25.9	25.9	25.6	25.4	25.4	25.2	25.2	25.0	25.0	24.8	24.8	24.6	24.6	24.4	24.3	24.1	24.1	24.1	24.1	23.9	c
	Score	272	232.5	231.5	83	81	78	74	70.5	70.5	70.5	69.5	69	S.	68.5	68.5	68	99	67.5	67.5	29	S	66.5	99	65.5	65.5	Š.	65.5	65	2
	Result No.	-	7	e	4	S	9	7	80	σ	10	11	12	13	14	12	16	17	18	19	50	21	22	23	24	25	36	27	28	c

NAD-dependent form hypothetical prote molybdenum cofacto	hemagglutinin prec dnaK-type molecula hypothetical prote	dnaK-type molecula elastin precursor DNA repair protein	hypothetical prote spidroin 2, dragli CREB-binding prote	hypothetical prote 19E-binding protei	hypothetical prote hemagglutinin prec
C98152 AI3135 A84169	НМІ VНМ ННК W 7 A Т 2 1 3 9 4	S51712 EART B70804	T29299 A44112 T13828	T22572 A54889	T15155 HMIVTN
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114 114 278	566 640 640	656 864 480	589 627 3190	215 262	471 565
23.7 23.7 23.7	23.7 23.7	23.7 23.7 23.5	23.5 23.5 23.5	23.3	23.3
64.5 64.5	64.5 64.5 64.5	64.5 64.5 64.5	2 4 4 4 4 4	63.5	63.5 63.5
30 31 32	6 4 6 1	36 37 38	39 410	4 4 8 3	4 4 5

ALIGNMENTS

N'Alternate names; outer membrane protein P70 C;Species: Bordetella parapertussis C;Date: 07;Apr-1994 *sequence_revision 07-Apr-1994 *text_change 08-Oct-1999 C;Accession: S15204; S14659 R:Li, L.J.; Dougan, G.; Novotny, P.; Charles, I.G. Mol. Microbiol, 5, 409-417, 1991
A; Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo A; Reference number: S15204; MUD:91251771; PMID:2041476 A; Accession: S15204 A; Molecule type: DNA A; Residues: 1-922 < LIL>
A;Cross-references: EMBL:X54547; NID:g39761; PIDN:CAA38419.1; PID:g39762 C;Genetics: A;Gene: prn C;Keywords: membrane protein
Query Match 100.0%; Score 272; DB 2; Length 922; Best Local Similarity 100.0%; Pred. No. 3.6e-21; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 QAATIRRSDAPAGGAVPGGAVPGGFGPLLDCWYGVDVSDSTVDLAQ 51

RESULT 2

68K Outer membrane protein P.68 pertactin - Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C; Accession: A47675 R; Li, J.; Pairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Pairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G. J.; Gen. Microbiol. 138, 1697-1705, 1992 A; Title: Cloning, nucleotide sequence and heterologous expression of the protective o A; Contents: CN7531

A; Accession: A47675

A; Status: preliminary A; Modecule type: nucleic acid A; Residues: 1-911 (LII> A; Cross-reference;: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397 A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

2; Query Match 85.5%; Score 232.5; DB 2; Length 911; Best Local Similarity 90.2%; Pred. No. 5.3e-17; Matches 46; Conservative 0; Mismatches 0; Indels 5

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Gaps

1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51

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Gaps

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Cisuperfamily: elastin
Cisuperfamily: elastin
Ciseywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-660/Product: elastin #status predicted <MAT>
F;850-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAlternate names: tropoelastin
C;Species: Mus musculus (house mouse)
C;Apecies: Mus musculus (house mouse)
R;Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A;Filte: Use of an intron length polymorphism to localize the tropoelastin gene to r
A;Reference number: A55721; MUID:95130069; PMID:7829060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Zea mars (maize)
C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Date: 20 Feb-1995 #sequence_revision 20 Feb-1995 #text_change 29-Oct-1999
C; Accession: S25103
S; Windaht, S.Y.; Suner, M.M.; Bell, P.J.; Vaudin, M.; Greenland, A.J.
S; Windaht, S.Y.; Suner, M.M.; Bell, P.J.; Vaudin, M.; Greenland, A.J.
A; Reference number: S25103
A; Recession: S25103
A; Status: preliminary
A; Status: preliminary
A; Status: Pype: man
A; Residuse: 1-128 GWRLA
A; Residuses: 1-128 GWRLA
A; Residuses: EMBL:X67324; NID:922646; PIDN:CAA47738.1; PID:922647
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A;Residues: 1-860 <WYD>
A;Cross-references: GB:U08210; NID:g473273; PIDN:AAA80155.1; PID:g473274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 1; Length 860;
Pred. No. 3.1;
3; Mismatches 11; Indels
                                                                                                                                                                                                                                        Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: cultivar Columbia; BAC clone F14P22 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATIRRGDAPAGGAVPG----GAVPG----GAVPGGFGP 32
                                                                                                                                                                                                                                        Score 81; DB 2
Pred. No. 0.42;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GDAPAGGAVPGGAVPGGAVPG----GFGPLLDGW 37
                                                                                   A;Map position: 3
A;Introns: 239/3; 267/3; 348/3; 404/3; 442/3
A;Note: F14P22.160
C;Superfamily: ATP-dependent RNA helicase DBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.2%;
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.7%;
Best Local Similarity 44.1%;
Matches 15; Conservative
A; Cross-references: EMBL: AL137082
                                                                                                                                                                                                                                     29.8%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elastin precursor - mouse
                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
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R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.; Submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23011
A; Accession: T45677
                                                                                                                                                                                                                                                                          P.; Morriss
                                                                                                                                                                                                               C. Accession: A32560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morris: Proc. Natl. Acad. Sci. U.S.A. 86, 3554.3558, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 3554.3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.; Reference number: A32560; MuID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T35389
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL079348; PIDN:CAB45488.1; GSPDB:GN00070; SCOEDB:SC66T3.32c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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ATP-dependent RNA helicase-like protein - Arabidopsis thaliana
N;Alternate names: protein F14P22.160
N;Alternate names: protein F14P22.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable serine-threonine protein kinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
                                                                                                                                                                                   Species: Bordetella pertussis
Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross_references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054 A;Note: it is uncertain whether Met-1 or Met-3 is the initiator C;Keywords: membrane protein F;1-34/Domain: signal sequence #status predicted <SIG>F;1-34/Domain: signal sequence #status predicted <SIG>F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 QRATIRRGDALAGGAVPGGAVPGGRVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QRATIRRGDAPAGGAVPGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
      254 QRATIRRGDAPA----GGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                    outer membrane protein P.69 precursor - Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 231.5; DB 2;
Pred. No. 6.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 RGDAPAGGAVPGGAVPGGFGP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain A3(2) C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: SCOEDB:SC66T3.32c
C; Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.1%;
Best Local Similarity 82.1%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.5
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z21576
A; Accession: T35389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-783 <MUR>
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A; Residues: 1-646 <DAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-910 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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RESULT 4

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Gaps

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Matches

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Gaps

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Length 1772;

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R:Dally, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Blochem. Parasitlol. 36, 289-285, 1989
A:Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: cloni
A:Reference number: A45531; MUID:90014982; PMID:2797064
                                                                                                                                                                      A; Status: preliminary
A; Molecule type: DNA
A; Residues: 454-1094 CDAL>
A; Cross-references: GB:J03975; NID:g160081; PID:g160082
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
              A; Cross-references: GB: J04668; NID: 9160492; PID: 9160493
                                                                                                                                                                                                                                                                                                                                                                      Score 70.5; DB Pred. No. 15; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDAPAGGAVPG -- GAVPGGAVPGGFGPLLDG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Residues: 1-641 <CER>
A) Cross-references: GB:AF188289
C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 GGMPGGGGMPGGGAPGG-FPGG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GDAPAGGAVPGGAVPGG 29
                                                                                                                                                                                                                                                                                                                                                                   Query Match
25.9%;
Best Local Similarity 44.1%;
Matches 26; conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.6%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.1
Matches 13; Conservative
                                                                                                                                                    A; Accession: A45531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: J01053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dnax-type molecular chaperone hsp70 - Plasmodium cynomolgi

N;Alternate names: heat shock protein hsp70
C;Species: plasmodium cynomolgi
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A49242
R;Eckert, V.; Sanchez, L.; Cochrane, A.; Enea, V.
Exp. Parasitol. 75, 323-328, 1992
A;Title: Plasmodium cynomolgi: the hsp 70 gene.
A;Reference number: A49242; MuID:93050041; PMID:1426134
A;Accession: A49242
A;Accession: A49242
A;Accession: A49242
A;Accession: A49242
A;Nolecule type: nucleic acid
A;Accession: A69242
A;Nolecule type: nucleic acid
A;Residues: 1-686 AccK.
A;Cross-references: GB:M90978; NID:gl60349; PIDN:AAA29625.1; PID:gl60350
A;Note: sequence extracted from NCBI backbone (NCBIN:118975, NCBIP:118976)
C;Function: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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C;Species: Plasmodium yoelli
C;Species: Plasmodium yoelli
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C;Accession: A45532; A45531
R;Lewis, A.P.
Rol. Biochem. Parasitol. 36, 271-282, 1989
A;Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface A;Reference number: A45532; MUID:90014981; PMID:2797063
                                                                                                                          C; Accession: A28121
R; Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
R; Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
R; Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
R; Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
R; Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
A; Title: The 3' portion of the gene for a Plasmodium yoelii merozoite surface antigen A; Reference number: A28121; MUID:88124889; PMID:2448778
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: Branslated the codon GTA for residue 429 as Leu
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           š
                                                                                    Species: Plasmodium yoelii
Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 TILAADAPATPEGAVPGAVPGAVPGAVPGAVPGS------GTDTRVAGSSVD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TIRRGDAPA-----GGAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 686;
                                                       major merozoite surface antigen – Plasmodium yoelii (fragment)
C:Species: Plasmodium yoelii
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5; DB 2;
Pred. No. 5.7;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llarity 44.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.9%;
Best Local Similarity 46.9%;
Matches 15; Conservative
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les 26; Conserv
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A;Molecule type: DNA
A;Residues: 1-1772 <LEW>
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Matches
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RESULT 8
A28121
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R;de Oliveira, D.B.; Seurinck, J.; Inze, D.; Van Montagu, M.; Botterman, J. Plant Call 2, 427-438, 1990
Plant Call 2, 427-438, 1990
A;Title: Oliferential expression of five Arabidopsis genes encoding glycine-rich prot A;Reference number: JQ1060; MUID:93044485; PMID:2152168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycine-rich protein 4 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-pec-1991 #sequence_revision 31-bec-1991 #text_change 21-Jul-2000
C;Accession: JQ1063
                                                                                                                                                                                                                                                     C;Species: Rhizopus nigricans
C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
C;Accession: PC7036
                                                                        Gaps
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A;Residues: 1-112 <DEO>
A;Cross-references: GB:S47413; NID:g259448; PIDN:AAB24076.1; PID:g259449
A;Experimental source: strain C24
                                             4 TIRRGDAPA-----GGAVPG---GAVPG---GAVPGGFGPLLDGWYGVD--VSDSTVD
Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                           Ricerilla, B.; Cresnar, B.; Breskvar, K.
Blochem. Blophys. Res. Commun. 265, 494-498, 1999
A;Title: Induction of Hsp70 in the fungus Rhizopus nigricans. A;Reference number: UC7132; MUID:20025372; PMID:10558896
A;Accession: PC7036
A;Status: preliminary
A;Molecule type: mRNA
8
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                                                                                                                                                                                                                             heat shock protein 70 - Rhizopus nigricans (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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Pred. No. 6.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.4%; Score 69; DB Best Local Similarity 48.4%; Pred. No. 1.4; Matches 15; Conservative 3; Mismatches
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A;Experimental source: strain Bristol N2; clone T28H11
                                                                                                                                                                                                                                                                                                                                Submitted to the EMBL Data Library, December 1996.

A;Reference number: 220008
A;Accession: 175273
A;Accession: 175273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Bolccule type: DNA
A;Residues: 1-422 <W12>
A;Coss.references: EMBL: 283241; PIDN:CAB05818.1; GSPDB:GN00021; CESP:T12D8.8
A;Experimental source: clone T25C8
                                                                                                                                                                                                                                                              A;Cross-references: EMBL:281120; PIDN:CAB03349.1; GSPDB:GN00021; CESP:T12DB.8
A;Experimental source: clone T12D8
                    C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C; Accession: T24865; T25273
R; McMurray, A.
Submitted to the EMBL Data Library, October 1996
A; Reference number: 219944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ypothetical protein T28H11.5 - Caenorhabditis elegans
Species: Caenorhabditis elegans
bate: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 422;
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probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 88/1; 372/1
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nelson, J.; Wohldmann, P. submitted to the EMBL Data Library, July 1996 A;Description: The sequence of C. elegans cosmid T28H11. A;Reference number: 220582 A;Accession: T29167
hypothetical protein T12D8.8 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ATIRRGDAPAGGA-VPGGAVPGGAVPGGFGPLLDGWYGV 40
                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 5.6;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GGFPGAGGMPGGFPGAPGGAPGGMG 317
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A;Introns: 35/2; 157/2; 228/3; 375/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.4%;
Best Local Similarity 50.0%;
Matches 13; Conservative
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ilarity 41.0%;
Conservative (
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-405 <NEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: T28H11.5
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                                                                                                                                                                                                                                                                                                                 R; Gardner, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database :

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Q10265 schizosacch
P16770 human cytom
035984 mus musculu
P23118 strongyloce
P11133 influenza a
P26139 influenza a
P26139 influenza a
P10209 herpes simp
Q01877 pucchila gr
P47845 cyytotolagus
Q10707 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.95.
PERTACTIN (P.70).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordețella parapertussis.
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordețella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTINEALY.
OUTET | membrahe; Signal; Virulence; Repeat.
SIGNAL
SIGNAL
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                               PBX2_MOUSE
BIND_STRFN
HEMA_IAZH2
                                                                                                                        HEMA_IAEN7
HEMA_IAZCO
HEMA_IAVI7
                                                                                                                                                                                            UL25_HSV11
HS71_PUCGR
LEG3_RABIT
                                                                                                                                                                                                                                                                    YK98_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: |X54547| CAA38419.1; -
EMBL: A26144 CAA01786.1; -
EMBL: A19182 CAA01454.1; -
PIR: S15204 | S15204.
PIR: S14659; |S14659; |S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CN2591;
MEDLINE-91251771; PubMed-2041476;
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  643
424
424
430
430
550
550
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560
560
560
560
560
481
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1 QRAIIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ
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                    5.1.4_p5_4578
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                           112892 seqs, 41476328 residues
                    GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERT_BORPA
PERT_BORPE
PERT_BORBR
MF18_MAIZE
ELS_MOUSE
HS70_PLACB
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CUT2_CAEEL
BR3A_HUMAN
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HEMA_IAME2
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HS71_CANAL
ELS_RAT
RADA_MYCTU
SPD2_NEPCL
LEG3_RAT
HEMA_IATKP
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ELS_CHICK
LEG3_CANFA
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HS70_ALTAL
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                           (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
                 LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                 922;
                                                                                                                                                                                                                                                                                                                    254 QRATIRRGDAPAGGAVPGGAVPGGROFGFLLDGWYGVDVSDSTVDLAQ 304
                                                                                                                                                                                                                                                                                                  1 QRATIRRGDAPAGGAVPGGAVPGGRVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                            ; Score 272; DB 1;
; Pred. No. 7.3e-20;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        910 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE-89264462; Pubmed-2542937;
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REVISIONS TO 264 AND 332.
MEDLINE=92407514; Pubmed-
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                                                                                                                                                                                                                                   Similarity
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P14283;
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Matches 51
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Gaps

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Indels

Length 910;

B 1;

Score 241.5; DB 1 Pred. No. 7.6e-17;

3; Mismatches

47; Conservative

Matches

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Local Similarity

1 QRATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ 51

LINES). 5 x 5 AA TANDEM REPEATS OF G-G-A-V-P.

(APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P. A169871E20A2E7DB CRC64;

93452 MW; 88.8%; 83.9%;

910 AA;

SEQUENCE Query Match

(APPROXIMATE).

280 285 290 593

CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL

PERTACTIN (P.69).

POTENTIAL.

910 711 910 262

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SIGNAL

DOMAIN REPEAT

REPEAT REPEAT REPEAT REPEAT DOMAIN

Outer membrane; Signal; Virulence; Repeat.

InterPro; IPR004899; Pertact_sup. InterPro; IPR003992; pertactin. InterPro; IPR003991; pertactin_vir. Pfam; PF03122; Pertactin; 1. PRINTS; PR01482; PERTACTIN. PRINTS; PR01484; PRTACTINFAMLY.

PIR; A32560; A32560.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEO. MICTODIOI. 138:1697-1705(1992).

GEO. WICTODIOI. AGGLUTINOGEN THAT BINDS TO EUKARYOFIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

- SUBUNIT: MONOMER.

- SUBCELLULAR LOCATION: Outer membrane.

- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.

- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                    911 AA
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.; AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92407514; PubMed-1527510;
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                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                 Bordetella.
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EMBL; J04560; AAA22980.1; ALT_SEQ

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May 7, 2003, 16:38:52; Search time 26.0647 Seconds (without alignments) 403.166 Million cell updates/sec
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                           Run on:
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272 1 QRATIRRGDAPAGGAVPGGA.....PLLDGWYGVDVSDSTVDLAQ US-09-855-754B-7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_human:*
sp_invertebrate:* 8: sp_organelle:* sp_archea:* sp_bacteria:* sp_plant:* : sp_mammal:* SPTREMBL_21:* sp_fung1:* sp_phage: * sp_mhc:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_bacterlap:* sp_archeap:*

sp_unclassified:*

sp_rvirus:*

sp_vertebrate: *

sp_rodent:* sp_virus:*

SUMMARIES

		Description	O9k5a6 bordetella	O9k5g8 bordetella		_	09kiv3 bordetella	09kiv4 bordetella	O9s3m9 bordetella	O9s6nl bordetella	093199 bordetella	Q9s6m9 bordetella			069257 bordetella		Q8rsu0 bordetella	O9k5h6 hordetella
		ID	Q9K5G6	Q9K5G8	Q9K510	09AHP1	Q9KJY3	Q9KJY4	Q9S3M9	Q9S6N1	Q93L99	6M9S6Q	0N9S60	093705	069257	Q9ALQ1	Q8RSU0	09K5H6
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		Match Length DB	158	159	160	179	211	216	387	910	382	902	905	167	907	181	912	147
dР	Query	Match	100.0	100.0	100.0	100.0	100.0	95.4	88.8	88.8	98.6	98.6	88.6	87.9	87.3	87.1	86.4	85.5
		Score	272	272	272	272	272	259.5	241.5	241.5	241	241	241	239	237.5	237	235	232.5
	Result	No.	-	7	m	4	S	ø	7	&	თ	10	11	12	13	14	15	16

Q9k5hB bordetella	09k5h4 bordetella	Q9k5h0 bordetella	_		m		Q9kjy2 bordetella				09k5g2 bordetella		Q9s3m8 bordetella		_		Q9alp6 bordetella		8 nephila	nephila		_		nephila		Q9gpk0 heterodera	Q9vwn3 drosophila	Q8sx19 drosophila	
09к5н8	Q9K5H4	Q9K5H0	Q9K5H2	Q9ALQ5	Q9ALQ3	Q93ST1	Q9KJY2	Q9L4E2	O9ALP4	Q9K5G3	Q9K5G2	069259	09S3M8	088143	Q9AIX8	Q93L98	Q9ALP6	Q9ALP8	044358	Q9NHW2	Q9NHW4	044359	O9NHW3	Q9NHW1	Q9XAI1	Q9GPK0	O9VWN3	Q8SXL9	
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85.5	85.5	85.5	85.5	85.5	85.5	85.5	85.5	85.5	84.0	84.0	84.0		83.8	83.1	82.2	82.2	31.2	31.2	34.7	34.7	34.7	32.7	31.6	31.6	30.5	30.1	29.8	29.8	
232.5	232.5	232.5	232.5	ς.	~:	232.5	ς.	~	228.5	<u>.</u>			228	~	223.5	23	221	221	4	94.5	4		98		83	85	81	81	
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ALIGNMENTS

01-007-2000 (TrEMBLrel. 15, Created) 01-007-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Pertactin (Pi68) (Fragment). PRT; 09K5G6 09K5G6;

Bordetella bronchiseptica (Alcaligenes bronchisepticus). Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae; Bordetella. NCBL_TaxID=518;

MEDLINE-20359389; PubMed-10899896; SEQUENCE FROM N.A. STRAIN=CAT1;

Boursaux-Eude C., Guiso N.; "Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000) 158 158 158 AA; 15062 MW; F8ECD81013EBFDCC CRC64; NON_TER SEQUENCE

; ; Query Match
100.0%; Score 272; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 51; Conservative 0; Mismatches 0; Indels (ŏ

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Gaps

159 A.A. PRELIMINARY; Q9K5G8 Q9K5G8; RESULT 2 g

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Keil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
amino acid repeats.";
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                                                                                                                                                                                                                                                                                                                                                 Length 179;
                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTV-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
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211 AA; 20946 MW; E751FFA1510D99A4 CRC64;
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179 AA: 17270 MW; 325502FFB5483DF7 CRC64;
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1larity 100.0%; Pred. No. 2e-21;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e-21;
tive 0; Mismatches 0;
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-JUN-2001 (TrEMBLrel 17, ref.
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                                                                                                                                 STRAIN-MBORD831;
MEDLINE-21117018; PubMed-11179374;
Register K.B.;
                                                                                                                                                                                              bronchiseptica pertactin.";
Infect. Immun. 69:1917-1921(2001).
MBEJ: AF298589; AAK16690.1; ...
InterPro; IPR003992; pertactin.
PRINTS; PR01482; PERTACTIN.
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 Pertactin (Fragment).
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tes 51; Conserv
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09KJY4;
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertusis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
                                                                                                                                                                                                               Boursaux-Eude C., Guiso N.; "Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:415-417(2000).
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                               Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (P.68) (Fragment).
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Pred. No. 1.5e-21;
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100.0%; Pred. No. 1.5e-21;
ive 0; Mismatches 0;
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MEDLINE-20359389; PubMed-10899896;
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01-JUN-2001
01-DEC-2001
                                                                                                                   Bordetella.
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Q9K510;
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Length 211;

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"Polymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends
and evidence for vaccine-driven evolution.";
Infect. Immun. 66:670-675(1998).
EMBL; AJ133784; CAB40080.1;
InterPro; IPR00392; pertactin.
InterPro; IPR00399; pertactin.
InterPro; IPR004899; pertactin.
Pfam; P00212; Pertactin: 1.
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Weber C., Boursaux-Eude C., Njamkepo E., Guiso N.;
Weber C., Boursaux-Eude C., Njamkepo E., Guiso N.;
"Polymorphism of Bordetella pertussis isolates circulating the last ten years in France, a country using the same effective whole-cell and the more than thirty years.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mooi F.R., VanOirschot H., Heuvelman K., vanderHeide H., Gaastra Willems R.R.J.;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AJ309315; CAC48161.1;
NON_TER 382 382
                                                                                                          van Oirschot H.F.L.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 AA; 93495 MW; AF38246F8D82E03D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA; 38333 MW; 2803BDA9581AC8E6 CRC64;
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Last annotation update)
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PRINTS; PRO1484; PRTACTNFAMLY.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=520;
                                    MCBI_TaxID-520;
                                                                                             STRAIN-B567;
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Matches 45;
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ID Q9S6M9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                  Kell D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
                                                                                                                                                                                                                                                                                                                                                                                      154 QRAIIRRGDAPAGGAVPGGAVPGGAVPGGRAVPGFGPLLDGWYGVDVSDSTVDLAQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 QRATIRRGDAPAGGAVPGGAVPGGFGPGFGFGPVLDGWYGVDSSSVELAQ 309
                                                                                                                                                                                                                                                                                                                                                                  1 QRATIRRGDAPA-----GGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRATIRRGDAPAGGAVPGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                             DB 2; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 387;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                         Query Match
95.4%; Score 259.5; DB 2; Length
Best Local Similarity 91.1%; Pred. No. 4.3e-20;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                           amino acid repeats.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF156768; AAF82392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 34 POTENTIAL.
35 >387 PERTACTIN.
387 387
387 AA; 38714 MW; 61195D45D347A1EB CRC64;
                                                                                                                                                                                                                                                        216 AA; 21328 MW; 639C97ED3A012306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Pertactin precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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83.9%; Pred. No. 6.5e-18;
tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 AA.
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Best Local Similarity
Matches 47; Conserva
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                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  216
                                  NCBI_TaxID-518;
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                 Bordetella
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SEQUENCE
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SEQUENCE
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0983M9;
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RESULT 8 09S6N1

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Query Match 88.6'
Best Local Similarity 88.2'
Matches 45; Conservative
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Best Local Similarity 77.0°
Matches 47; Conservative
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01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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PRN OR PRN6.
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SEQUENCE FROM N.A.
STRAIN=18323;
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SEQUENCE
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"Polymorphism in the Bordetella pertussis virulence factors
P.69/pertactin and pertussis toxin in The Netherlands: temporal trends
and evidence for vaccine-driven evolution.";
Infect. Immun. 66:670-675 (1988).
EMBL; AJ13245; CAB39891.1;
InterPro; IPR003991; pertactin.
InterPro; IPR004899; pertactin.vir.
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                                                                                                                                                                                                                                                                                                                                           Mool F.R., He Q., Van Oirschot H., Mertsola J.; "Variation in the Bordetella pertussis virulence factors pertuss toxin and pertactin in vaccine strains and clinical isolates in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%; Score 241; DB 2; Length 905;
88.2%; Pred. No. 1.8e-17;
tive 3; Mismatches 3; Indels
                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERTACTIN.
7AE0F69C1B305E52 CRC64;
                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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EMBL; AJ011015; CAA09460.1; -
Interpro; IPR003992; pertactin.
Interpro; IPR004899; pertactin_vir.
Interpro; IPR004899; Pertact.sup.
Pfan; PR01342; Pertact.n; 1.
PRINTS; PR01482; PERTACTIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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35 905 Pi
905 AA; 93071 MW;
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Pfam; PF03212; Pertactin; 1.
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Matches 45; Conservative
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                                                                                                                                             Bordetella pertussis.
                                                                                                 Pertactin precursor
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NCBI_TaxID=520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weber C., Boursaux-Eude C., Nicole G.;
"Polymorphism of Bordetella pertussis isolates circulating the last ten years in France, a country using the same effective whole-cell vaccine since more than thirty years.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ318056; CAC67458.1; ...
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                                                                                                                                                                                              Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella. NCBI_TaxID=520;
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Pred. No. 4.9e-18;
3; Mismatches 1; Indels
                                                                                    Score 241; DB 2; Length 90
Pred. No. 1.8e-17;
3; Mismatches 3; Indels
                                                                                                                                                                          1 QRATIRRGDAPAGGAVPGGAVPGGRGPLLDGWYGVDVSDSTVDLAQ
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
- PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
SEQUENCE 905 AA; 93114 MW; 74B155EDB61059B4 CRC64;
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167 AA; 15826 MW; E136B4CF809565F0 CRC64;
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Last annotation update)
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88.2%;
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07,
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van Loo I.H., Mooi F.R.;
"Changes in the Bordetella pertussis population in the first 20 years
after the introduction of vaccination.";
Submitted (Fib-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430832; CAD23609.1;
SEQUENCE 912 AA; 93680 MW; 7F417BA66B732EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ORATIRRGDAPAGGAVPGGAV------PGGFGPLLDGWYGVDVSDSTVDLA 50
                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.4%; Score 235; DB 2; Length 91
75.4%; Pred. No. 7.9e-17;
Live 3; Mismatches 2; Indels
                                                  Created)
Last sequence update)
Last annotation update)
       912 AA
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       PRT;
                                                01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
     FRELIMINARY;
                                                                                                                                                                       Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                         STRAIN-B442;
                                                                                                                       Pertactin.
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                                                                                                                                      Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;

"Intranasal murine model of Bordetella pertussis infection: II.

"Sequence variation and protection induced by a tricomponent acellular

"Vaccine."; 12651-2660(1999).

"Waccine."; 12651-2660(1999).

"REMBL; AJ006152; CAA06894.1; -..

"REMBL; AJ006160; CAA06802.2; -..

"REMBL; AJ00160; CAA06802.2; -..

"InterPro; IPR003991; pertactin." vir.

"InterPro; IPR004899; Pertactin." vir.

"PR03312; Pertactin." vir.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 237.5; DB 2; Length
Pred. No. 4.3e-17;
3; Mismatches 2; Indels
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Pred. No. 8.7e-18;
3; Mismatches 4; Indels
van Oirschot H.F.L.M., Mooi F.R.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERTACTIN.
3A7D05F4094420EA CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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STRAIN-MBORD591;
MEDLINE-21117018; PubMed-11179374;
                                                                                                                       MEDLINE-99345256; Pubmed-10418915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93298 MW;
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82.1%;
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86.3%;
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Matches 44; Conservative
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907 AA;
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09ALQ1;
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Thu May
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76.0 45 76.0 45 76.0 45	74.2 51 23 74.2 922 13 74.2 922 23 72.2 922 23 58.8 46 23 58.8 911 12	58.8 911 13 58.8 911 23 53.6 36 23 62.0 59 23 61.7 36 23	6.40 6.40 6.40 6.40 7.40 7.40 7.40 7.40 7.40 7.40 7.40 7	100.2 100.2	34.1 20 23 33.8 445 22 30.2 15 23 30.2 137 22		ALIGNMENTS	T 1 188 AAE16188 standard; peptide; 56 AA. AAE16188;	MAR-2002 (first entry) bronchiseptica strain I-3 pertactin outer membrane protein region I	Pertactin; PRN; outer membrane protein; vaccine; therapy; antibiotic; antibacterial; region I. Bordetella bronchisentica	143-72.	001. 001; 2001WO-EP06457.	000; 2000US-206969P.	ASTE	maclouf N, Boursaux-eude C; 2002-097639/13.	containing polymorphisms of the Bordetella species, useful in in ections caused by Bordetella and
				***		39 91.5 40 91.5 42 91.5 44 91.5 45 91.5		RESULT 1 AAE16188 ID AAE16188 XX AC AAE16188;	26- B.		_	PD 29-NOV-2001. XX PF 23-MAY-2001;	XX PR 25-MAY-2000;		Guisc WPI;	AA Polypeptides PT pertactin in PT treating infe
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	es/sec		,								ed,			ica	eptica pertuss pertuss	tica al an al an al an
.4_p5_4578 pugen Ltd.	Seconds ts)	PVLDGWYGVDVSGSTVELAQ 56		s: 908470		eqp-embl/AA1980.DAT:* eqp-embl/AA1981.DAT:* eqp-embl/AA1983.DAT:* eqp-embl/AA1983.DAT:* eqp-embl/AA1984.DAT:*	eqp-embl/AA1985.DAT:* eqp-embl/AA1986.DAT:* eqp-embl/AA1987.DAT:* eqp-embl/AA1988.DAT:* seqp-embl/AA1988.DAT:*	<pre>seqp-embl/Aa1990.DAT:* seqp-embl/AA1991.DAT:* seqp-embl/AA1992.DAT:* seqp-embl/AA1993.DAT:* seqp-embl/AA1994.DAT:* seqp-embl/AA1994.DAT:*</pre>	seqp-embl/AA1996.DAT:* seqp-embl/AA1997.DAT:* seqp-embl/AA1998.DAT:*	seqp-embl/Aa2000.DAT:* seqp-embl/Aa2001.DAT:* seqp-embl/Aa2002.DAT:*	ed by chance to have a f the result being printed ore distribution.		Description	bronch bronch	B. bronchiseptica Bordetella pertuss Bordetella pertuss	B. Dronchiseptica F647 monoclonal a FeM3 monoclonal a PeM4 monoclonal a
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	ت	54B-9 NAPAGGGVPGGAPVLDGWYGVDVSGSTVELAQ 5	Gapop 10.0 , Gapext 0.5 908470 segs, 133250620 residues	f hits satisfying chosen parameters: 908470 length: 0 length: 2000000000	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_101002:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1983.DAT:* /SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1983.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*	/SIDSZ/gcgdata/geneseq/genesegp-embl/AA1985.DAT:* /SIDSZ/gcgdata/geneseq/genesegp-embl/AA1986.DAT:* /SIDSZ/gcgdata/geneseq/genesegp-embl/AA1987.DAT:* /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1988.DAT:* /SIDSZ/gcgdata/qeneseg/genesegp-embl/AA1989.DAT:*	11: /SIDS2/gcgdata/geneseq/geneseqp-embl/Aa1990.DAT:* 12: /SIDS2/gcgdata/geneseq/geneseqp-embl/Ab1991.DAT:* 13: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Ab1992.DAT:* 14: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Aa1993.DAT:* 15: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Aa1993.DAT:* 15: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Ab1993.DAT:* 16: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Ab1994.DAT:* 16: /SIDS2/gcgdata/geneseqy/geneseqp-embl/Ab1994.DAT:*	/: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* /: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:* /: /SIDS2/gcgdata/geneseqp-embl/AB1998.DAT:* /: /SIDS2/gcgdata/geneseqp-embl/AB1998.DAT:*	1: /SIDS2/gcgdata/geneseq/genesegp-embl/AA2000.DAT:* 2: /SIDS2/gcgdata/geneseq/genesegp-embl/AA2001.DAT:* 1: /SIDS2/gcgdata/geneseq/genesegp-embl/AA2002.DAT:*	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being print derived by analysis of the total score distribution.	SUMMARIES	Query Match Length DB ID	56 23 AAB16188 B. 56 23 AAB16191 B.	56 23 AAE16189 B. bronchis 910 23 AAE16184 Bordetella 910 23 AAE17146 Bordetella 61 23 AAE17146 Bordetella	23 AAE16192 23 AAE17153 23 AAE17154 23 AAE17155

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
Claim 26; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AA;
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Sequence

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Gaps
                                               ;
                Length 56;
                                               Indels
             100.0%; Score 308; DB 23;
100.0%; Pred. No. 9.7e-25;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.00
Local Similarity 100.00
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1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 g ò

AAE16191 RESULT

AAE16191 standard; peptide; 56 AA.

AAE16191;

26-MAR-2002 (first entry)

B. bronchiseptica strain prn3 pertactin outer membrane protein region I.

Pertactin, PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region I.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P.

(INSP) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Disclosure; Fig 1b; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

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B. bronchiseptica strain prn1 pertactin outer membrane protein region I.
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                                                          Gaps
Bordetella in a material. The present sequence is B. bronchiseptica
pertactin outer membrane protein region I.
                                                                         1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPVLDGWYGVDVSGSTVELAQ 56
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                                         DB 23;
                                       Score 291; DB 23;
Pred. No. 5.4e-23;
1; Mismatches 2
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                                                                                                                                    AAE16189 standard; peptide; 56
                                         94.5%;
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                                                         53; Conservative
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                                         Query Match
Best Local Similarity
                        56 AA;
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Matches
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(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods invention relates to Bordetella bronchiseptica pertactin Disclosure; Fig 1b; 47pp; English. present

56 AA; Sequence

Gaps ö 3; Indels Score 281; DB 23; Pred. No. 5.7e-22; Pred. No. 5.7e 1; Mismatches 91.2%; 92.9%; Query Match 91.2 Best Local Similarity 92.9 Matches 52; Conservative

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1 QRATIRRGDAPAGGAVPGGAVPGGRAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 56 1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 ô g Location/Qualiflers 597..604 /note= "Conserved region"

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Pertactin; pinl; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                   Bordetella pertussis pertactin (Prn1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 35-38; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              (NEWE-) NEDERLANDEN MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000EP-0202309.
                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001WO-NL00493
               18-APR-2002 (first entry)
                                                                                                                                                                  Bordetella pertussis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal cells, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. pertussis pertactin outer membrane protein, p.69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                  Pertactin; PRN: outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                              Bordetella pertussis pertactin outer membrane protein, p.69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 281; DB 23;
Pred. No. 7.7e-21;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                   /note= "Pertactin region II"
                                                                                                                                                                                                                                                                                                            254..309
/note= "Pertactin region I"
568..609
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                             AAE16184 standard; Protein; 910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 31; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2001; 2001WO-EP06457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-206969P
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                     Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD26441
                                                                                                                                                                                                                                                                                                                                                                                                    WO200190143-A2
                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                    AAE16184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                            Key
Region
                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
         RESULT 4
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polio and infections caused by Haemorphilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is B. pertussis prn1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. bronchiseptica strain prn2 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                        1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                                     Length 910;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                             91.2%; Score 281; DB 23;
92.9%; Pred. No. 7.7e-21;
11ve 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16190 standard; peptide; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.9
Matches 52; Conservative
                                                                                                                                                                                                                                                                              910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200190143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE16190;
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AAE17146 standard; Protein; 910 AA.

AAE17146;

AAE17146 ID AAE1 XX AC AAE1

RESULT

g ò

1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ

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Couter membrane protein or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                                                                                                           Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to Bordetella bronchiseptica pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QRATIRRGDAPAGGAVPGGAV-----PGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F647 monoclonal antibody specific for region 1 of pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.6%; Score 254.5; DB 23; Length Best Local Similarity 87.5%; Pred. No. 2.7e-19; Matches 49; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pertactin outer membrane protein region I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
   Boursaux-eude C;
                                                                                                                                                                                                                                                                                          Disclosure; Fig 1b; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEWE-) NEDERLANDEN MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE17153 standard; Protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001; 2001WO-NL00493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                   WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AA;
Guiso-maclouf N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200200695-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE17153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mooi FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
NAME OF COLOR OF PARTY OF PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain prn4 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic. compositions for treating infections caused by Bordetella and in diagnostic methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 278.5; DB 23; Length 61;
Pred. No. 1.1e-21;
1; Mismatches 2; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; antibiotic; antibacterial; region I.
                                                                                                                                                                                                                                                                                                                         Guiso-maclouf N, Boursaux-eude C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1b; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%;
86.9%;
                                                                                                     23-MAY-2001; 2001WO-EP06457.
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                                                                                                                                                                         25-MAY-2000; 2000US-206969P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                 (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-097639/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertactin; PRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190143-A2
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                          29-NOV-2001
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RESULT 7

AAE16192;

Sequence

Matches

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Gaps

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caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region 1 of pertactin used for epitope mapping and vaccination.

45 AA;

Sequence

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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polito and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune responses against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present used for epitope mapping and vaccination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PeM3 monoclonal antibody specific for region 1 of pertactin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATIRRGDAPAGGAVPGGAVPGGAVPGGFGPGFGPGFGPVLDGWYGVDV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 234; DB 23;
Pred. No. 3.1e-17;
0; Mismatches 3;
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Example 1; Fig 2a; 52pp; English.
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/note= "Epitope"
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Best Local Similarity 93.3%;
Matches 42; Conservative
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      Length 45;
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Pred. No. 3.1e-17;
0; Mismatches 3;
Score 234; DB 23;
Pred. No. 3.1e-17;
0; Mismatches 3;
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26..35
/note= "Epitope"
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   76.0%;
93.3%;
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Matches 42; Conservative
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les 42; Conserv
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Query Match
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Pertactin; prnl; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
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                                                                                                                   PeM70 monoclonal antibody specific for region 1 of pertactin
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/note= "Epitope"
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diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy;
immune response; antibody.
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Pred. No. 3.1e-17;
0; Mismatches 3;
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2002 (first entry)
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Best Local Similarity 93.3
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-139897/18.
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AAE17157
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, polio and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections sequence is a monoclonal antibody specific to region I of pertactin used for epitope mapping and vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
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Pred. No. 3.1e-17;
0; Mismatches 3; Indels
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llarity 93.3%;
Conservative
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The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prol). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and other infectious diseases of mammals including diphtheria, tetanus, pollo and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and/or diagnostic purposes, particularly for treating or preventing infections sequence is a monoclonal antibody specific to region 1 of pertactin used for epitope mapping and vaccination.
                                                                                                                                                                             New polypeptides derived from Bordetella pertussis pertactin, useful as a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B. bronchiseptica strain I-1 pertactin outer membrane protein region I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region I.
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Pred. No. 3.1e-17;
0; Mismatches 3; Indels
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                                                          (NEWE-) NEDERLANDEN MIN WELZIJN
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93.3%;
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Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polypeptides derived from Bordetella pertussis pertactin (Prn1). The polypeptide is useful in the preparation of vaccines against B. pertussis, B. parapertussis, B. bonochiseptica and other infectious diseases of amammals including diphtheria, tetanus, polico and infections caused by Haemophilus influenza b. The polypeptide is especially useful for eliciting an immune response against Bordetella sp. Antibodies against the polypeptide may be used for pharmaceutical and diagnostic purposes, particularly for treating or preventing infections caused by Bordetella pertussis or Bordetella parapertussis. The present sequence is a monoclonal antibody specific to region I of pertactin used for epitope mapping and vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine; diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy; immune response; antibody.
                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides derived from Bordetella pertussis pertactin, useful a vaccine against infections caused by Bordetella strains, and other infectious diseases of mammals, e.g. diphtheria, tetanus, or polio
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Pred. No. 3.1e-17;
0; Mismatches 3;
          Location/Qualiflers
31..35
/note= "Epitope"
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/note= "Epitope"
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93.3%;
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                                                                                                                                    03-JAN-2002
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Best Local 3
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Region
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                 Key
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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when sed in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region I.

Sequence

Gaps 5; Query Match

Query Match

74.2%; Score 228.5; DB 23; Length 51;
Best Local Similarity 80.4%; Pred. No. 1.3e-16;
Matches 45; Conservative 2; Mismatches 4; Indels 5

1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 ò qq

Search completed: May 7, 2003, 16:47:03 Job time : 30.0971 secs

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7, 2003, 16:41:51; Search time 9.25383 Seconds (without alignments) 178.054 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-010-928B-4

US-09-010-928B-2

US-08-455-069-4

US-08-425-069-4

US-08-356-978B-6

US-09-247-806-9

US-09-247-806-9

US-09-247-806-9

US-09-247-806-10

US-09-247-806-10

US-09-247-806-10

US-09-26-978B-18

US-09-26-978B-18

US-09-26-978B-18

US-09-26-978B-18

US-09-26-978B-18

US-09-26-978B-18

US-09-010-928B-7

US-08-556-978B-59

US-08-556-978B-18
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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228.5
212
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116
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00001000000000000000000000000000000000	RESULT 1 US-08-460-26 Sequence 2 Sequence 4 GENERAL TIT TIT TIT TIT TIT TIT TIT TIT TIT TI	Query Match Best Local S Matches 51 Qy 1 QRAT Db 254 QRAT
777 733 700 669 669 700 700 700 700 700 700 700 700 700 70	SGULT 1 -08-460-269C-2 Sequence 2, Appl 1 Patent No. 619754 GENERAL INFORMAT TITLE OF I NUMBER OF CONFESSION CONFESSION CONFUTER IF COMPUTER IF COMPUT	Match ocal Sin s 51; l QRATII
22222222222222 222222222222222 22222222	ALIGI LT 1 #640-269C-2 quence 2, Application US/08460269C quence 2, Application US/08460269C tent No. 6197548 GENERAL INFORMATION: ROMANOS, MICHAEL A. TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: 2200 Clarendon Blvc CITY: ARLINGTON STATE: VA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: TBM PC COMPATIBLE COMPUTER: TBM PC COMPATION SOFTWARE: PATENTION UNMBER: 37,06; REGISTRATION NUMBER: 37,06; REGISTRATION NUMBER: 37,06; REGISTRATION NUMBER: 37,06; REGISTRATION NUMBER: 37,06; RECOUNTER: COMPATION: 22: CECURNCE CHARACTERISTICS: LEALPHNOW: (703) 243-6410 TOPOLOGY: Linear MOLECULE TYPE: ADDRESS POLICALE TYPE: ADDRESS POLICAL TYPE: ADDRESS POLICA	h Similarity 51; Conser ATIRRGDAPAG
35 35 35 35 35 35 35 35 35 45 45 43 43 43 44 43 44 43 44 44 43 44 44 44	E ADDRE ADDR	88.0%; larity 91.1%; conservative dDAPAGGGVPGGAVE
	PEFREY MICHAN MICHAN MICHAN 17 17 17 17 17 17 17 17 17 17 17 17 17	* * * ; * * ; * * ; * * ; * * ; * * ;
US-08-209-747-52 US-08-458-298-52 US-08-556-9788-46 US-08-963-168C-9 US-08-963-168C-9 US-08-963-168C-9 US-08-541-139-14 US-08-542-051-32 US-08-542-051-32 US-08-542-051-32 US-08-542-051-33 US-08-542-051-33 US-08-542-051-38 US-08	GUMENTS GUMENTS Zelano vd., Sul MS-DOS e #1.0, /460,269 67 Popov-2	tch 88.0%; Score 271; DB 4; Length 910; al Similarity 91.1%; Pred. No. 5.6e-22; Indels 0.51; Conservative 1; Mismatches 4; Indels 0. QRATIRRGDARGGOVPGGAVPGGFDPGGFCPGGFCPCMYGVYGGTVPLAQ
4	ROLOGOUS PROTEIN 6 Branigan, P.C. te 1400 Version #1.30 C	3 4; Length 3-22; 4; Indel. LDGWYGVDVSGS /LDGWYGVDVSGS
sednence sed	NI C	. 56
7 2 3 4 4 6 7 7 7 8 7 8 7 7 8 7 8 7 7 8 7 7 8 7 8		Gaps
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APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TIRRGDAP------AGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 907;
                                                                                                                                                                                                                                                                                                                                                                                               Score 212; DB 4; Length 911;
Pred. No. 1.6e-15;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/09/010,928B FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120.5; DB 2
Pred. No. 1.7e-05;
1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: BIRCH, STEWART, KOLASCH & BIRCH 8110 GATEHOUSE RD. SUITE 500E
                                       ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/460,269C
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09010928B
Patent No. 5994099
GENERAL INFORMATION:
                                                                                                                                                                                                                                                LENGTH: 911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy Jr., Gerald M REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    68.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 amino acids amino acids
                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-010-928B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 8110 GATEHOU
CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STAT
ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-010-928B-4
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Sequence 4, Application US/08460269C
Batent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAREL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                   ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 922;
                                                                                                                                                                                                                                                Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Brani,
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 228.5; DB 4,
Pred. No. 2.5e-17;
2; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Ze
STREET: 2200 Clarendon Blvd
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                           Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION: APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.2%;
Best Local Similarity 80.4%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22201
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         RESULT 2
US-08-460-269C-6
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TRANSFORMED CELL
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TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CEI
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ATTRRGDAPAGGVPGGAVPGGFDPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                   Length 870;
                                                                                                                                                                                                                                                                                                                                         8 GDAPAGGGV-PGGAVPGGFDPGGFGPGGFGP--VLDGWYGVDVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.7%; Score 91.5; DB 1;
41.5%; Pred. No. 0.016;
tive 3; Mismatches 25;
                                                                                                                                                                                                                                   Score 116; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE; Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                        Pred. No. 5e-05;
                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MULPHY JI., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/POCKET NUMBER: 1447-106P
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08425069
Patent No. 5728810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis, Randolph V.
Xu, Ming
Hinman, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
    NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 2997
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                 37.7%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 595 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 205-8050
                                                                                                          870 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.53
Matches 22; Conservative
                                                                                                                                                                                                                                                                          Conservative
                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 870 amino act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                    protein
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ADDRESSEE: Birch, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                             amino acid
                                                                                                                                                                                                                                                Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lewis,
                                                                                                                                                              ; MOLECULE TYPE:
US-09-010-928B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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COUNTRY:
                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-425-069-4
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                                    Patent No. 5994099
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       576 GGAGGSGGVGPGGSGPGGYGPGGYGPGGSGPGGYGPGGSGS 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GDAPAGGGV-PGGAVPGGFDPGGFGPG--VLDGWYGVDVSGS 50
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , DB 2;
4.3e-05;
                                                                                                                                                                                                  SSEE: BIRCH, STEWART, KOLASCH & BIRCH ;: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: BIRCH, STEWART, KOLASCH & BIRCH
P: 8110 GATEHOUSE RD. SUITE 500E
FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 116;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                       UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                   Sequence 28, Application US/09010928B
Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09010928B
Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.78;
56.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-010-928B-28
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                 VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2; CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22042
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JS-09-010-928B-28
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-010-928B-2
                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                   STATE:
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DB 4; Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90.5; DB 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                      US/08/556,978B
                                                                                                                                                                                       08/077,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09247806
Patent No. 6280747
                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 08/077,60
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
RECISTRATION UNBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9
OPERATING SYSTEM: MICROSOFF SOFTWARE: MICROSOFF
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.4%;
Best Local Similarity 43.8%;
Matches 21; Conservative 3
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Best Local Similarity 43.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Nephila clavipes
US-09-247-806-9
                                                                                   CURRENT. APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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; MOLECULE TYPE: peptide
US-08-556-978B-60
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US-09-247-806-9
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: XL, Ming
APPLICANT: XL, Ming
APPLICANT: MINGALIB
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: COTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60, Application US/08556978B
Patent No. 6268169
GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; DB 2; 1
0.016;
ches 25;
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 91.5; DB pred. No. 0.016 3; Mismatches
                                                                                                      Sequence 4, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MUTPhy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 241-1300
(703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.7%;
Best Local Similarity 41.5%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                              Virginia
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELAWARE
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US-08-556-978B-60
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Gaps

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GENERAL INFORMATION:

APPLICANT: PHILLIPPE, Michel

APPLICANT: PHILLIPPE, Michel

APPLICANT: GRSON, Jean-Claude

APPLICANT: ARRANDEAU, Jean-Pleire

TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT

TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN

TITLE OF INVENTION: ANALOG

FILE REFERENCE: 6388-0365-0

CURRENT APPLICATION NUMBER: US/09/247,806
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Pred. No. 0.0037;
2; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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UNITED STATES OF AMERICA

19898

COUNTRY:

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH

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Score 90.5; DB 4; Length 714; Pred. No. 0.025; Mismatches 22; Indels
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                                                                                                                      8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Voulie, Pierre G.
APPLICANT: Coulie, Pierre G.
APPLICANT: Lucas, Sophie
APPLICANT: Hoon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 90; DB 2;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
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0; Mismatches
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                                                                                                                                                                                                                                     Sequence 8, Application US/08845998
Patent No. 5879892
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Patent No. 6130052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECISTRATION NUMBER: (0,21)
REFERENCE/POCKET NUMBER: L(FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.2%;
                      29.4%;
illarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 420 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-845-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                      Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02210
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                                                                                                                                                                                                RESULT 13
US-08-845-998-8
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APPLICANT: GARSON, Jean-Claude
APPLICANT: GARSON, Jean-Claude
TITLE OF INVENTION: COSMETT ON DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER FILING DATE: 1999-02-11
SALIER FILING DATE: 1998-02-11
SALIER PILING DATE: 1998-02-11
SEQ ID NO:
LENGTH: 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90.5; DB 4; Length 714; Pred. No. 0.025; 2; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:protein US-09-247-806-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                  NOVEL RECOMBINANTLY PRODUCED SPIDER SILK ANALOGS
                                                                                                                                                                                                                                   E: DISKETTE, 3.50 INCH
IBM PC COMPATIBLE
SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD FOR WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR-9389-A
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                   STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                               CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/07,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-247-806-10
Sequence 10, Application US/09247806
Fatent No. 6280747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....OGY: unknown ; MOLECULE TYPE: protein US-08-556-9788-61
                                                       NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU 1
                                                                                                                                                                                                              COMPUTER READABLE FORM MEDIUM TYPE: DISKET
                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
APPLICANT: FAHNESTC
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                  WILMINTON
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                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                            19898
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APPLICANT: Coulle, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thiery
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
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Gaps
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                                                                                                                                                                                                                                                                                                                                                               29.2%; Score 90; DB 4; Length 420; 60.0%; Pred. No. 0.016; Live 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 GGGPGGGGPGGGGGGGGGGGGGG 179
                                                                    NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERNCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GDAPAGGGVPGGAVPGGFDPGGFGPGFGP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 7, 2003, 16:56:58
Job time: 10.3447 secs
        APPLICATION NUMBER: 08/845,998
                                                                                                                                                                       TELEFAX: (61)720-2441
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-430-854-8
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29.2%; Score 90; DB 4; Length 420;
Best Local Similarity 60.0%; Pred. No. 0.016;
Matches 18; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
                                          E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPHONE: (617)720-3441
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GDAPAGGGVPGGAVPGGFDPGGFGP 37
                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 420 amino acids
amino acid
GY: linear
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-206-537-8
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                     STATE: MA
COUNTRY: US
TO: 02210
                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                            FILING DATE
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Simet, Charles
APPLICANT: Locas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEGKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

Sequence 8, Application US/09430854 Patent No. 6271019 GENERAL INFORMATION:

RESULT 15 US-09-430-854-8

ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

02210

STATE: M COUNTRY:

APPLICATION NUMBER: US/09/430,854

CLASSIFICATION: PRIOR APPLICATION DATA:

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Sequence 9, Appl. Sequence 194, App Sequence 60, Appl. Sequence 119, Appl. Sequence 14, Appl. Sequence 14, Appl. Sequence 15, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 37, Appl. Sequence 34, Appl. Sequence 34, Appl. Sequence 16, Appl. Sequence 21, Appl.

Sequence:

Run on:

Searched:

Database

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Sequence 12, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUTANAY.
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOUGSAUX-EUDE, CAROLINE
APPLICANT: BOUGSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEAT
TITLE OF INVENTION: BEGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT PAPLICATION UNBER: US/09/855,754
CURRENT PILING DATE: 2000-09-10
PRIOR APPLICATION UNBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHELLY
SOFTWARE: PATCHELLY
SOFTWARE: PATCHELLY
SOFTWARE: PATCHELLY
SOFTWARE: PATCHELY
SOFTWARE
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US-078-770-194

US-09-847-956A-60

US-09-841-321A-60

US-09-841-321A-60

US-10-235-674-14

US-10-283-689-14

US-09-919-172-41

US-09-919-172-41

US-09-964-761-35807

US-09-964-761-35807

US-09-881-260-25

US-09-817-969A-37

US-09-841-321A-37

US-09-841-321A-37

US-09-934-323-2

US-09-934-323-2

US-09-934-323-3

US-09-934-323-3

US-09-934-323-3

US-09-934-323-3

US-09-934-323-3

US-09-934-323-3

US-09-984-323-3

US-09-984-323-3

US-09-984-323-3

US-09-984-323-3

US-09-984-323-3

US-09-984-323-3

US-09-984-323-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-010-4
US-09-837-969A-21
US-09-841-321A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                      US-09-855-754-12
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Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 6012, Ap
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                                                                                                                                                    (without alignments)
306.927 Million cell updates/sec
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                                                                                                                                                                                                                                                1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ
                                                                                                                                  ; Search time 16.7905 Seconds
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/ cgn2_6/prodata/2/puppaa/PCT_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO6_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO6_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO7_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO9_NEW_PUB.pep:*
/ cgn2_6/prodata/2/puppaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/puppaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
/ cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 US-09-855-754-9
9 US-09-855-754-10
9 US-09-855-754-11
9 US-09-855-754-11
9 US-09-855-754-7
10S-09-855-754-7
10S-09-855-754-7
10S-09-855-754-7
10S-09-855-754-6
US-09-855-754-6
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US-09-855-754-6
US-09-851-597-9
1 US-09-812-882-6
US-09-812-882-6
US-09-812-882-6
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US-09-812-882-6
US-09-812-882-6
US-09-812-882-8
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                                                                                                                                                                                                                                                                                                                                                 349150 seqs, 92025710 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                  7, 2003, 16:53:34
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length: 2000000000
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Match Length
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274.5
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90.5
88
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CURRENT APPLICATION NUMBER: US/09/855,754
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US-09-855-754-13
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LENGTH: 910
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US-09-855-754-5
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TITLE OF INVENTION: POLYEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND SORDETELLA
TITLE OF INVENTION: RANDONGHISEPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: FOLTPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: FOLTPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
GURRENT PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
RIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PARENTE 1200-05-25
SOFTWARE: PARENTE 1200-05-25
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 12
LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 291; DB 9;
Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT CORGANISM: Bordetella bronchiseptica US-09-855-754-10
                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Bordetella bronchiseptica
US-09-855-754-12
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APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-855-754-10
; Sequence 10, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
; APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              ch 94.5%;
l Similarity 94.6%;
53; Conservative
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Best Local Similarity
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US-09-855-754-11
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LENGTH: 56
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Best Local
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDETSEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPGFGPVLDGWYGVDVSDSSVELAQ 309
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 4.8e-21;
1; Mismatches 2;
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89.0%; Score 274; DB 9;
Best Local Similarity 91.1%; Pred. No. 1.7e-19;
Matches 51; Conservative 1; Mismatches 4
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 61
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                                                                                                                                                                                                                             ); TYPE: PRT
() ORGANISM: Bordetella bronchiseptica
US-09-855-754-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 5, Application US/09855754
Publication No. US20020192237Al
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella pertussis
US-09-855-754-5
                                                                                                                                                                                                                                                                                                                                                  90.4%;
86.9%;
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 86.9
Matches 53; Conservative
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SEQ ID NO 4
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         SEQ ID NO 6
LENGTH: 922
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                                                      TYPE: PRT
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Best Local
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
GURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Publication to. US2002019237A1
GENERAL INFORMATION:
APPLICANT: BUURSAUX-EUDE, CAROLINE
APPLICANT: BUURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLUOF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTERPRETATION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTERPRETATION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                                                   Length 51;
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Pred. No. 9.5e-19;
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION UNDER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 51
                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                              ch 82.6%;
1 Similarity 87.5%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Matches 49; Conserv
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Matches
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FALLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60,206-969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VET: 2.1
SED ID NO SECULIAR OF SECULIAR
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APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CHRRENT PILLION DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 020206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                       1 ORATIREGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
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                                                                                                                                           Length 922;
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                                                                                                                                      DB 9;
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Pred. No. 1.4e-14;
2; Mismatches 2
                                                                                                                                 Score 228.5; DB 9
Pred. No. 5.3e-15;
                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-8
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US-09-855-754-4
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;; Sequence 8, Application US/09855754
;; Publication No. US20020192237A1
; GENERAL INFORMATION:
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ilarity 75.0%;
Conservative 2
                                                                                                                                      74.2%;
80.4%;
                                                                                                                                                                                                                                 45; Conservative
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                                                                                                                                                              Best Local Similarity
Matches 45; Conserv
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Length 714;

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Similarity
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US-09-861-597-2
Query Match
Best Local S
Matches 21
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APPLICANT: GARSON, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REPREMENDE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-02-11
PRIOR FILING DATE: 1999-02-11
SPIOR PILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 14
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APPLICANT: GARSON, Jean-Claude
APPLICANT: GRASON, Jean-Claude
APPLICANT: ARRADDBAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ARABLOG
FILE REPERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
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                                                                                                                              254 QRAIIRRGDAPAGGAVPGGAV------PGGFGPLLDGWYGVDVSDSTVDLAQ 299
                                                               10;
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                                                                                                        1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
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                     Length 911;
                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GQQGPSGPGSAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.033;
                     Score 212; DB 9;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/247, 806
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: FR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GSAAAAAGPGQGPGGYGPGQQGPGGYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09861597 Patent No. US20020064539A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Sequence 9, Application US/09861597
Patent No. US20020064539Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 29.4%;
1 Similarity 43.8%;
21; Conservative
                     68.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PHILLIPPE, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Nephila clavipes
US-09-861-597-9
                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                     Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-861-597-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10
LENGTH: 714
                                                                                                                                                                                                              RESULT 11
US-09-861-597-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chilkcti, Ashutosh
TITLE OF INVENTION: Fusion Peptides Isolatable by Phase Transition
FILE REFERENCE: 4176-101
CURRENT APPLICATION NUMBER: US/09/812,382
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                             3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GDAPAGGGVPGGAVPGGFDPG----GFGPGGFGPVLDGWYGVDVSGSTV 52
                                                                                                                20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                         8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 AAAAASGPGQQGPGGYGPGQQGPGGYGP---GQQGLSGPGSAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 APAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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Score 90.5; DB 10;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 10;
; 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88; DB 1
Pred. No. 0.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 87.5; D
Pred. No. 0.26
3; Mismatches
                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/861,597 CURRENT FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR PELING DATE: 1999-02-11
PRIOR PELING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 529
                                                                                                                                                                                                                                            Sequence 6, Application US/09812382 Patent No. US20010034050A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09861597 Patent No. US20020064539A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.4%;
Best Local Similarity 43.5%;
Matches 20; Conservative
29.4%;
llarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Nephila clavipes US-09-861-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.6
Best Local Similarity 49.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: ELP[V5A2G3-90]
US-09-812-382-6
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RESULT 18

US-09-925-300-1381

Sequence 1381, Application US/09925300

Sequence 1381, Application US/09925300

Sequence 1381, Application US/09925300

Sequence 1382, Application US/09925300

CORRENT: CTAIG ROSEN,

APPLICANT: CTAIG ROSEN,

APPLICANT: CTAIG ROSEN,

APPLICANT: CTAIG ROSEN,

APPLICANT: CALGAT ROSEN

TITLE REFERENCE: PAIO1

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT PILLNG DATE: 2000-03-08

FRIOR FILLNG DATE: 2000-03-08

FRIOR FILLNG DATE: 1999-03-12

FROM FILLNG DATE: 1999-03-12

COCATION: (507)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

COCATION: (562)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals A.7%; MAME/KEY STEE

COTHER INFORMATION: Xaa equals A.7%; MAME/KEY STEE

COCATION: (562)

COTHER INFORMATION: Xaa equals A.7%; MAME/KEY STEE

COCATION: (562)

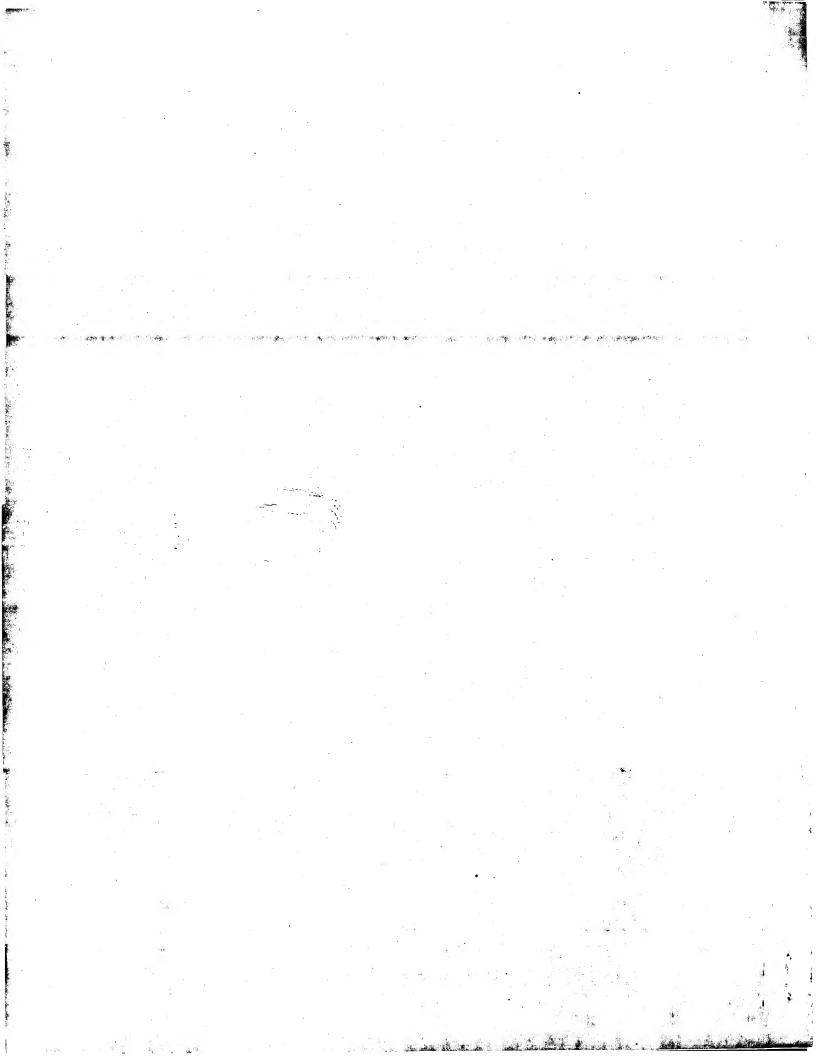
COTHER INFORMATION: Xaa equals A.7%; MAME/KEY STEE

COCATION: (562)

COTHER INFORMATION: Xaa equals A.7%; MAME/KEY STEE
```

q

Search completed: May 7, 2003, 17:30:49 Job time: 18.7905 secs



GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 7, 2003, 16:41:02; Search time 10.494 Seconds (without alignments) 513.008 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-855-754B-9 308 1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ 56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	outer membrane oro		Ë	probable serine-th	qlycine-rich cell	spidroin 2, dragli	elastin precursor	hypothetical prote	octamer binding tr	ATP-dependent RNA	probable cell wall	hypothetical prote	heat shock protein	dnaK-type molecula	hypothetical prote	keratin 10, type I		fibrillin-2 precur	hypothetical prote		RNA helicase RH11	ATP-dependent RNA	elastin precursor	probable immediate	dnaK-type molecula	elastin precursor	leukophysin - huma	MFS18 protein - ma	Aluna Tona Manager
SUMMARIES	ΩI	A32560	S15204	A47675	T35389	T09262	A44112	EAMS	B86181	159234	T45677	T40618	T15126	PC7036	S41372	H84217	A31994	KRHU0	A54105	T24865	A49242	T51742	T45671	EART	T03166	S51712	A26601	G01226	S25103	A54507
	DB	2	~	~	~	~	7	Н	~	7	~	~	~	~	7	7	~	Н	~	~	~	7	N	-	~	~	~	7	N	~
	å Query Match Length	910	922	911	783	16	627	860	200	420	646	273	259	641	645	133	561	593	2918	422	989	224	603	864	1300	959	784	235	128	198
d	Query Match	88.0	74.2	68.8	34.4	31.0	29.7	29.2	29.5	29.5	29.1	27.6	27.3	26.8	26.8	26.6	26.6	26.6	26.6	26.5	26.3	26.1	26.1	26.1	26.1	26.0	26.0	25.8	25.5	25.3
	Score	271	228.5	212	106	95.5	91.5	91	90	90	89.5	82	84	82.5	82.5				82	81.5	81	80.5	80.5	80.5	80.5	80		79.5	78.5	78
	Result No.	-	7	e	ಶ	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	76	27	58	53

glycine-rich prote protein R09B5.8 (1	hypothetical prote	transcription fact	hypothetical prote	. polyketide hydroxy	dnaK-type molecula	dnaK-type molecula	hypothetical prote	hypothetical prote			•	Ч	_
S01821 G88949	T00799	A49642	T29299	T35608	S11456	JC4610	A97443	AC2661	A70812	T20801	T32734	T22078	T49890
7 7	7	0	7	7	~	7	~	~	~	~	~	7	7
252 82	201	420	589	627	650	651	699	699	749	1126	1215	112	185
25.3	7.8	œ.	₩.	æ	ω.	œ.	89.	œ.	æ	8	Φ.	. 7	.7
25	25	24	24	24	24	24	24	24	24	· 24	77	24	24
78 77.5	77.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	92	92
	-		-	_		-	1			-		-	
30	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	KESULT 1
	A32560
	outer membrane protein P.69 precursor - Bordetella pertussis
	C;Species: Bordetella pertussis
	C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
	C; Accession: A32560
	R;Charles", I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morr
	Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
	A; Title: Molecular cloning and characterization of protective outer membrane protein
	A;Reference number: A32560; MUID:89264462; PMID:2542937
٠.	A; Accession: A32560
	A; Molecule type: DNA
	A/Residues: 1-910 <cha></cha>
	A; Cross-references: GB:J04560; NID:9144053; PIDN:AAA22980.1; PID:9144054
	A; Note: it is uncertain whether Met-1 or Met-3 is the initiator
	C; Keywords: membrane protein
	$F;1-34/{ m Domain}$: signal sequence #status predicted <sig></sig>
	F;35-910/Product: Outer membrane protein P6.9 #status predicted <mat></mat>
	*; Pred: No. 1.1e-18;
	Marches 51; Conservative 1; Mismarches 4; indeis 0; Gaps 0;
	Qy 1 ORATIREGDAPAGGGVPGGAVPGFDPGGFGPGFGPVLDGWYGVDVSGSTVELAQ 56
	Db 254 QRATIREGDALAGGAVPGGAVPGGRQPGGFGPVLDGWYGVDVSGSSVELAQ 309

	RESULT 2 S15204 Pertactin - Bordetella parapertussis N;Alternate names: outer membrane protein P70 C;Species: Bordetella parapertussis C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999 C;Accession: S15204; S14659
يب	R;Li, L.J.; Dougan, G.; Novotny, P.; Charles, I.G. Mol. Microbiol. 5, 409-417, 1991
-	A;Title: P,70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo A;Reference number: S15204; MUID:91251771; PMID:2041476
	A;Accession: S15204 A;Molecule type: DNA
	f A; Residues; 1-922 <lil> A; Cross-references: EMBL: X54547; NID: q39761; PIDN: CAA38419.1; PID: q39762</lil>
	C;Genetics: A;Gene: prn C;Keywords: membrane protein

1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56 2, Query Match 74.2%; Score 228.5; DB 2; Length 922; Best Local Similarity 80.4%; Pred. No. 1.4e-14; Matches 45; Conservative 2; Mismatches 4; Indels 5;

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Gaps

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A44112
Spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
Spidroin 2, dragline silk fibroin, dragline
Nalternen enames: silk fibroin, dragline
Nalternen enames: silk fibroin, dragline
C; Species: Nephila clavipes
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Mar-1998
C; Accession: A4412; S27824
R; Hinman, M.B.; Lewis, R.V.
J; Biol. Chem. 257, 19320-19324, 1992
A; Title: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavip
A; Reference number: A44112; MUD: 92406876; PMID: 1527052
A; Residue: preliminary
A; Molecule type: mRNA
A; Residues: preliminary
A; Residues: preli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine F:1-27/Domain: signal sequence #status predicted <SIG>F:28-860/Product: elastin #status predicted <MAT>F:28-855/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastin precursor - mouse
N'Alternate names: tropolastin
C;Species: Mus musculus (house mouse)
C;Dete: 18-Aug-1995 #sequence_revision 16-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the tropoelastin
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA
                                                                                                                                                     Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Indels
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wydner, R.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C. Genomics 23, 125-131, 1994
A;Title: Use of an intron length polymorphism to localize A;Reference number: A55721; MUID:95130069; PMID:7829060
A;Cross-references: EMBL:L47748; NID:91350525; PID:91350526
C;Genetics:
A;Gene: EMB31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91.5; DB 2;
Pred. No. 0.15;
3; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 1;
Pred. No. 0.23;
                                                                                                                                                         ;
                                                                                                                                                             Score 95.5; DB 2,
Pred. No. 0.0084;
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                          8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFG 36
                                                                                                                                                                                                                                                                                                                                                     9 GPGPGGPGGPGGWGPG---PGGFGPGGFG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.5%;
                                                                                                                                                         31:0%;
nilarity 65.5%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.7%;
Best Local Similarity 41.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: $27824
A;Molecule type: mRNA
A;Residues: 19'627 <HIZ>
A;Cross-references: EMBL:M92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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A; Residues: 1-860 <WYD>
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A55721
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                                                                                                                                                                                                                                                   19;
                                                                                                                                                                            Query Match
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                                                                                                                                                                                    obx outer membrane protein P.68 pertactin - Bordetella bronchiseptica (Species: Bordetella bronchiseptica C.5pecies: Bordetella bronchiseptica C.5pecies: Bordetella bronchiseptica C.5pecession: A47675 # sequence_revision 18-Nov-1994 # text_change 08-Oct-1999 C.5Accession: A47675 # sequence TR.11, J.12. Pairweather, N.P.; Novotny, P.; Dougan, G.; Charles, I.G. J. Gen. Microbiol. 138, 1697-1705, 1992 A;Tille: Cloning, nucleotide sequence and heterologous expression of the protective outed A;Reference number: A47675; MUID:92407514; PMID:1527510 A;Accession: A.75751 A;Accession: A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, June 1999
A; Reference number: 221576
A; Accession: T35389
A; Status: preliminary: translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross references: EMBL; AL079348; PIDN: CAB45488.1; GSPDB:GN00070; SCOEDB: SC66T3.32c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: A47675
A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-911 <LII-5
A,Residues: 1-911 <LII-5
A,Cross-references: 68:X54815; GB:S46416; NID:939396; PIDN:CAA38584.1; PID:939397
A,Note: sequence extracted from NCB1 backbone (NCBIN:113318, NCBIP:113319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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C;Species: Picea glauca (white spruce)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable serine-threonine protein kinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 212; DB 2; Length 911;
Pred. No. 5.3e-13;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
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R; Dong, J.Z.; Dunstan, D.I.
submitted to the EMBL Data Library, June 1996
A; Description: Gene expression during somatic embryogenesis.
A; Reference number: 216588
A; Recession: T09262
A; Accession: T09262
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A;Molecule type: mRNA
A;Residues: 1-76 <DON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%; Score 106; DB 2;
ilarity 54.5%; Pred. No. 0.0076;
Conservative 1; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-783 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: SCOEDB:SC66T3.32c
C; Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 68.8%;
1 Similarity 75.0%;
42; Conservative
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Matches 24; Conserv
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T09262
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Matches
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N'Alternate names: protein Fi4P2.160
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Nov-2000
C'Accession: T45677
R'D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, Submitted to the Protein Sequence Database, January 2000
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A; Residues: 1.273 <LIXN>
A; CTOSS - references: EMBL: AL034563; PIDN: CAA22526.1; GSPDB:GN00067; SPDB:SPBC660.06
A; Experimental source: strain 972h-; cosmid c660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable cell wall protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T2086.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T151.26
C;Accession: T151.26
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                                                                                                                                         ATP-dependent RNA helicase-like protein - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T40618
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M. submitted to the EMBL Data Library, December 1998
A; Reference number: Z21941
A; Accession: T40618
A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89.5; DB
Pred. No. 0.25;
9; Mismatches
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 239/3; 267/3; 348/3; 404/3; 442/3
Note: F14P22.160
C;Superfamily: ATP-dependent RNA helicase DBP1
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A; Cross-references: EMBL: AL137082
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31.3%;
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Best Local Similarity 31.33
Matches 26; Conservative
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21; Conservative
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C, Superfamily: WW repeat
F;8-48/Domain: WW repeat
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A; Molecule type: DNA
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Matches 21;
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
C; Accession: 159234
A; Title: Differential expression of four members of the POU family of proteins in activa
A; Ritle: Differential expression of four members of the POU family of proteins in activa
A; Reference number: 159234; MUID:94052142; PMID:8434287
A; Retence number: 159234
A; Retence number: 159234
A; Residues: 1420 cRRS>
A; Res
                                                                                                                                                                                                                                                                            hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B86181
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosoma l of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-200 <STO>
A; Cross-references: GB; AE005172; NID: 97211985; PIDN:AAF40456.1; GSPDB:GN00141
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GGAVPGGFDPGGFGPGGFGPVLDGWYGVDVS 48
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œ
                                                          2 RATIRRGDAPAGGGVPG----GAVPGGFD----PGGFGPGGFGPVLDGWYGVDVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 2; Length 200;
Pred. No. 0.072;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90; DB 2; Length 420;
Pred. No. 0.15;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Map position: 1
C:Superfamily: glycine-rich cell wall structural protein 1
   20;
   Mismatches
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llarity 36.1%;
Conservative
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llarity 60.0%;
Conservative
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B86181
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 18;
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23;
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Best Local S:
Matches 22,
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Gaps -----GG 29

33;

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Gaps

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C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein co C;Superfamily: heat shock protein 70
C;Reywords: ATP; cytosol; heat shock; molecular chaperone; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: H84217
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja, Jung, K.H.; Alam, M.; Frettas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer. A.D.; Ebhardt, H.; Lowe, T.M.; A;Tille: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                 //A; Molecule type: protein
// A; Residues: 4-10;137-143;158-164;221-227;329-335;362-368;388-394;425-431;573-579;609-
                                 A;Cross-references: EMBL:229379; NID:9443914; PIDN:CAA82570.1; PID:9443915
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:AE004437; NID:q10580192; PIDN:AAG19108.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                        Length 645;
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Pred. No. 0.29;
3; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 DAPAGGGVPGGAVPGGFDPGGFGPGFGPVLDGWYGVDVSGSTVE 53
                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                  Score 82.5; DB 2;
Pred. No. 1.2;
1; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7, 2003, 16:55:20
                                                                                                                                                                                                                                                                                                                                                     Ouery Match 26.8%;
Best Local Similarity 48.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.68;
42.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.6
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: H84217
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-133 <STO>
        A:Residues: 1-645 <TIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May
Job time: 11.494 secs
                                                                                      A; Accession: S71636
                                                                                                                                                                                            A; Gene: HSA1; HSP72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: VNG0597H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E 107
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                                                                                                                                                                      C; Genetics
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                                                                                                                                                                                                                   A;Cross-references: EMBL:AF000193; NID:g1946986; PID:g1946988; PIDN:AAB52890.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone T2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Accession: 34137.
A.Accession: 34137.
A.Accession: 34137.
A.Bolecule type: DNA
A.Residues: 1-645 < DIE>
A.Cross-references: RBBL: 229379; NID:g443914; PIDN:CAA82570.1; PID:g443915
R.Titcrenko, V.I.; Evers, M.E.; Diesel, A.; Samyn, B.; van Beeumen, J.; Roggenkamp, R.; Yantle: Identification and characterization of cytosolic Hansenula polymorpha proteins A.Reference number: S71636; MUID:96437974; PMID:8840502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rhizopus nigricans
C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
C;Accession: PC7036
R;Cernila, B; Cresnar, B.; Breskvar, K.
Biochem. Biophys. Res. Commun. 265; 494-498, 1999
A;Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
A;Reference number: JC7132; MUID:20025372; PMID:10558896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dnak-type molecular chaperone HSA1 - yeast (Pichia angusta)
N.Alternate names: heat shock protein hsp72
C;Species: Pichia angusta
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Apr-2000
C;Accession: S41372; S71640; S71636
R;Diesel, A.A.; Roggenkamp, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84; DB 2; Length 259;
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GDAPAGGGVPGGAVPGGFDPGGFGP-----GGFGPVLDGWYGVDVSG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Diesel, A.A.; Roggenkamp, R.R. submitted to the EMBL Data Library, January 1994 A;Description: HSP70 genes of the yeast Hansenula polymorpha A;Reference number: $41372
R; Beck, C.; Wamsley, P. submitted to the EMBL Data Library, April 1997 A; Description: The sequence of C. elegans cosmid T20B6. A; Reference number: Z18297 A; Accession: T15126 A; Status; preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heat shock protein 70 - Rhizopus nigricans (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: Phaseolus glycine-rich protein 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82.5; D
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AF188289
C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 GGMPGGGGMPGGGAPGGF-PGG 629
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                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%;
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68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.29
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3
Best Local Similarity 44.7
Matches 21; Conservative
                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-259 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-641 <CER>
                                                                                                                                                                                                                                                                                           A;Gene: CESP:T20B6.3
A;Map position: 3
A;Introns: 9/2; 231/1
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us-09-855-754b-9.rsp

GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 7, 2003, 16:31:49 ; Search time 5.43782 Seconds (without alignments) 427.133 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-855-754B-9 308 1 QRATIRRGDAPAGGGVPGGA.....PVLDGWYGVDVSGSTVELAQ 56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P14283 bordetella	_		-	_	Q01851 homo sapien	_	P53421 pichia angu			_			Q99372 rattus norv	candid	P07916 gallus gall	homo s				P10495 phaseolus v	Q01877 puccinia gr	P38486 canis famil	P42534 streptomyce		P09789 petunia hyb	P21522 schistocerc	Q01546 homo sapien	_	P27483 arabidopsis	P08699 rattus norv	P06394 bos taurus	P35908 homo sapien
	ΩI	PERT BORPE	PERT_BORPA	PERT_BORBR	SPD2_NEPCL	ELS_MOUSE	BR3A_HUMAN	BR3A_MOUSE	HS71_PICAN	K1CJ_HUMAN	FBN2_HUMAN	DDX9_MOUSE	HS70_PLACB	HS70_BLAEM	ELS_RAT		ELS_CHICK	DDX9_HUMAN	K2C1_HUMAN	MF18_MAIZE	HS70_SCHJA	GRP1_PHAVU	HS71_PUCGR	LEG3_CANFA	HYDL_STRCO	HS7C_BOVIN	GRP1_PETHY	ROA1_SCHAM	K220_HUMAN	ELS_BOVIN	GRP_ARATH	LEG3_RAT	K1CJ_BOVIN	K22E_HUMAN
	DB	-	Н	Н	-	Н	-		Н	Н	Н	-1	Н	Н	Н	Н	-	-	-	Н	-	Н	Н	-	-	-	Н	Н		-	٦.	Н	-	Т
	Match Length	910	922	911	627	860	423	421	644	593	2911	1380	989	649	864	655	750	1270	643	128	198	252	648	295	627	650	384	342	638	747	338	261	526	645
*	Match	91.2	74.2	68.8	29.7	29.5	29.5	27.8	26.8	26.6	26.6	26.5	26.3	26.1	26.1	26.0	26.0	25.8	25.6	25.5	25.3	25.3	25.3	24.8	24.8	24.8	24.7	24.5	24.5	24.4	24.2	24.0	24.0	23.9
	Score	281	228.5	212	91.5	91	90	85.5	82.5	82	æ	81.5	œ	80.5	80.5	80	80	79.5	79	78.5	78	78	78	76.5	76.5	76.5	9.	75.5	'n.	75	74.5	74	74	73.5
Boanlt	No.	1	7	m	❖	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

	F3//OD dances caro	P12035 homo sapien	092125 xenopus lae	P87047 paracoccidi	Q61555 mus musculu	P47953 cricetulus	P19013 homo sapien	Q92804 homo sapien	090473 brachydanio	P10569 acanthamoeb	P10591 saccharomyc	
CDD PARCE	GRES_DAUCA	K2C3_HUMAN	ANX7_XENLA	HS70_PARBR	FBN2_MOUSE	LEG3_CRILO	K2C4_HUMAN	RB56_HUMAN	HS7C_BRARE	MY SC_ACACA	HS71_YEAST	YZ08_MYCTU
-	4	-	-	-	Н	Н	-	Н	-	н	-	-
101	130	629	512	649	2907	244	534	592	649	1168	641	1901
7 5 5	7.07	23.5	23.4	23.4	23.4	23.2	23.2	23.2	23.2	23.1	22.9	22.9
- 13	2	72.5	72	72	. 72	71.5	71.5	71.5	71.5	7.1	70.5	70.5
7.5	*	35	36	37	38	39	40	41	42	43	44	. 45

ALIGNMENTS

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DOR NO DO

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EMBL; X54815; CAA38584.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CN7531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERT_BORBR
Q03035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERT_BORBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
DR NOOR DR NOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mach by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Outer membrane.
-i- DISBASE: MAX CONTRIBUTE TO THE DISBASE STATE OF WHOOPING COUGH.
-i- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                                                                          LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                               (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 281; DB 1; Lengtn >2.
Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
                                                                                                                                                                                       PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                            (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                    Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                            IPR003991; pertactin_vir.
    InterPro; IPR003992; pertactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                               93452 MW;
                                                                       PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X54547; CAA38419.1; ...
EMBL; A26124; CAA01786.1; -..
EMBL; A19182; CAA01454.1; -..
                          InterPro; IPR003991; pertacti
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 92.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               910 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Hes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                       266
271
276
276
281
579
                                                                                                                      Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERT_BORPA
P24328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                    CHAIN
PROPEP
SITE
                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERT_BORPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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--I- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERFACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i-SUBCELLULAR LOCATION: Outer membrane.
-i-DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-i-MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
                                                                                                                                                                                                                                                                                                                                                                CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertactin precursor (Outer membrane protein P.68) (P.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 228.5; DB 1
Pred. No. 8.6e-14;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                               PERTACTIN (P.70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
                                                                                                                                                                                                                              Outer membrane; Signal; Virulence; Repeat.
SIGNAL 1 34 POTENTIAL.
PIR; S15204; S15204.
PIR; S14659; S14659.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IRR003991; pertactin.
Pfan; PF03212; Pertactin.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 80.4 ses 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
275
280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
603
                                                                                                                                                                                                                                                                                                            647
922
262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
575
922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=518;
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us-09-855-754b-9.rsp

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APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELASTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:95317; Eln.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
                                                                                       12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71955 MW;
                                                                                                                                           54184 MW;
                                                                                                                                                           29.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U08210; AAA80155.1; -.
                                                                                                                                                 Query Match
Best Local Similarity 41.00.
                                                                                                                                                                   41.58;
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860
                                                                                                                                  516
627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         860 AA;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
    chromosome 7
                                                                                                                                                                                                                                                       ELS_MOUSE
P54320;
                                                                                                                        REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
   DOMAIN
                                           REPEAT
REPEAT
                                                                                       REPEAT
REPEAT
                                                                                                       REPEAT
REPEAT
                            REPEAT
                                                              REPEAT
REPEAT
                    REPEAT
                                      REPEAT
                                                                                REPEAT
                                                                                                                                                                                                                                                ELS_MOUSE
                                                                                                                                                                                                                                       RESULT 5
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                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                      CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EURARYOTIC CELL
                                                                                                                                                                                                                                              QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Chellcerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
                                                                                                                                                                                                            Score 212; DB 1; Length 911;
Pred. No. 2.7e-12;
2; Mismatches 2; Indels 10;
                                                                                                                                                                          3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spidroin 2 (Dragline silk fibroin 2) (Fragment).
                                                                                              PERTACTIN (P.68).
POTENTIAL.
                                                                                                                                                                                                                                                                                                        627 AA.
                                                                      Signal; Virulence; Repeat.
EMBL; A19180; CAA01453.1; -.
PIR; A47675; A47675.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                  LINES)
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92406876; Pubmed=1527052;
Hinman M.B., Lewis R.V.;
                                                                                                                                                                                                                                                                                                                                                           Nephila clavipes (Orb spider).
                                         Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                            93995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M92913; AAA29381.1; -. Silk; Repeat.
                                                                                                                                                                                                            ch 68.8%;
1 Similarity 75.0%;
42; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                    911
712
911
262
                                                                                                                                        701
266
266
271
276
570
911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-6915;
                                                                      Outer membrane;
                                                                                                                                                                                                                                                                                                      SPD2_NEPCL
P46804;
                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                     Local
                                                                                             CHAIN
PROPEP
SITE
                                                                                                                                         SITE
                                                                              SIGNAL
                                                                                                                                                                           REPEAT
                                                                                                                                                          REPEAT
                                                                                                                                                                  REPEAT
                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                SPD2_NEPCL
                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENOMICS 23:125-131(1994).
-1- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND NUCHAL LIGAMENT, WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY
-1- SÜBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C: TISSUE-Lung;
MEDINE-95130069; PubMed=7829060;
Wydner K.S., Sechler J.L., Boyd C.D., Passmore H.C.;
"Use of an intron polymorphism to localize the tropoclastin gene to mouse chromosome 5 in a region of linkage conservation with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTO AN EXTENSIBLE 3D NETWORK.
-- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
-- PIM: THE CROSSLINKS ARE MADE OF DEAMINATED LYS.
                                                                                                                                                3
                                                                                                                                                                                                                                                       ATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                             Length 627;
CB9B63779B2C594B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCOBESAAE1EDD7F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein; Repeat; Signal; Connective tissue.
SIGNAL
                                                                          5; DB 1;
0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-1996 (Rel. 34, Last annotation update)
Elastin precursor (Tropoelastin)
                                                                                                           Pred. No. 0.15
3; Mismatches
                                                                      Score 91.5;
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RESULT 7
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                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PLEACENTA;

MEDLINE-93027214; PubMed-1357630;

MEDLINE-93027214; PubMed-1357630;

A Collum R.G., Fisher P.E., Datta M., Mellis S., Thiele C., Huebner K.,

Collum R.G., Fisher P.E., Datta M., Morly T., Deblinho R.A., Alt F.W.;

A Cocce C.M., Israell M.A., Thell T., Moroy T., Deblinho R.A., Alt F.W.;

A novel POU homeodomain gene specifically expressed in cells of the developing mammalian nervous system.*;

Nucleic Acids Res. 20:4919-4925(1992).

THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A SUBSET OF NEURONOL LINEAGES. MAY PLAY A ROLE IN DETERMINING OR MAINTAINING

THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

THE IDENTITIES OF A SMALL SUBSET OF VISUAL CORD AND EYE.

TISSUE SPECIFICITY: BRAIN. SEEMS TO BE SPECIFIC TO THE RETINA.

PRESENT IN THE DEVELOPING BRAIN, SPINAL CORD AND EYE.

THE DEVELOPMENTAL STAGE: EXPRESSION PEAKS EARLY IN BERRYOGENESIS

(DAY 13.5) AND IS UNDETECTABLE 14 DAYS AFTER BITTH.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95348789; PubMed-7623109;
Xiang M., Zhou L.-J., Macke J.P., Yoshioka T., Hendry S.H., Eddy R.L.,
Shows T.B., Nathans J.;
"The Brn-3 family of PoU-domain factors: primary structure, binding
specificity, and expression in subsets of retinal ganglion cells and
somatosensory neurons.";
J. Neurosci. 15:4762-4785(1995).
                                  Gaps
                                                                                    SEQUENCE FROM N.A.
MEDLINE-94052142; PubMed-9234287;
MEDLINE-94.052142; PubMed-9234287;
MEDLINE-94.052142; PubMed-9234287;

"Differential expression of four members of the POU family of proteins in activated and phorbol 12-myristate 13-acetate-treated
                                                                 20
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  BR3A_HUMAN STANDARD; PRT; 423 AA.
601851; 015318; 014986;
01-JUL-1993 (Rel. 26, created)
01-JUL-1993 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 91) respecific homeobox/FOU domain protein 3A (BRN-3A) (OCT-T1)
POU4FI OR BRN3A OR RDC1.
                                  .;
8
                                                                 2 RATIRRGDAPAGGGVPG----GAVPGGFD----PGGFGPGGFGPVLDGWYGVDVSGS
DB 1; Length 860;
                                  20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 90:10260-10264(1993).
               0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                  6; Mismatches
 Score 91;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U10063; AAA57161.1; -. EMBL; U10062; AAA57161.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 85-423 FROM N.A.
 29.5%;
                                  23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASS-4 SUBFAMILY
 Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jurkat T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue-Placenta;
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    rissue-Retina;
                                                                                                                                                      RESULT 6
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MEDLINE-94215319; PubMed-8162704; Theil T., Zechner U., Klett C., Adolph S., Moeroey T.; "Chromosomal localization and sequences of the murine Brn-3 family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
PROSITE; PS500401; HOMEOSOX_2; 1.
Transcription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 3A (BRN-3A) (BRN-3.0).
POU4F1 OR BRN3A OR BRN3 OR BRN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.2%; Score 90; DB 1; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3AE4732E1309F34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TS -> H (IN REF. 3).
A -> R (IN REF. 1).
GAG -> ARR (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN REF. 3).
GP -> AA (IN REF. 3).
GP -> PR (IN REF. 3).
GP -> AA (IN REF. 3).
GP -> AA (IN REF. 3).
G -> A (IN REF. 3).
G -> A (IN REF. 3).
A -> S (IN REF. 3).
A -> S (IN REF. 3).
A -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AER -> GS (IN REF.
AQR -> PS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Pred. No. 0.15
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POU-IV BOX.
POLY-HIS.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental control genes.";
Cytogenet. Cell Genet. 66:267-271(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 GGGPGGGGPGGGGGGGGGGGGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFGP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALA-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
                                                                                                                                                                                                              PRINTS; PRO0028; POUDOMAIN.
ProDom; PD000010; Homeobox; 1.
ProDom; PD0000583; POU_domain; 1.
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU domain.
Pfam; PF00166; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42939 MW;
EMBL; X64624; CAA45907.1;
                                                                                 Genew; HGNC:9218; POU4F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.2
Best Local Similarity 60.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                      FRANSFAC; T01876; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                  P10037;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Developmental
                                                                                                        MIM; 601632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BR3A_MOUSE
P17208;
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Saccharomycetes;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | [1] | SEQUENCE FROM N.A. MEDLINE-89125611; PubMed-2464696; Rieger M., Franke W.W.; Rieger M., Franke W.W.; Rieger M. T. Franke W.W.; "Indentification of an orthologous mammalian cytokeratin gene. High degree of intron sequence conservation during evolution of human mineral nio.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 DAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVE 53
                                                                         Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID-4905;
15-JUL-1999 (Rel. 38, Last annotation update)
Heat-shock protein 70 1 (HSP72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 AA
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                                                                       STRAIN-ATCC 34438;
MEDLINE-96437974; PubMed-8840502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 229379; CAA82570.1; -. HSSP; P19120; 3HSC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fam; PF00012; HSP70;
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                       Gaps
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Franscription regulation; Nuclear protein; DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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Pred. No. 0.38;
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(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLY-RICH.
ALA-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GGGPGGGGPGGGPGG-GGGGGPGGGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GDAPAGGGVPGGAVPGGFDPGGFGPGGFG 36
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                                                     STRAIN-T6 / TW1; TISSUE-TESTIS;
MEDLINE-90221898; PubMed-1970171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S09237; S09237.
HSSP; P10037; 1A07.
MGD; MGI:102525; Pou4f1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; PoU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roDom; PD000010; Homeobox; 1.
roDom; PD000583; POU_domain; 1.
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PS00465; POU_2;
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SMART; SM00352; POU: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compton J.G., Bale S.J.; "Preferential sites in keratin 10 that are mutated in epidermolytic
                         MEDLINE-88122104; PubMed=2448602; Darmon M.Y., Semat A., Darmon M.Y., Vasseur M.; Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                           Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides the C-terminal V2 subdomain due to variable numbers and sizes of diveine loops.";
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                                                                                                                                                                                                                                                                  Microsequences of 145 proteins recorded in the two-dimensional gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126. MEDLINE-94216497; PubMed=7512983; Syder A.D., Yu Q.-C., Paller A.S., Gludice G., Pearson R., Fuchs "Genetic mutations in the K1 and K10 genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                              MEDLINE-92386600; PubMed-1381287; Cheng J., Syder A.J., Yu Q.-C., Letal A., Paller A.S., Fuchs E. The genetic basis of epidermolytic hyperkeratosis: a disorder differentiation specific epidermal keratin genes."; cell 70:811-819(1992).
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Vandekerckhove J.;
                                                                                                                                           undergo structural rearrangements within repeats."; dene 116:245-251(1992).
                                                                                                                                  Tkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                                                             protein database of normal human epidermal keratinocytes."
Electrophoresis 13:960-969(1992).
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J. Clin. Invest. 93:1533-1542(1994).
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MEDLINE-94117868; PubMed-7507150;
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                                                                                                         SEQUENCE OF 197-593 FROM N.A.
MEDLINE-92339897; PubMed-1378806;
                                                                                   Mol. Biol. Rep. 12:277-283(1987)
                                                                                                                                                                                                         SEQUENCE OF 180-184 AND 577-589.
             OF 130-593 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C -1- POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN
THE GLY-RICH REGION (POSITIONS 490-560).
C -1- DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF EPIDERMOLYTIC
HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL
CCHARACTERIZED BY BLISTERING AND AMARKED THIOKENING OF THE STRATUM
CORNEUM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH
REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS.
MITHIN A FEW WEEKS, THE EFYTHRODERMA AND BLISTER PORMATION
DIMINISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL
C DOMINANY, BUT MOST CASES ARE SPORADIC.
C DOMINANY BUT MOST CASES ARE SPORADIC.
C LOSSESCE DEFECTS IN KRT10 ARE THE CAUSE OF ANNULAR EPIDERMOLYTIC
C LCHTHYOSIS (ABI), A DISTINCAL PHONOTYPIC VARIANT OF EPIDERMOLYTIC
C HYPERKERATOSES. IT RESEMBLES CLINICAL AND HISTOLOGGIC FRAUTRES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arin M.J., Longley M.A., Anton-Lamprecht I., Kurze G., Huber M.,
Hohl D., Rothnagel J.A., Roop D.R.;
Hohl D., Rothnagel J.A., Roop D.R.;
"A novel substitution in keratin 10 in epidermolytic hyperkeratosis.";
"J. Invest. Dermatol. 112:506-508(1999).
-!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
KERATIN 10 IS GEMERALLY ASSOCIATED WITH KERATIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                    Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
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    McMillan J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND I (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8].
-! SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN POSITIONS 513 TO 555.
                                                                                                                         "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
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McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan ,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genetic and clinical mosaicism in a type of epidermal nevus.";
New Engl. J. Med. 331:1408-1415(1994).
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MEDLINE-99072665; PubMed-9856845;
Suga Y., Duncan K.O., Heald P.W., Roop D.R.;
"A novel helix termination mutation in keratin 10 in annul epidermolytic ichthyosis, a variant of bullous congenital ichthyosiform erythroderma.";
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MEDLINE=95059228; PubMed=7526210;
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Aarhus/Ghent-2DPAGE; 7405; IEF
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EMBL; M77663;
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Nature 352:330-334(1991).
                                                                       VARIANTS CCA HIS-1114.
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MEDLINE-91304567; PubMed-1852206;
Lee B., Godfrey M., Vitale E., Horl H., Mattei M.-G., Sarfarazi M.,
Tsipouras P., Ranirez F., Hollister D.;
"Linkage of Marfan syndrome and a phenotypically related disorder to
two different fibrillin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure and expression of fibrillin-2, a novel microfibrillar component preferentially located in elastic matrices."; Cell Biol. 124:855-863(1994).
              InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Fran; Pr00038; filament; 1.
PRINTS; PR001248; TYPEIKERATIN.
PROSTE; PS00226; IF; 1.
Intermediate filament; Colled coll; Keratin; Disease mutation;
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MEDLINE-94165150; Pubmed-8120105;
Zhang H., Apfelroth S.D., Hu W., Davis B.C., Sanguineti C.,
Bonadio J., Mecham R.P., Ramirez F.;
                                                                                                                                                                                                                                                                                    DB 1; Length 593;
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R -> H (IN EHK).
/FTId=vAR_003827.
R -> C (IN EHK).
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R -> P (IN EHK).
/FTId-vAR_003829.

R -> S (IN EHK).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrillin 2 precursor.
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5; Mismatches
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1 Similarity 44.7%;
21; Conservative
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P35556;
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			BP 7LIKE 41, -LIKE 43, -LIKE 44, -LIKE 44, -LIKE 45, -LIKE 45, -LIKE 47, SIMILARITY	SIMILARITY
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Kistelow P., Miazek A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: UNWINDS DOUBLE-STRANDED DNA AND RNA IN A 3' TO 5'
DIRECTION. GENERATES MULTIPLE SECONDARY STRUCTURES THAT INFLUENCE
RNA-BINDING PROTEINS. MAY PLAY A ROLE IN X-LINKED GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 GFAPSGNGNGYGPGGTGFIPIPGGNGFSPGVGAGGQGPIIT---GLTILNQTIDI 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDX9_MOUSE STANDARD; PRT; 1380 AA.
070133; 035931; 054703;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATP-dependent RNA helicase A (Nuclear DNA helicase II) (NDH (DEAD-box protein 9) (MHEL-5).
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STRAIN-129/Sv;
MEDLINE-98149984; Pubmed-9480750;
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ilarity 35.5%; Pre
Conservative 10;
 [2]
SEQUENCE OF 386-919 FROM N.A.
STRAIN-C57BL/6;
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Genomics 47:365-371(1998).
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hes 22;
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DDX9_MOUSE
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HS70_BLAEM
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                       SIMILARITY: CONTAINS 2 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
DEAH BOX.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
Heat shock 70 kDa protein (HSP70) (Cytoplasmic antigen) (74.6 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eckert V., Sanchez L., Cochrane A.H., Enea V.;
**plasmodium cynomolgi: the hsp 70 gene.";
Exp. Parasitol. 75:33-328(1992).
-1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN THE ASEXUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY. DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00690; DEAH ATP.
PROSITE; PS00690; DEAH ATP.
PROSITE; PS0137; DS_RBD; 2.
Hellcase; RNA-binding; DNA-binding; Repeat; Nuclear protein;
DOMAIN 3 71 DRBM 1.
DOMAIN 182 254 DRBM 1.
NP_BIND 413 420 ATP (POTENTIAL).
NP_BIND 513 516 DEAH BOX.
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-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium cynomolgi (strain Berok).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AGGGVPGGAVPGGFDPGGFGPGGFG 36
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-> V (IN REF. 2)
0F23755C291D2FE1 CRC64;
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InterPro: IPR002464; DEAH.box.
InterPro: IPR001159; DS.RBD.
InterPro: IPR001650; Helicase_C.
                                                                                                                                                                                                                                               Pfam; PF00035; dsrm; 2.
Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00358; DSRM; 2.
SMART; SM00490; HELICC; 1.
                                                                                                                                               EMBL; U91922; AAC05725.1; -.
EMBL; AF023530; AAC05301.1; -
EMBL; U92080; AAB72087.1; -.
                                                                                                                                                                      EMBL; U92080; AAB72087.1; -. MGD; MGI:108177; Ddx9.
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37.3%;
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19; Conservative
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674
748
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1380 AA;
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Q05746;
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MEDLINE-95129910; PubMed-7828923;
Stefanl R.M.; Gomes S.L.;
A unique intron-containing hsp70 gene induced by heat shock and during sporulation in the aquatic fungus Blastocladiella emersonii.";
Gene 152:19-26(1995).
- I SIMILARIȚY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Chytridiomycota; Blastocladiales; Blastocladiaceae;
Blastócladiella.
NCBL_TaxID-4308;
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  Swiss Institute of Bioinformatics and the Bioinformatics Institute. There are no reprofit institutions as long as its content this statement is not removed. Usage by
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Pred. No. 1.5;
3; Mismatches 1
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(Rel. 33, Last sequence update)
(Rel. 33, Last annotation update)
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ProDom; PD000089; HSP70. 1.
PROSITE; PS00297; HSP70.1; 1.
PROSITE; PS0129; HSP70.2; 1.
PROSITE; PS01036; HSP70.3; 1.
ATP-binding; Heat shock; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74602 MW;
                                                                                                                                   EMBL; M90978; AAA29625.1; -. PIR; A49242; A49242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.3%;
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HSSP; P08109; 1CKR.
InterPro; IPR001023; HSp70.
Pfam; PF00012; HSP70; 1.
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InterPro; IPR001023; Hsp70.
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Best Local Similarity
These 23; Conserve
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between the
the European
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01-FEB-1996 (
01-FEB-1996 (
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HS71_CANAL P41797;
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-!- FUNCTION: MAJOR STRUCTURAL PROTEIN OF TISSUES SUCH AS AORTA AND

-!- EUNCTION: WHICH MUST EXPAND RAPIDLY AND RECOVER COMPLETELY.

-!- SUBUNIT: THE POLYMERIC ELASTIN CHAINS ARE CROSS-LINKED TOGETHER
INTO AN EXTENSIBLE 3D NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX OF ELASTIC FIBERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                  Gaps
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Pierce R.A., Alatawi A., Deak S.B., Boyd C.D.;
"Elements of the rat tropoelastin gene associated with alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-3104668; Pubmed-1702399;
Pleace R.A., Deak S.B., Stolle C.A., Boyd C.D.;
"Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.";
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MEDLINE-88330868; PubMed=2971041;
Deak S.B., Pierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
"Rat tropoelastin is synthesized from a 3.5-kilopase mRNA.";
J. Biol. Chem. 263:13504-13507(1988).
                                                                                                                                                                                                                                                                   Length 649;
                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                          70833 MW; 152D5CF67B924A8D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          12 AGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVE 53
                                                                                                                                                                                                                                                                         DB 1;
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01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Elastin precursor (Tropoelastin) (Fragment).
                                                                                                                                                                                                                                                                   Score 80.5; Di
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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AAA42271.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 29:9677-9683(1990).
                  PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01039; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
ATP-binding; Chaperone.
                                                                                                                                                                                                                                                                      26.1%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                          649 AA;
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Best Local Similarity
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EMBL, M86372; 2
EMBL, M86355; 2
EMBL, M86355; 2
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M86364; 1
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Q99372;
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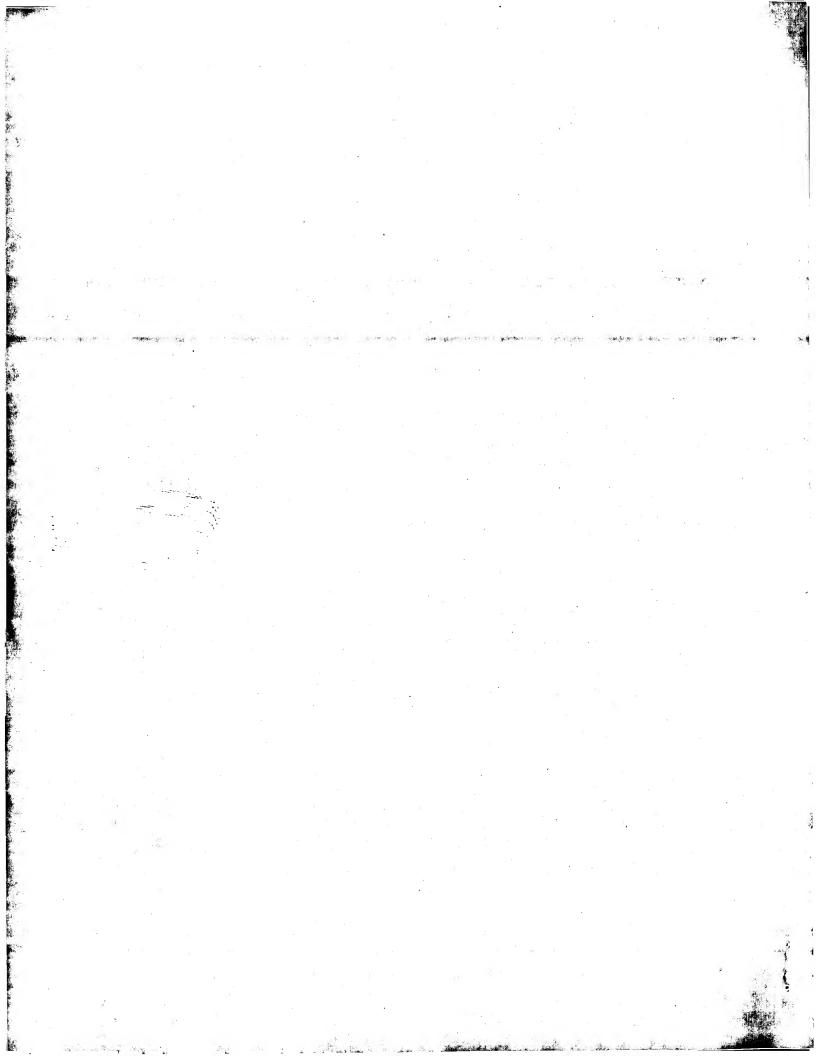
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mach by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95262895; PubMed-7744244;
Eroles P., Sentandreu M., Blorza M.V., Sentandreu R.;
"Cloning of a DNA fragment encoding part of a 70-KDa heat shock
protein of Candida albicans.";
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--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                          Length 864;
                                                                                                                                                                                                                         MISSING (IN CERTAIN ISOFORMS)
MISSING (IN CERTAIN ISOFORMS)
MISSING (IN CERTAIN ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
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EMBL; M86375; AAA42272.1; GINED.
EMBL; M86375; AAA42272.1; JOINED.
SEMBL; M86375; AAA42272.1; JOINED.
Structural protein; Connective tissue; Repeat; Signal;
Alternative splicing.
NON TER
<1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                        456894BB09E79FD4 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Heat shock protein SSA1.
                                                                                                                                                                                                                                                                                                                                  Score 80.5; F
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                                                                                                                                                                                                                                                                                                           72786 MW;
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63.0%;
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Candida albicans (Yeast).
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17; Conservative
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307
308
823
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STRAIN-ATCC 20955;
Cassone A.C., la V.
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ACETYLATION (BY SIMILARITY). A -> G (IN REF. 2). MY: 634743E4D6DAD9D5 CRC64;
1 175 70192 N
175 655 AA;
MOD_RES CONFLICT SEQUENCE
FT

10; Gaps Query Match 26.0%; Score 80; DB 1; Length 655; Best Local Similarity 50.0%; Pred. No. 1.8; Matches 24; Conservative 1; Mismatches 13; Indels

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Search completed: May 7, 2003, 16:48:04 Job time : 7.43782 secs



us-09-855-754b-9.rspt

Title: Perfect score:

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O9xail streptomyce
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"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4817,4817(2000).
EMBL; AJZ50093; CAB76447.1;
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009kjy4
0098fig9
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Q9b1u8 d
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Bardeta; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBL_TaxID-518;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (E.68) (Fragment).
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100.0%; Pred. No. 7.4e-24;
11ve 0; Mismatches 0;
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09K5G6
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Matches 56;
            254.5
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AC Q9K5G2;
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1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ
                                                                                                   7, 2003, 16:38:52 ; Search time 28.6201 Seconds
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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sp_invertebrate:*
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308 308 301 291 290.5 287 281 281 278.5 276 276

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Result

274.5 268.5 260.5 255.5

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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
BEBBL, AJ55004; CAB76448.1; -...
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                                                                                                                                                                                                               Length 161;
                                              Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                    Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Pred. No. 3.8e-23;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Register K.B.,
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.",
Infect. Immun. 69:1917-1921(2001).
EMBL; AY072ZF6; AAG38452.1;
InterPro; IPR003992; pertactin.
PRINTS; PR01482; PERTACTIN.
                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                           161 AA; 15435 MW; 7FACB18F1FD0507E CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Pertactin (P.68) (Fragment).
                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                            100.0%; Score 308; DB 2;
100.0%; Pred. No. 7.5e-24;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
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01-AUG-1998 (TrEMBLrel. 07, Created)
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MEDLINE-21117018; PubMed-11179374;
                                                                                                                 MEDLINE-20359389; PubMed-10899896;
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98.2%;
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                                                                                                                                                                                                                       Local Similarity 100.
les 56; Conservative
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nes 55; Conservative
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159 AA;
                                                                                             SEQUENCE FROM N.A.
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                                                                  Bordetella.
NCBI_TaxID=518;
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NON_TER
SEQUENCE
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Q9ALP4;
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Matches
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069259
ID 06925
AC 06925
DT 01-AU
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ID Q
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Fry N.K., Neal S., Harrison T.G., Miller E., Matthews R., George R.C.;
"Genotypic Variation in the Bordetella pertussis Virulence Factors
"Genotypic Variation in the Bordetella pertussis Virulence Factors
pertactin and Pertussis Toxin in Historical and Recent Clinical
Isolates in the United Kingdom.";
Infect. Immun. 69:5520-5528(2001).
EMBL; AJ001515; CAA0698.2;
EMBL; AJ0011093; CAA00477.1;
EMBL; AJ001362; CAA07477.1;
EMBL; AJ001362; CAA07477.1;
EMBL; AF348485; AAK92093.1;
InterPro; IPR003999; pertactin.
InterPro; IPR003999; pertactin.vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Polymorphism in the Bordetella pertussis virulence factors P.69/pertactin and pertussis toxin in The Netherlands: temporal trends and evidence for vaccine-driven evolution.";
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SERANT-287, AND AL1561;
MEDLINE-99345256; PubMed-10418915;
BOUTSAUX-ENDE C., Thiberge S., Carletti G., Guiso N.;
Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98114370; PubMed-9453625;
Mooi F.R., VanOirschot H., Heuvelman K., vanderHeide H., Gaastra W.
Willems R.R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
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Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 910;
                                                                                                                                          Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-JUN-2002 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin precursor (Pertactin outer membrane protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERTACTIN.
9035EE1F07A52BC8 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Pertactin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 AA
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PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine 17:2651-2660(1999)
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910
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35 9
910 AA;
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                                                                                                                                                                                                             Bordetella.
NCBI_TaxID-520;
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PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
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  01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                 Pertactin precursor.
PRN OR PRN6.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                       Bordetella.
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Best Local 3
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Q9S3M9
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                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                       94.3%; Score 290.5; DB 2; Length 184; 78.9%; Pred. No. 5e-22; Live 0; Mismatches 0; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptic Bertacin.;
Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptic Bertacin.;
Infect. Immu. 69:1917-1921(2001).
Infect. Immu. 69:1917-1921(2001).
InterPro: IPRO03992; Pertactin.
PRINTS; PR01482; PERTACTIN.
NON_TER 195 195 195 195 SEQUENCE 195 AA; 18724 MW; 7409C189267C2D71 CRC64;
                                                                              Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007274; AAG38450.1;
InterPro; IPR003992; pertactin.
PRINTS; PR01482; PERTACTIN.
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195 AA; 18724 MW; 7409C189267C2D71 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                        STRAIN-ST. LOUIS;
MEDLINE-21117018; PubMed-11179374;
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STRAIN-MBORD901;
MEDLINE-21117018; Pubmed-11179374;
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Best Local (
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069257
ID 06929
AC 06929
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STRAIN-C2;
MEDLINE-99345256; PubMed-10418915;
MEDLINE-99345256; PubMed-10418915;
Boursaux-Eude C., Thiberge S., Carletti G., Guiso N.;
Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular vaccine.";
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"Intranasal murine model of Bordetella pertussis infection: II.
Sequence variation and protection induced by a tricomponent acellular
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Bordetella.
                                                                                                                Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Similarity 94.6%; Pred. No. 5.6e-21;
53; Conservative 1; Mismatches 2; Indels
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            van Oirschot H.F.L.M., Mool F.R.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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CHAIN 35 907 PERTACTIN.
SEQUENCE 907 AA; 93298 MW; 3A7D05F4094420EA CRC64;
07, Created)
07, Last sequence update)
21, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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EMBL; AJ3005152; CAA06894.1; -
EMBL; AJ32095; CAA10566.1; -
EMBL; AJ006160; CAA06902.2; -
InterPro; IPR003992; pertactin,
InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
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Mool F.R., VanOirschot H., Heuvelman K., Vanderheide H.G., Gaastra W., Willems R.J.; Polymorphism in the Bordetella pertussis virulence factors P.69/pertactin and pertussis toxin in The Netherlands: temporal trends and evidence for vaccine-driven evolution."; Infect. Immun. 66:670-675(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fry N.K., Neal S., Li Y.T., Hanauer S., Blank E., Harrison T.G.; "Sequence variation in the pertactin and pertussis toxin genes and amplified fragment length polymorphism analysis of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ORATIRRGDAPAGGGVPGGAV----PGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA
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Pertactin and Pertussis Toxin in Historical and Recent Clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                        Boursaux Eude C., Thiberge S., Carletti G., Guiso N.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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4AF56A29BAAFFED0 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.4%; Score 278.5; DB 2 Best Local Similarity 86.9%; Pred. No. 4.1e-20; Matches 53; Conservative 1; Mismatches 2
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MEDLINE-21391812; PubMed-11500425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pertactin_vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolates in the United Kingdom.";
Infect. Immun. 69:5520-5528(2001).
                                                                                      STRAIN=B345;
MEDLINE=98114370; PubMed=9453625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vi
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1
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PRINTS; PR01484; PRTACTNFAMLY.
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EMBL; AJ007361; CAA07476.1;
EMBL; AF348484; AAK92092.1;
EMBL; AF348482; AAK92090.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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915
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915 AA;
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                    BI_TaxID-520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella,
                                                                                                                                                                                                                                                                                                          STRAIN-HAV;
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Q9AIX8
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                                                                                                                                                                                                                                                               254 QRATIRRGDAPAGGAVPGGAVPGGRAVPGFGPGFGPGFGPVLDGWYGVDVSGSSVELAQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98114370; PubMed-9453625;
Mool F.R., VanOlrschot H., Heuvelman K., vanderHeide H., Gaastra Willems R.R.J.;
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                                                                                                                                                                                                                                        1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P.69B protein precursor (Pertactin outer membrane protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.2%; Score 281; DB 2; Length 910; 92.9%; Pred. No. 2.3e-20;
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                                                                                                                                                    Length 387;
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                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Oirschot H.F.L.M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93495 MW; AF38246F8D82E03D CRC64;
                                           1 34 POTENTIAL.
35 >387 PERTACTIN.
387 AA; 38714 MW; 61195D45D347Aleb CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                    Score 281; DB 2;
Pred. No. 9.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915 AA.
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1; Mismatches
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InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
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PRINTS; PR01484; PRIACTNFAMLY.
EMBL; AJ006154; CAA06896.1; -.
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Pfam; PF03212; Pertactin; 1.
                                                                                                                                               91.2%;
ilarity 92.9%;
Conservative
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Bordetella pertussis.
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                                                               CHAIN
NON_TER
SEQUENCE
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Best Local
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Q9S6N1;
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Pfam;

Matches

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Indels

Length 915;

George R.C.;

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van Loo I.H., Mool F.R.;
"Changes in the Bordetella pertussis population in the first 20 years after the introduction of vaccination.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430832; CAD23609.1; -.
SEQUENCE 912 AA; 93680 MW; 7F417BA66B732EF7 CRC64;
                                                                                                                                                                                                                      1 ORATIRREDAPA-----GGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                           1 QRATIREGDAPAGGG-----VPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Polymorphism of Borderella pertuasis isolates circulating the last
ten years in France, a country using the same effective whole-cell
vaccine since more than thirty years.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ318056; CAC67458.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 268.5; DB 2; Length 167;
85.2%; Pred. No. 7.5e-20;
1ive 1; Mismatches 3; Indels 5
                                                                                                                                                          Score 274.5; DB 2; Length 912;
Pred. No. 1e-19;
1; Mismatches 2; Indels 5;
   Bacteria, Proteobacteria, beta subdivision, Alcaligenaceae, Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 AA; 15826 MW; E136B4CF809565F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                     0937U5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Pertactin (Fragment).
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Last annotation update)
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(TrEMBLrel, 17, I
(TrEMBLrel, 19, I
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Similarity 86.9%;
53; Conservative 1
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Best Local Similarity 85.29
Matches 52; Conservative
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                                                   SEQUENCE FROM N.A.
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NCBI_TaxID-520;
                            NCBI_TaxID=520;
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01-JUN-2001 (
01-JUN-2001 (
01-DEC-2001 (
                                                               STRAIN-B442
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Pred. No. 7.4e-20;
1; Mismatches 2; Indels 10; Gaps
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                                                                                                                                                                                   10;
                                                                                                                                                           Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella.
NCBL_TaxID=520;
                                                                                                                                                                                   2; Indels
pertussis isolates from Missouri, USA.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR218010.1; -..
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; Pertactin.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
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                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                          Score 276; DB 2;
Pred. No. 6.8e-20;
1; Mismatches 2,
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(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 89.6%;
al Similarity 80.3%;
53; Conservative
                                                                                                                                                           89.6%;
80.3%;
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                                                                                                                                                                                   Conservative
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                                                                                                                                   851 AA;
                                                                                                                                                                      Similarity
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314 SVELAQ 319
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SVELAQ 310
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01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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Local Sim.
53;
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PRN.
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SEQUENCE
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Best Local
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QBRSU0
1D QBRSU
OR 01-JU
DT 01-JU
DT 01-JU
DF 01-JU
OF PERTAI
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Q93L98
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Gaps

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Search completed: May 7, 2003, 16:53:10 Job time: 29.6201 secs

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Sequence 23, Appli
Sequence 27, Appli
Sequence 76981, A
Sequence 76981, A
Sequence 21434, A
Sequence 31444, A
Sequence 11629, Sequence 11629,
Sequence 21, Appli
Sequence 21, Appli
Sequence 24, Appli
Sequence 27, Appli
Sequence 37, Appli
Sequence 67, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Aprilation US/09855754
GENERAL INFORMATION:
APPLICANT: BOUNGAUX-EUDE, CAROLINE
APPLICANT: BOUNGAUX-EUDE, CAROLINE
APPLICANT: BOUNGAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
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US-09-855-754-19

US-09-855-754-19

US-09-855-754-14

US-09-855-754-20

US-09-855-754-21

US-09-855-754-21

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US-09-791-537-112007

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US-09-791-537-112007

US-09-791-537-11629

US-09-791-537-11629

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US-09-791-537-12007

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US-09-380-693A-38
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11arity 100.0%; Pred. No. 1e-12;
Conservative 0; Mismatches 0;
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US-09-855-754-17
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Matches 52; Conserv
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SOFTWARE: F.
SEQ ID NO 17
LENGTH: 52
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US-09-855-754-17
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                                                                                                                                     7, 2003, 16:47:16 ; Search time 131.727 Seconds (without alignments) 254.511 Million cell updates/sec
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1: \cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: \cgqn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
3: \cgqn2_6/ptodata/1/paa/USON_COMB.pep:*
4: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
5: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
6: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
7: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
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26: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
27: \cgn2_6/ptodata/1/paa/USON_COMB.pep:*
                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-18
US-09-855-754-13
US-09-791-537-37413
US-09-791-537-85698
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Minimum DB 8 Maximum DB 8

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES OF PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2001-09-10
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TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI HORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNICABLIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 52
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US-09-855-754-16
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US-09-855-754-15
; Sequence 15, Application US/09855754
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                           US-09-855-754-16; Sequence 16, Application US/09855754; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
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Matches 51; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 52; Conserv
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LENGTH: 56
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LENGTH: 59
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Sequence 37413, Application US/09791537

Sequence 37413, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH:: 911
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEC ID NOS: 153055
SOFTWARE: Patentin version 3.0
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDCHIELAPPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILLS REFERENCE: 03495-0306-00000

FILLE REFERENCE: 03495-0306-00000

FILLE REFERENCE: 2001-09-10

PRIOR FILLING DATE: 2001-09-10

PRIOR FILLING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SSEQ ID NO 15

LENGTH: 52
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Pred. No. 7e-10;
0; Mismatches 0; Indels :
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Pred. No. 6e-11;
0; Mismatches 0;
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US-09-791-537-37413
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US-09-855-754-15
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSBIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISBEPTICA, THERR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CORRENT APPLICATION NUMBER: 06/206-969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTING PATE: 2000-06-25
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                         559 GAKAPPAPKPAPQPGPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPGRELSAA 610
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                                                                                                                                       Length 911;
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                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                       DB 21;
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                                                                                                                                       Score 271; DB 21
Pred. No. 7e-10;
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Pred. No. 7e-10;
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                                             ; TYPE: PRT; CRGANISM: Bordetella bronchiseptica US-09-791-537-85698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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96.2%;
                                                                                                                                     Query Match 90.9%;
Best Local Similarity 96.2%;
Matches 51; Conservative
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Matches 51; Conserv
SEQ ID NO 85698
LENGTH: 911
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LENGTH: 58
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DB 22;

Score 267;

89.68;

Query Match

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Sequence 50286, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biologia, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE; 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO $20286;
LENGTH; 922
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APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: RECTONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITILE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
                                 Gaps
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                            Indels
    Pred. No. 1.2e-10;
0; Mismatches 1;
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Pred. No. 1.3e-09;
0; Mismatches 1;
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Pred. No. 1.3e-09;
0; Mismatches 1;
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US-09-791-537-50236
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US-09-855-754-14
; Sequence 14, Application US/09855754
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Sequence 6, Application US/09855754
GENERAL INFORMATION:
  84.98;
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Best Local Similarity 87.9%;
Matches 51; Conservative
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1larity 87.9%;
Conservative
Best Local Similarity 87.9 Matches | 51; Conservative
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Patentin Ver.
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Best Local Similarity
Matches 51; Conserv
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US-09-791-537-50286
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LENGTH: 922
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US-09-855-754-6
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TITLE OF INVENTION:
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US-09-855-754-23
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LENGTH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PAPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                           APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 60/206,969
PRICA PLICATION NUMBER: 60/206,969
PRICA PLICATION DATE: 2001-09-10
PRICA PLICATION DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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Pred. No. 1.3e-09;
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Pred. No. 3.3e-09;
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GENERAL INFORMATION
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                         : BOURSAUX-EUDE, CAROLINE
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90.68;
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88.7%;
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 47; Conserv
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US-09-855-754-21
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US-09-855-754-20
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LENGTH: 48
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LENGTH: 49
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA, AND BORDETELLA, PARAPERTUSSIS, AND INFILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT FILLNG DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PRETACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDOTELLA PARETR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.2e-08;
1; Mismatches 1;
IMMUNOGENIC COMPOSITIONS
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                                                                                                                     CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
FRANCE: PROPERTY OF THE PROPERTY OF THE PATENTY OF 
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US-09-855-754-22
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US-09-855-754-21
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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18; Conservative
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APPLICANT: BOURSAUX-EUDE,
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/9855,754B
CURRENT FILING DATE: 2001-05-16
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Pred. No. 1.5e-12;
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Sequence 17, Apriloation US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-7548-17
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Best Local Similarity 100.0%; Pr
Matches 52; Conservative 0;
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03409-0206-00000
CURRENT APPLICATION NUMBER: 2001-05-16
CURRENT FILING DATE: 2001-05-16
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Pred. No. 1.1
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Pred. No. 1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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; ORGANISM: Bordetella bronchiseptica
US-09-055-754B-15
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                   Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOURSAUX-EUDE,
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SOFTWARE: PatentIn Ver.
NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 52; Conserv
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US-09-855-754B-15
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                     SOFTWARE: Par
SEQ ID NO 16
LENGTH: 59
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LENGIH: 52
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                                                          Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                    22
                                                                                                                                Length 911;
                                                          Indels
                                                                                                    1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                 Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Score 271; DB 5; L/
Pred. No. 7.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 271; DB 5;
Pred. No. 4.2e-10;
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                                                               0; Mismatches
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APPLICATION NUMBER: US/10/227,353
FLLING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lebovitz, Richard M. RECISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                             Sequence 4, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   GUISO-MACLOUF, NICOLE
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                   90.9%;
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COMPUTER READABLE FORM:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
                     Query Match 90.9
Best Local Similarity 96.2
Matches 51; Conservative
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RESULT 9
US-10-227-353-6
SEQ ID NO 6
LENGIH: 922
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTELLA OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/465,754B
CURRENT PILING DATE: 2000-05-16
PRIOR PEDELICATION NUMBER: 60/206,969
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/0855,754B
CURRENT PILING DATE: 2001-0516
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Pred. No. 4.2e-10;
0; Mismatches 0;
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Pred. No. 1.4e-10;
0; Mismatches 1;
                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-227-353-4
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                  TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-19
               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                          LENGTH: 911 amino acids TYPE: amino acid
                                                                                                   SEQUENCE CHARACTERISTICS
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ilarity 96.2%;
Conservative
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ilarity 87.9%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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SOFTWARE: Patentin Ver. 2.1
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nes 51; Conserv
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                  Length 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                         1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                Score 267; DB 5;
Pred. No. 7.6e-10;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 267; DB 6;
Pred. No. 7.6e-10;
0; Mismatches 1
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FILING DATE: 26-Aug-2002
PRIOR AFPLICATION DATA:
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NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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US-09-855-754B-14
Sequence 14, Application US/09855754B
SERICAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-7548-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 922 amino acids TYPE: amino acid
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87.9%;
                                                                                89.68;
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Best Local Similarity 87.99
Matches 51; Conservative
                                                                              Query Match
Best Local Similarity 87.9°
Matches 51; Conservative
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TELEFAX: (703) 24
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2001-05-16

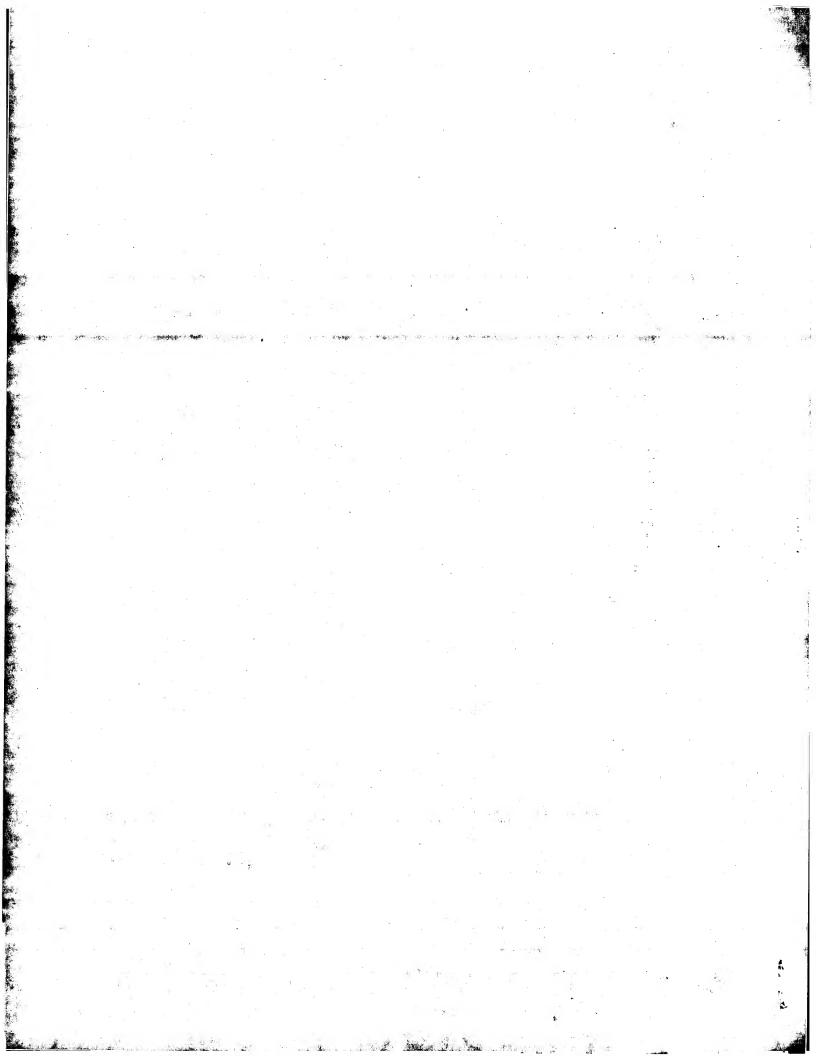
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CURRENT FILING DATE:
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LENGTH: 42
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIESPITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
          REPEATED
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRARETUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGHISEPTICA, THERE USE IN DIÁGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0226-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 49;
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Pred. No. 3.5e-09;
0; Mismatches: 0; Indels
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Pred. No. 1.4e-09;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-14
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88.7%;
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90.6%;
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 88.7
Matches 47; Conservative
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Best Local Similarity
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REPEATED
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.2e-08;
1; Mismatches 1;
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85.7%; Pred. No. 1.4e-08;
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING
TITLE OF INVENTION: REGIONS OF PERTACTIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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                                                                                                                                                                                          Bordetella bronchiseptica
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Best Local Similarity 88.9%;
Matches 48; Conservative
PRIOR APPLICATION NUMBER: 60/.
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
                                                                              SOFTWARE: Patentin Ver. 2.1
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                                                     NUMBER OF SEQ ID NOS: 25
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
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US-09-855-754B-21
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LENGTH: 52
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                                                                                                                                    Gaps
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SOFTWARE: PatentIn version 3.1
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Pred. No. 4e-06;
1; Mismatches 0; Indels
                                                                                    Score 207; DB 5; Length 42;
Pred. No. 6.7e-07;
1; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR PILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
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78.8%;
                                                                                    Query Match 69.5%;
Best Local Similarity 78.8%;
Matches 41; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local Similarity 78.8
Matches 41; Conservative
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US-10-282-122A-51012
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US-09-380-693A-50
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1 GARAPPAPKPAPQPGPPGPP......QRQPEAPAPPAGRELSAA
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1: cgn2_6/ptodata/1/paa/PCGC_COMB.pep:*
2: cgn2_6/ptodata/1/paa/USOG_COMB.pep:*
3: cgn2_6/ptodata/1/paa/USOG_COMB.pep:*
4: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
5: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
6: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
7: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
8: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
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11: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
12: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
13: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
14: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
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16: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
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12: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
13: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
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15: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
16: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
17: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
18: cgn2_6/ptodata/1/paa/USOB_COMB.pep:*
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Compugen Ltd.
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                            GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Maximum DB
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Sequence 38, Appl Sequence 53, Appl Sequence 22218, A Sequence 50, Appl

Sequence 1323, Ap Sequence 5, Appli Sequence 8, Appli

Sequence 23, Appl Sequence 2, Appl Sequence 76981, A Sequence 76981, A Sequence 76981, A Sequence 21274, A Sequence 11200, Sequence 11629, Sequence 2, Appl Sequence 3, Appl Sequence 24, Appl Sequence 21, Appl Sequence 21, Appl Sequence 2285, A Sequence 2116, Appl Sequence 2285, A Sequence 2285, A Sequence 2285, A Sequence 2118, Appl Sequence 2116, Appl Sequence 2285, A Sequence 2285, A Sequence 2118, Appl Sequence 2118, Appl

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APPLICANT: BOURSACY-EUDE, CAROLINE
APPLICANT: BOURSACY-EUDE, NICOLE
TITLE OF INVENTION: POLIPPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATE: LONG. 24
SEQ ID NOS: 24
SEQ ID NOS: 24
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 56
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1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 56

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Sequence 18, Appl Sequence 19, Appl Sequence 50286, A Sequence 6, Appli Sequence 16, Appli Sequence 15, Appl

US-09-855-754-18 US-09-855-754-19 US-09-791-537-50286 US-09-855-754-6 US-09-855-754-15

2222222

56 922 922 53 53

94.1 94.1 94.1 94.1 91.5

322 303 303 303 294.5

Result 2 Sequence Sequence Sequence Sequence

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Gaps

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Length 922; Indels 26

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PREMACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, ITTLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTILLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: BORDETELLA PRRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISBETICA, THEIR USE IN DIAGNOSTICS, AND STILE OF INVENTION: IMMUNGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 24
REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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Pred. No. 2.1e-12;
0; Mismatches 0;
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Pred. No. 6.3e-12;
0; Mismatches 1;
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CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-16
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                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09855754 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.5%;
Best Local Similarity 91.7%;
Matches 55; Conservative (
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Best Local Similarity 94.8%;
Matches 55; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
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US-09-855-754-15
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APPLICANT: Debe, Joseph
APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HREHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50286
LENGTH: 922
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-BUDE, CAROLINE
APPLICANT: GIISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                          APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN FILLE NEFRENCE: 03495-0206-00000
FILLE REFERENCE: 03495-0206-00000
PRICHENT PELLING DATE: 2001-09-10
PRICHENT PILLING DATE: 2001-09-10
PRICH PILLING DATE: 2001-09-10
PRICH PILLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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           1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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94.8%; Pred. No. 6.3e-12;
tive .0; Mismatches 1;
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Pred. No. 5.7e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50286, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella parapertussis US-09-791-537-50286
                                                                                                                                                            Sequence 19, Application US/09055754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 94.1%;
Best Local Similarity 94.8%;
Matches 55; Conservative
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Best Local Similarity
Matches 55; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-791-537-50286
                                                                                                                   RESULT 2
US-09-855-754-19
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LENGTH: 58
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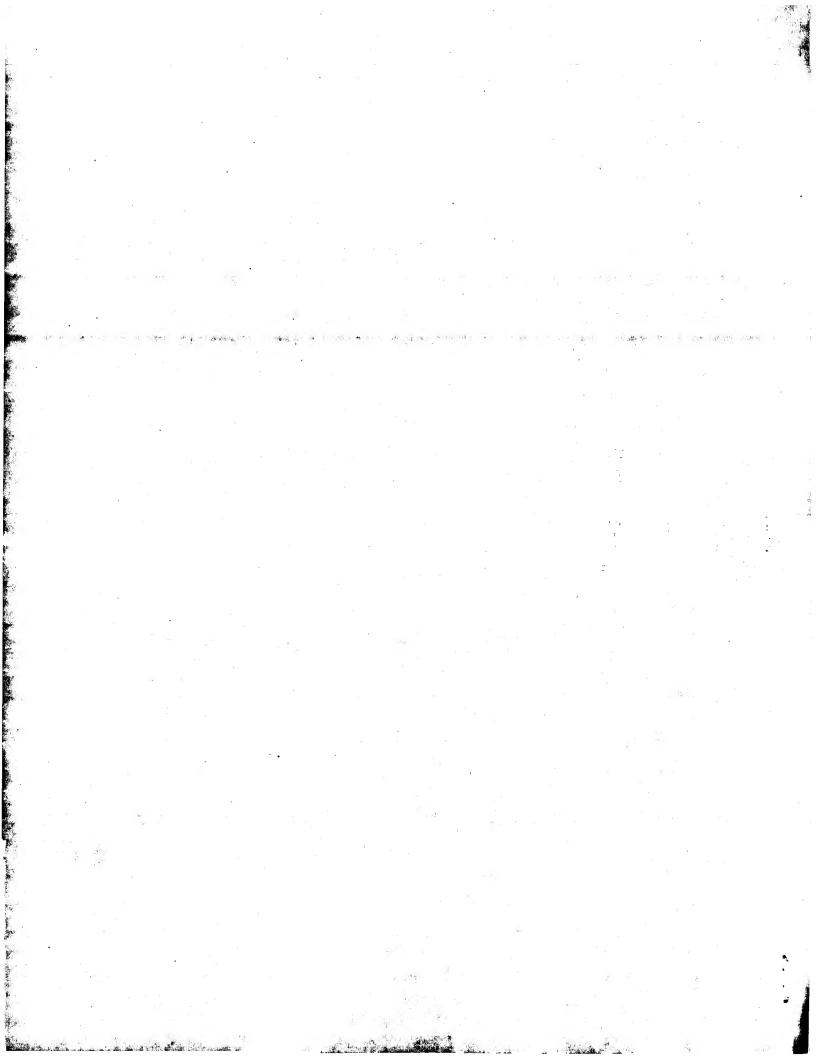
DB 22; Length 59;

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APPLICATE: CGISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGTELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
CURRENT PAPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: REGIONS OF PERPACTIN IN BONDERPLISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BONDETELLA PREPETLE.
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 9.4e-11;
0; Mismatches 0;
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Pred. No. 1.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09855754 GENERAL INFORMATION:
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                                                                                                                                                                            US-09-855-754-4; Squence 4. Squence 4. Squence 4. Squence 4. GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: BOURSAUX-EUDE, CAROLINE
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91.1%;
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ilarity 92.9%;
Conservative
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Best Local Similarity 91.19
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
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APPLICANT: GUISO-MACLOUF
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Best Local Similarity
Matches 52; Conserv
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debc, Derck
APPLICANT: Dencer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: 105/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 37413
LENGTH: 911
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Sequence 85698, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NOWBER: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                         Length 52;
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Pred. No. 7.8e-12;
0; Mismatches 0;
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Pred. No. 9.4e-11;
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92.9%; Pred. No. 9.4e-11;
tive 0; Mismatches 0;
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US-09-791-537-85698
   60/206,969
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1 Similarity 92.9%;
52; Conservative
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ilarity 92.9%;
Conservative
PRIOR APPLICATION NUMBER: 60/3 PRIOR FILING DATE: 2000-05-25
                                                                NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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Best Local Similarity 92.9
Matches 52; Conservative
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Best Local Similarity
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LENGTH: 911
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Best Local S
Matches 52
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERBUCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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                                           APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR PELLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 1.6e-10;
.....nes 0;
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Pred. No. 4.2e-10;
0; Mismatches 0;
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US-09-855-754-20
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                          APPLICANT: BOURSAUX-EUDE, CAROLINE
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85.7%;
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87.58;
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SEQ ID NO 20
LENGTH: 48
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Best Local Similarity
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Best Local Similarity
GENERAL INFORMATION:
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LENGTH: 49
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TITLE OF INVENTION: POLYMOTPIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: POLYMOTPIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03405-0206-00000
CURRENT PAPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION DATE: 2001-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0306-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 5.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                   CURRENT APPLICATION NUMBER: US/09/855,754
                                                                   CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754-22
                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica US-09-855-754-21
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APPLICANT: BOURSAUX-EUDE, CAROLINE
TITLE OF INVENTION: IMMUNOGENIC FILE REFERENCE: 03495-0206-00000
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86.0%;
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 54
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us-09-855-754b-18.rapn

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 05/09-0659
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Sequence 19, Appl
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nnce 12544, A nnce 51470, A nnce 9452, Ap nnce 9652, Ap nnce 6756, Ap nnce 80, Appl nnce 92543, A nnce 92543, A nnce 28564, A nnce 28564, A nnce 28564, A nnce 24873, A nnce 24873, A nnce 24873, A		THE REPEATED SSIS,	0; Gaps 0;	ል - 4 የ የ
Sequence Seq		ton US/09855754B EUDE, CAROLINE CLOUF, NICOLE POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE R RECIONS OF PERTACTIN IN BORDETELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IMMUNOSENIC COMPOSITIONS S-0206-00000 NUMBER: 00/206,969 00-05-25 er. 2.1 a bronchiseptica	; Length 56; 3; 0; Indels	GAKAPPAÈKPAPQPGPQPGPQPQPQPPQPPQPPQPPQRQPEGABAAAGRELSAA
US-10-156-761-12544 US-110-282-122A-51470 US-10-224-995A-3465 US-09-949-016-9652 US-09-949-016-6756 US-60-423-586-80 US-60-423-586-80 US-09-724-676-92543 US-10-724-676-92543 US-10-282-122A-48029 US-10-282-122A-48029 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-28564 US-10-366-683-288564 US-10-366-683-288564 US-10-366-683-288564 US-10-366-683-288564 US-10-366-683-288564 US-10-366-683-288564 US-10-366-683-28873 US-10-366-683-28873 US-10-366-683-2883	ALIGNMENTS	54B E CONTAINING POLYA CONTAINING POLYA TRAPERTUSSIS, A RARAPERTUSSIS, A COMPOSITIONS //855,754B 969	Score 322; DB 5; Pred. No. 1.3e-13 Mismatches 0	PPOPPOROPEA
000000000000000000000000000000000000000	AL	SULT 1 SQUE 1 SQUE 1 SQUE 1 SQUE 1 SQUE 1 SQUE 1 APPLICATION US/09855754B GENERAL INFORMATION: APPLICANT: BOUGSAUX: EUDE, CAROLINE APPLICANT: BOUGSAUX: EUDE, NICOLE TITLE OF INVENTION: POLYPEPTIDES CONTAINING P TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BRONDHISEPTICA, THEIR US TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS CURRENT APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2001-05-16 PRIOR FILING DATE: 2000-05-25 NUMBER OF SEQ ID NOS: 25 SOFTWARE: PATENTIN VOY: 2.1 SEQ ID NO 18 LENGTH 56 TYPE: PRT ORGANISM: BORGETELIA bronchiseptica -09-855-754B-18	100.0%; Scoi 100.0%; Pred tive 0; Mi	1 GAKAPPAFKPAPQPGPOPGPOPGPOPGI
324 324 324 324 324 324 3264 3264 3264 3		ULT 1 194-855-7548-18 196-855-7548-18 196-855-7548-18 196-855-7548-18 196-855-7548-18 196-856-7548-18 196-856-7548-18 196-856-7548-18 196-856-7548-18 196-855-7548-18 196-855-7548-18 196-855-7548-18 196-855-7548-18 196-855-7548-18	th Similarity 100 56; Conservative	1 GAKAPPAFKPAPOGPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOPOP
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FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQP--GPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                        Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                        Score 303; DB 5;
Pred. No. 1.9e-12
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Pred. No. 1e-11;
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                                                                                                        ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-19
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09855754B GENERAL INFORMATION:
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US-09-855-7548-6
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94.8%;
                                                                                                                                                                        94.18;
94.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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SOFTWARE: Patentin Ver. 2.1
                        PatentIn Ver. 2.1
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    NUMBER OF SEQ ID NOS: 25
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Matches 55; Conserv
                                                                                                                                                                                              Similarity
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US-10-227-353-6
                            SOFTWARE: Pe
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                                                                                          TYPE: PRT
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Best Local
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISSPITICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORNCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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Pred. No. 1e-11;
0; Mismatches
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
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                                                                                                                     REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-227-353-6
                                                                      NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09855754B GENERAL INFORMATION:
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ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                      TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                               LENGTH: 922 amino acids
                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.18;
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91.7%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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PRIOR FILING DATE: 2000-0
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US-09-855-754B-15
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CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILLING DATE: 2001-05-16 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILLING DATE: 2000-05-25
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
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; ORGANISM: Bordetella bronchiseptica
.US-09-855-754B-17
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                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        (703) 243-5410
                                                                                                                  FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 911 amino acids TYPE: amino acids
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APPLICANT: GUISO-MACLOUF, NICOLE
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92.9%;
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NUMBER OF SEQ ID NOS: 25
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Best Local Similarity 92.93
Matches 52; Conservative
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 60,206,969
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
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ROMANOS, MICHAEL A.
TILLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 911;
                                                                                                                                                                                                                                                                                        Length 52;
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                                                                                                                                                                                                                                                                                   Score 285; DB 5;
Pred. No. 2.2e-11;
0; Mismatches 0;
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION WUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION WUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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                                                                                                                                                                                                                     ORGANISM: Bordetella bronchiseptica
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ilarity 92.9%;
Conservative
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Local Similarity 92.9%;
nes 52; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 52; Conserv
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US-10-227-353-4
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APPLICANT: GUÍSO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYDEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYDEPTIDES CONTAINING POLYMORPHELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AMMINGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
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SOFWMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
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87.6%; Score 282; DB 5;
Best Local Similarity 91.1%; Pred. No. 3.4e-11;
Matches 51; Conservative 1; Mismatches 0
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Pred. No. 1.3e-10;
0; Mismatches 0
                                                                                                                                              APPLICATION NUMBER: US/08/460, 269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
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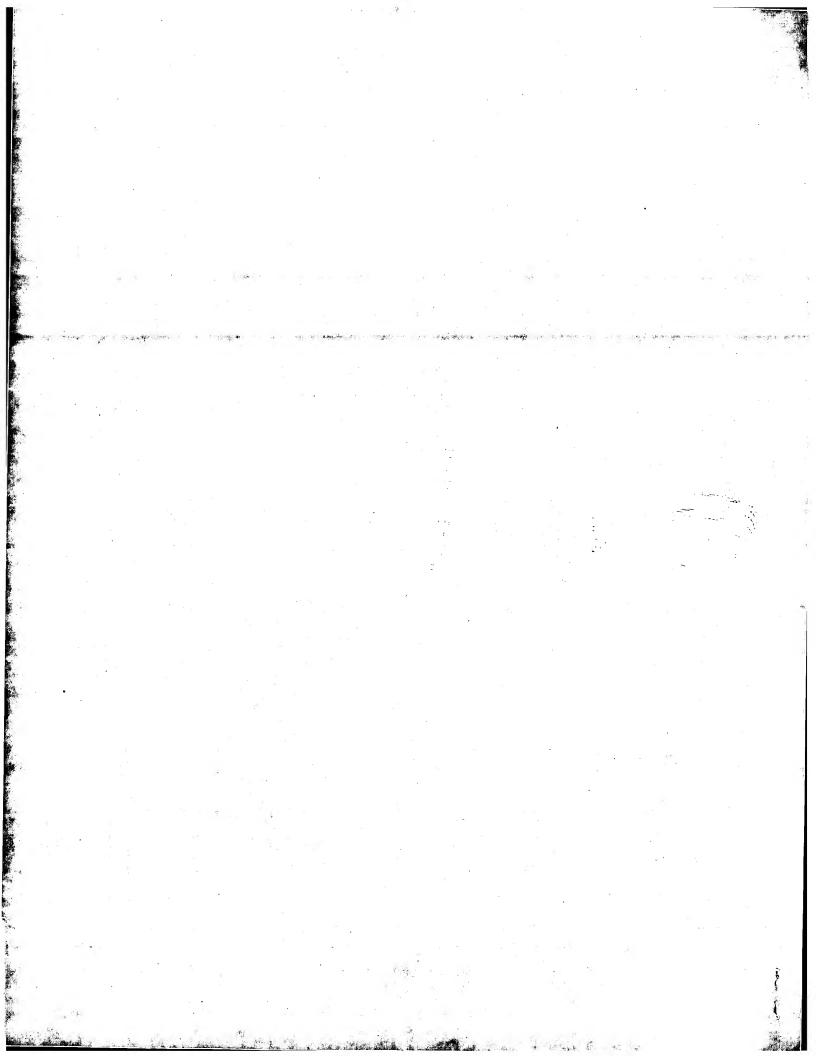
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RESULT 13
US-09-855-754B-22
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LENGTH: 42
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 120/99/855,754B
    POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-0206-00000
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Pred. No. 3.9e-10;
0; Mismatches 0;
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Pred. No. 9.7e-10;
0; Mismatches 0;
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYN
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORE
TITLE OF INVENTION: BORDETELLA PARAPERIUSSIS, AR
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PLING DATE: 2000-05-25
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CURRENT APPLICATION NUMBER: US/09/855,754B
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-855-754B-20; Sequence 20, Application US/09855754B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-14
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85.7%;
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87.5%;
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Matches 48; Conservative
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PRIOR FILING DATE: 2000-05
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Best Local Similarity
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ORGANISM:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,7548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTINI IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-0206-00000
CORRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILLING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                      Length 52;
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                                                                                                                                                                                                                                                                                                                   Score 257; DB 5; Le
Pred. No. 1.2e-09;
0; Mismatches 2;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09855754B GENERAL INFORMATION:
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     2001-05-16
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Best Local Similarity 86.0%;
Matches 49; Conservative
CURRENT FILING DATE: 2001-05
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 52
                                                        2000-05-25
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Matches 49; Conservative
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SOFTWARE: Patentin Ver. 3
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Pred. No. 4.7e-06;
0; Mismatches 1; Indels 14; Gaps
                                                                                                                     Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51012
LENGTH: 768
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                                                                                                                     14;
                                                                         Score 210; DB 5; Length 42;
Pred. No. 8e-07;
0; Mismatches 1; Indels
                                                                                                               1; Indels
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; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/206,848
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APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/267,636
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APPLICATION NUMBER: 60/207,727
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                                                                         Query Match 65.2%;
Best Local Similarity 73.2%;
Matches 41; Conservative
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Best Local Similarity 73.2%;
Matches 41; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:49 Job time : 34.0085 secs



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Best Local S
Matches 58
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Sequence 50286, A
Sequence 6, Appli
Sequence 18, Appl
Sequence 16, Appl
Sequence 15, Appl
                                                                                                 ; Search time 146.927 Seconds
  (without alignments)
  254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
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20: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
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23: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
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25: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
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27: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/USOR_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-791-537-50286
US-09-855-754-6
US-09-855-754-18
US-09-855-754-15
US-09-855-754-15
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALCHLIN VET. 2.1
SEQ ID NO 19
                                                                                                    Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 78841, A
Sequence 76968, A
Sequence 76961, A
Sequence 76961, A
Sequence 21274, A
Sequence 212007,
Sequence 24, Appl
Sequence 21, Appl
Sequence 2285, Appl
Sequence 2218, Appl
Sequence 2217, Appl
Sequence 22118, Appl
Sequence 22118, Appl
Sequence 22217, Appl
Sequence 22218, Appl
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1 US-09-791-537-37413

1 US-09-855-754-4

2 US-09-855-754-12

2 US-09-855-754-12

2 US-09-855-754-21

2 US-09-855-754-21

2 US-09-855-754-21

2 US-09-855-754-21

2 US-09-855-754-21

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2 US-09-855-754-2

2 US-09-857-754-2

2 US-09-811-507-2218

8 US-09-417-507-2218

8 US-09-417-507-2215

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8 US-09-417-507-2215
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llarity 100.0%; Pred. No. 7.4e-15;
Conservative 0; Mismatches 0;
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Gaps

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA, THEIR USE IN DIAGNOSTICS, AND IN FITLE OF INVENTION: IMMUNGEBRIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.7e-12;
0; Mismatches 0;
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Pred. No. 8.5e-13;
0; Mismatches 1;
                                                   BRONCHISEPTICA, THEIR USI
IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BORDETELLA PRARPERTUSSI TITLE OF INVENTION: BRONCHISEPTICA, THEIR UTITLE OF INVENTION: IMMUNGENIC COMPOSITION FILE REFERENCE: 03455-0206-00000 CURRENT APPLICATION NUMBER: 05/09/855,754 CURRENT FILING DATE: 2001-09-10 PRIOR FILING DATE: 2000-05-25 PRIOR FILING DATE: 2000-05-25 SOFTWARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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GENERAL INFORMATION:
APPLICANT: BOURSAUX EDDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09855754 GENERAL INFORMATION:
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Best Local Similarity 95.0%;
Matches 57; Conservative
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SOFTWARE: PatentIn Ver.
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US-09-855-754-16
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SEQ ID NO 16
LENGTH: 59
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LENGTH: 56
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Best Local S
Matches 55
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                                                                                                                                               Sequence 50266, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: 18/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50286
LENGTH: 922
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONGEFELLA PRABERUGSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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Pred. No. 7.9e-14;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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Best Local Similarity
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Best Local Similarity
Matches 58; Conserv
                                                                                                           RESULT 2
US-09-791-537-50286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-791-537-50286
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BOUGSADY. EUDE, CAROLINE

APPLICANT: BOUGSADY. EUDE, CAROLINE

APPLICANT: BOUGSADY. EUDE, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS,

TITLE OF INVENTION: BRONCHISEPTIOS, THERR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS

TITLE OF INVENTION INMERS: US/09/855,754

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VET: 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTION IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGERIC COMPOSITIONS
FILE REPERRUCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US,09/855,754
CURRENT RILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER: PACENTING DATE: 2000-05-25
NUMBER: PACENTING DATE: 2000-05-25
NUMBER: PACENTING DATE: 2000-05-25
NUMBER: PACENTING DATE: 2000-05-25
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Pred. No. 1.6e-10;
0; Mismatches 0;
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Pred. No. 1.7e-10;
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Best Local Similarity 87.9%;
Matches 51; Conservative (
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ilarity 89.7%;
Conservative
         559 GAKAPPAPKPAPQPGPQPG
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Best Local Similarity
Matches 52; Conserv
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US-09-855-754-22
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US-09-855-754-17
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US-09-855-754-17
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TTLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
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89.7%; Pred. No. 1.6e-10;
tive 0; Mismatches 0;
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Pred. No. 1.6e-10;
0; Mismatches 0;
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Pred. No. 1.4e-11;
0; Mismatches 0
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Darzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
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; Sequence 85698, Application US/09791537
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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US-09-791-537-85698
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89.7%;
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Best Local Similarity 89.7%;
Matches 52; Conservative
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Best Local Similarity 89.7
Matches 52; Conservative
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Best Local Similarity
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LENGTH: 911
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-247-544-2
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LENGTH: 52
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Matches 48
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                                    TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 12001-09-10
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APPLICANT: BUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: PORDETELLA PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPERTITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 2.7e-10;
0; Mismatches 0;
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Pred. No. 2.4e-10;
); Mismatches 5;
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: BOURSAUX-EUDE, CAROLINE
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 49; Conserv
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SEQ ID NO 22
LENGTH: 54
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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Pred. No. 7.1e-10;
0; Mismatches 0;
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  IMMUNOGENIC COMPOSITIONS
                                               CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                         CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION WUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 48
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                              ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-855-754-21
; Sequence 21, Application US/09855754
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08247544
GENERAL INFORMATION:
APPLICANT: CHARLES, IAN G.
APPLICANT: FAIRWEATHER, NEIL F.
TITLE OF INVENTION: IMMUNOGENIC FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: VACCINES NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        76.7%;
llarity 82.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOURSAUX-EUDE,
                                                                                                                                                                                                                                                                                                                                                                                  L Similarity
48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22201-4714
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMARE: Patentin Release #1.0, Version #1.25
SOCTAMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSITCATION NUMBER: US 08/048,059
FILING DATE: 19-APR-1993
PRIOR APPLICATION NUMBER: US 07/798,045
FILING DATE: 19-APR-1991
PRIOR APPLICATION NUMBER: US 07/756,589
FILING DATE: 04-SEP-1990
PRIOR APPLICATION NUMBER: US 07/576,589
FILING DATE: 04-SEP-1989
PRIOR APPLICATION NUMBER: US 99/1388.0
FILING DATE: 21-APX-1990
PRIOR APPLICATION NUMBER: US 90/1388.0
FILING DATE: 21-APX-1990
ATTORNEY/AGENT INFORMATION:
FELECHMONE: CRAMACORE NUMBER: 25,327
FELECHMONE: CRAMACORE NUMBER: 25,327
FELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONE: CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Search completed: May 7, 2003, 17:21:57 Job time: 146.927 secs

Query Match 70.4%; Score 236; DB 6; Length 39; Best Local Similarity 100.0%; Pred. No. 1.4e-08; Matches 39; Conservative 0; Mismatches 0; Indels

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Gaps

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8 08:49:00 2003
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7, 2003, 16:48:21 ; Search time 34.1874 Seconds (without alignments) 289.347 Million cell updates/sec
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335
1 GAKAPPAPKPAPQPGPQPGP......QRQPEAPAPQPPAGRELSAA
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                   May
                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                               Scoring table:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

length: 0 length: 2000000000

/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:* Pending_Patents_AA_New:*
.: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
.: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
.: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
.: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 19, Appl	9	9	18	16,	15,	4 , A	4	17	22,	14,	20,	21,	23,	5101	u,	'n	24,	4170		Sequence 11684, A	Sequence 11684, A				
TD .	US-09:855-754B-19	US-09-855-754B-6	US-10-227-353-6	US-09-855-754B-18	US-09-855-754B-16	US-09-855-754B-15	US-09-855-754B-4	US-10-227-353-4	US-09-855-754B-17	US-09-855-754B-22	US-09-855-754B-14	US-09-855-754B-20	US-09-855-754B-21	US-09-855-754B-23	US-10-282-122A-51012	US-09-855-754B-5	US-10-227-353-2	US-09-855-754B-24	US-10-218-140-4170	US-60-452-680-19541	US-60-453-135-11684	US-60-453-050-11684	US-10-017-161-1982	US-10-282-122A-51472	US-10-224-999A-3465	US-10-282-122A-51470
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Length	58	922	922	26	59	52	911	911	52	54	49	48	52	42	768	910	910	39	900	1218	1218	1218	523	632	487	324
Query Match	100.0	100.0	100.0	90.4	89.1	84.8	84.8	84.8	79.7	79.1	78.7	76.7	76.4	62.4	62.4	62.4	62.4	56.3	50.0	50.0	50.0	50.0	49.9	49.9	45.5	44.6
Score	335	335	335	303	298.5	284	284	284	267	265	263.5	257	256	209	209	209	209	188.5	167.5	167.5	167.5	167.5	167	167	152.5	149.5
Result No.	-	7	٣	4	ις.	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

APPLICANT: 1001SAUX-EUDE, CAROLINE
APPLICANT: BOUISAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTION IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BROWNENESPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000

Sequence 6, Application US/09855754B GENERAL INFORMATION:

US-09-855-754B-6

RESULT 2

CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16 PRIOR PELLOATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25

Gaps 58

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GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHIEDEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS THE REPERRACE: 03495-0206-00000 CURRENT APPLICATION NUMBER: 93,09,9855,754B
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: FREGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGHISRPTICS, THEIR USE IN DIAGNOSTICS, AND INTILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GUISO-WACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAKAPPAPKPAPQPGPQPGPQPP--GPQPPQPPQPPQPPQPPGRPAPAPQPPAGRELSAA
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Pred. No. 3.5e-12;
0; Mismatches 1
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Pred. No. 6.7e-12;
0; Mismatches 0
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09855754B
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%;
95.0%;
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94.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 95.0
Matches 57; Conservative
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Matches 55; Conserv
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US-09-855-754B-15
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGGUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922
                                                                                                                                                                              Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 335; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.2e-13;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                 Score 335; DB 5;
Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-AUG-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-855-754B-18; Sequence 18, Application US/09855754B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                      ) ORGANISM: Bordetella parapertussis US-09-855-754B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
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                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
                     SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                             58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703)
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                   Query Match
Best Local Similarity
                        SOFINATION SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-227-353-6
                                                                                         TYPE: PRT
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US-10-227-353-4
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TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVERTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVERTION: BRONCHISSPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                           Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                         Score 284; DB 5;
Pred. No. 4.6e-11;
0; Mismatches 0;
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Pred. No. 2.6e-10;
0; Mismatches 0
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
                                                   PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
                                                                                                                                                                                               ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10227353 GENERAL INFORMATION:
                                     2001-05-16
                                                                                                                                                                                                                                                         84.8%;
ilarity 89.7%;
Conservative
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89.7%;
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SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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es 52; Conserv
                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                  US-09-855-754B-15
                                                                                                                                                                                                                                                                                                 52;
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US-10-227-353-4
                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                           Query Match
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Matches
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT PRILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/206, 969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPGRELSAA 610
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                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 267; DB 5;
Pred. No. 5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 284; DB 6;
Pred. No. 2.6e-10;
0; Mismatches 0
                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                              NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOFOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                     ENCÉ CHARACTERISTICS:
LENGTH: 911 amino acids
TYFE: amino acid
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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87.9&;
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Best Local Similarity 89.77
Matches 52; Conservative
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SOFTWARE: Patentin Ver.
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Matches 51; Conserv
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US-09-855-754B-17
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US-09-855-754B-22
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT ELLING DATE: 2001-05-16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONEFIELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                     TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
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Pred. No. 7.8e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 265; DB 5;
Pred. No. 6.7e-10;
0; Mismatches 5
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US-09-855-754B-14
; Sequence 14, Application US/09855754B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-22
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84.5%;
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l Similarity 84.5%;
49; Conservative (
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Best Local Similarity 84.57
Matches 49; Conservative
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PRIOR FILING DATE: 2000-05
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Matches 49; Conserv
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ORGANISM: 1
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POETONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MANUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                          0; Indels
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1 Similarity 84.5%; Pred. No. 2.3e-09;
49; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                     Score 257; DB 5;
Pred. No. 1.9e-09;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILLING DATE: 2001-08-16
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                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-20
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAROLINE
CURRENT FILLING DATE: 2001-05-1
PRIOR APPLICATION NUMBER: 60/20
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                     76.7%;
82.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                       48; Conservative
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PRIOR FILING DATE: 2000-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOURSAUX-EUDE,
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-09-855-754B-23
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SEQ ID NO 23
LENGTH: 42
                                                                                                                                                                    LENGTH: 48
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FILE REFERENCE: ELITERA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                  Gaps
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                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 51012 LENGTH: 768
                                                                                                                                16;
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Pred. No. 8e-06;
0; Mismatches 1; Indels 16;
                                                                                 Score 209; DB 5; Length 42;
Pred. No. 1.4e-06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                   Sequence 51012, Application US/10282122A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R FILING DATE: 2000-05-23

R APPLICATION NUMBER: 60/207,727

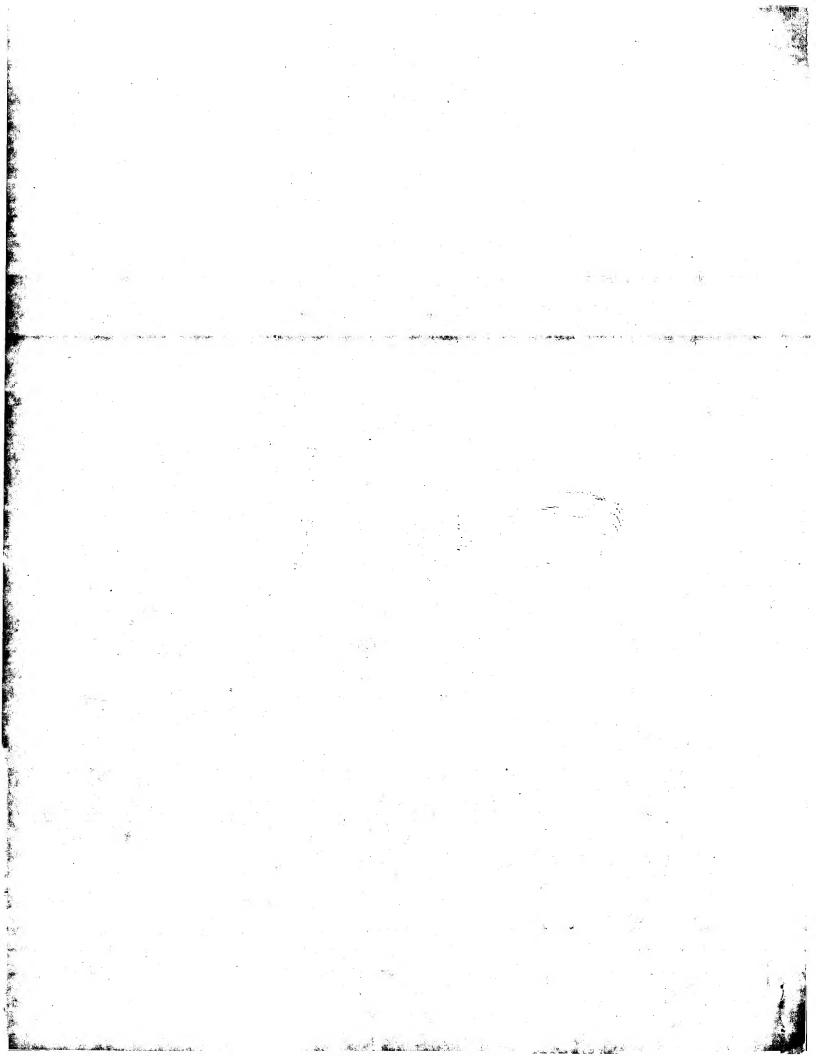
R FILING DATE: 2000-05-26

R APPLICATION NUMBER: 60/230,335

R FILING DATE: 2000-09-06

R APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/191,078
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APPLICATION NUMBER: 60/206,848
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APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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US-10-282-122A-51012
                                                                                 Query Match 62.4%;
Best Local Similarity 70.7%;
Matches 41; Conservative
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Best Local Similarity 70.7%;
Matches 41; Conservative
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Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:49 Job time : 34.1874 secs



Sequence 18, Appl Sequence 50, Appl Sequence 51, Appl Sequence 21, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 23, Appl Sequence 75841, A Sequence 76961, A Sequence 76961, A Sequence 76961, A Sequence 76961, A Sequence 7842, A Sequence 112007, Sequence 11207, Sequence 24, Appl Sequence 11207, Sequence 1120, Appl Sequence 24, Appl Sequence 2285, Appl Sequence 2281, Appl

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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRRACTIN IN BORDETELLA PRITLE OF INVENTION: BORDETELLA PRECIOUS
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT APPLICATION NUMBER: 06/206,969
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
2 US-09-855-754-18

2 US-09-855-754-19

1 US-09-71-537-50286

2 US-09-855-754-21

2 US-09-855-754-22

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-16

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1 US-09-791-537-78443

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1 US-09-791-237-78255

2 US-08-247-544-8

1 US-09-380-693A-49

1 US-09-380-693A-51

2 US-08-247-544-8

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2 US-08-247-544-8

1 US-09-380-693A-51

2 US-08-247-544-31

2 US-08-247-544-31

2 US-08-31-418-2285

2 US-08-247-541-333

2 US-08-247-541-333

2 US-08-241-611-323

2 US-08-241-611-323

2 US-09-896-0030-11
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US-09-855-754-20
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Sequence 20, Application US/09855754
GENERAL INFORMATION:
     202.5
202.5
202.5
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Sequence 14, Appl
Sequence 15, Appl
Sequence 37413, A
Sequence 8569, A
Sequence 4, Appll
                                                                                                                                                             7, 2003, 16:47:16 ; Search time 121.595 Seconds (without alignments) 254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPPQ......QRQPEAPAPQPPAGRELSAA
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(9902_6/ptodata/1/paa/US06_COMB.pep:*
(9902_6/ptodata/1/paa/US01_COMB.pep:*
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(9902_6/ptodata/1/paa/US01_COMB.pep:*
(9902_6/ptodata/1/paa/US012_COMB.pep:*
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(9902_6/ptodata/1/paa/US012_COMB.pep:*
(9002_6/ptodata/1/paa/US012_COMB.pep:*
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6/ptodata/1/paa/US094_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
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6/ptodata/1/paa/US097_COMB.pep:*
6/ptodata/1/paa/US099_COMB.pep:*
6/ptodata/1/paa/US099
                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-14
US-09-855-754-15
US-09-791-537-37413
US-09-791-537-85698
US-09-855-754-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   4569144 seqs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                          Run on:
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Length 48;

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Query Match
Best Local Similarity 92.3%;
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver.
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US-09-855-754-4
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APPLICANT: BOURGAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPATATATINI IN BORDETELLA
TITLE OF INVENTION: BRONGHISEPATICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: USO/99/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABETUSSIS, AND BONDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
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1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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0;
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Pred. No. 3.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella bronchiseptica
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; Sequence 15, Application US/09855754
; GENERAL INFORMATION:
                                                                                                                           Sequence 14, Application US/09855754 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOURSAUX-EUDE, CAROLINE
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ilarity 98.0%;
Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Matches 48; Conserv
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Best Local Similarity
Matches 48; Conserv
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; ORGANISM: BO
US-09-855-754-14
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LENGTH: 52
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Sequence 85698, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bloomia.x. Inc.
APPLICANT: Bloomia.x. Inc.
APPLICANT: Dabe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFRENCE: 251/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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TITLE OF INVENTION: POLYBEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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92.3%; Pred. No. 5.6e-10;
ive 0; Mismatches 0;
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Pred. No. 5.6e-10;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: 0S/09/855,754
CURRENT FILING DATE: 2001-09-10
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-791-537-37413
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TYPE: PRT
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CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 18
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 04495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                            Length 911;
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Pred. No. 6.5e-11;
0; Mismatches 0; Indels
                                                                                                                                                                     0; Indels
                                                                                                                        Score 260; DB 22;
Pred. No. 5.6e-10;
0; Mismatches 0;
                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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US-09-855-754-18
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PRIOR FILING DATE: 2000-05-25
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
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; GENERAL INFORMATION:
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85.7%;
                                                                                                                          95.6%;
92.3%;
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Best Local Similarity 85.77
Matches 48; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Matches 48; Conservative
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SEQ ID NO 4
LENGTH: 911
                                                                                                                          Query Match
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Length 58;

DB 22;

Score 257;

94.58;

Query Match

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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                         Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: REGIONS OF PERTACTIVI IN BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THERR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DAIE: 2001-09-10
                                                          GAKAPPAPRAPQPG-----PQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA
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                       Indels
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Pred. No. 9.1e-10;
0; Mismatches 0;
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Pred. No. 9.1e-10;
0; Mismatches 0;
  Pred. No. 7.8e-11;
); Mismatches 0
                                                                                                                                                                                                                                                                                                                                    FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50286
LENGTH: 922
                                                                                                                                                                                                   Sequence 50286, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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82.8%;
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Best Local Similarity 82.8%;
Matches 48; Conservative
  82.8%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
Best Local Similarity 82.8 Matches 48; Conservative
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Best Local Similarity
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US-09-791-537-50286
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SEQ ID NO 17
LENGTH: 52
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Best Local 9
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Matches
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT PELLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 05/01-09-10
PRIOR FILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/85,754
CURRENT FILLING DATE: 2001-0910
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: RECIOUS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.2%; Score 248; DB 22; Length 54; B5.2%; Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 249; DB 22;
Pred. No. 2.5e-10;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
88.5%;
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 52
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Matches 46; Conserv
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TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BROBETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND FITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FILE REFERENCE: 03495-0206-00000
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
                                                    CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFFWARE: PATENTIN Ver. 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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ORGANISM: Bordetella bronchiseptica
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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SOFTWARE: PatentIn Ver. 2.1
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US-09-855-754-23
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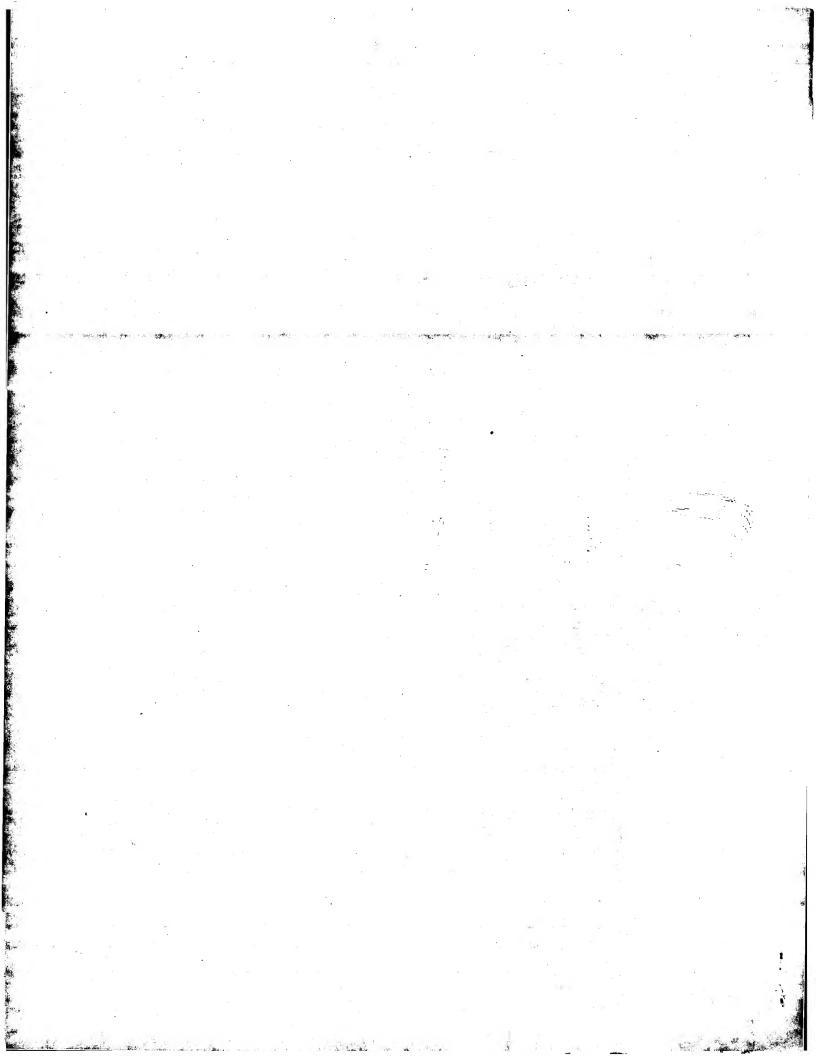
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; SOFTWARE: Patentin Ver. 2.1
; SEO ID NO 23
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
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Query Match 82.0%; Score 223; DB 22; Length 42;
Best Local Similarity 87.5%; Pred. No. 1.3e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 6; Gaps
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Search completed: May 7, 2003, 17:21:58 Job time: 122.595 secs



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Sequence 19, Appl
Sequence 6, Appli
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2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-724-676A-84275

84274 Sequence 84274, A 8-84278 Sequence 84274, A 8-84278 Sequence 84278, A 8-84280 Sequence 84280, A 8-84280 Sequence 84280, A 8-84277 Sequence 84277, A 8-84277 Sequence 84277, A 8-84279 Sequence 84277, A 8-84279 Sequence 84277, A 8-84279 Sequence 84279, A 8-84279 Sequence 84276, A 8-84276 Sequence 84276, A 8-84276 Sequence 54828, A 8-51472 Sequence 51477, A 8-6988 Sequence 51477, A 8-6988 Sequence 51477, A 8-6988 Sequence 51477, A Sequence 51427, A Sequence 69888, A 8-224 Sequence 69888, A 8-224 Sequence 69888, A 8-224 Sequence 69882, A 9-9652, Ap Sequence 69621, App		POLYMORPHISMS OF THE REPEATED BORDETELLA PERTELLA IS, AND BORDETELLA USE IN DIAGNOSTICS, AND IN NS	; DB 5; Length 48; 3.2e-11; hes 0; Indels 0; Gaps 0;	POPPAGRELSAA 48 POPPAGRELSAA 48	G POLYMORPHISMS OF THE REPEATED IN BORDETELLA PERTUSSIS, SIES, AND BORDETELLA TOSE IN DIAGNOSTICS, AND IN CONS
1760 5 US-09-724-676-84274 1776 5 US-09-724-676A-84278 1778 5 US-09-724-676-84278 2328 5 US-09-724-676-84278 2328 5 US-09-724-676-84280 2346 5 US-09-724-676-84277 2346 5 US-09-724-676-84277 2781 5 US-09-724-676-84277 2781 5 US-09-724-676-84279 2781 5 US-09-724-676-84279 279 5 US-09-724-676-84279 279 5 US-09-724-676-84276 279 6 US-10-282-122A-51472 273 6 US-10-282-122A-6988 1390 6 US-10-282-122A-6988 1390 6 US-10-092-900A-224	ALIGNMENTS	B NTAINI TACINI THEI MPOSIT 55,7541	.0%; Score 272 .0%; Pred. No. 0; Mismatcl	GAKAPPAKRAPOPEGPOPPOPPOPPOROPPEAPAPOPPAGRELSAA 1111 1 1 1 1 1 1 1 1 1 1	rainin Actin Pertug Positi
126 66.3 126 66.3 126 66.3 126 66.3 126 66.3 126 66.3 126 66.3 127 66.3 128 66.3 129 66.3 129 66.3 129 66.3 120.5 64.3 120.5 44.3		RESULT 1 Sequence 20, Application US/09855754; GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE TITLE OF INVENTION: REGIONS OF PER TITLE OF INVENTION: REGIONS OF PER TITLE OF INVENTION: BRONCHISEPTICA TITLE OF INVENTION: IMMUNGENIC CON FILE REFERENCE: 03495-0206-00000 CURRENT FILING DATE: 2000-05-15 PRIOR PELING DATE: 2000-05-25 NUMBER OF SEQ 1D NOS: 25 NUMBER OF SEQ 1D NOS: 25 LENGTH: 48 TYPE: PRT ORGANISM: BOLGETEILB DIONCHISEPTIC US-09-855-754B-20	/ Match 100 Local Similarity 100 les 48; Conservative	1 GAKAPPAPKPAPQI 	754B-14 14, Applicat INFORMATION: WERE BORGSAUX WERS GUISO-WERE F INVENTION: F INVE
22222 22222 23222 2322 2322 2322 244444 244444444		RESULT 1 US-09-855-75 SEQUENCE IN RENERAL IN REPLICANT TITLE OF TI	Query M Best Lo Matches	da Db	RESULT 2 US-09-855- Sequence Seneral APPLICA TITLE OI TIT

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US-09-855-754B-18
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND INAFILE OF INVENTION: IMMUNGBENTC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT PILLING DATE: 2001-05-16
PRIOR PELLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.1
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TITLE OF INVENTION: POLYMPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 1.5e-10;
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Pred. No. 2e-10;
                                                                                                                                                                                                                          0; Mismatches
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-754B-15; Sequence 15, Application US/09855754B; GENERAL INFORMATION:
                                                                                                            ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-14
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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1 Similarity 92.3%;
48; Conservative
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1 Similarity 98.0%;
48; Conservative
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
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Best Local Similarity
Matches 48; Conserv
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Best Local Similarity
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US-09-855-754B-15
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US-09-855-754B-4
                                               SEQ ID NO 14
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
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  Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                1 GAKAPPAPKPA----PQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.6%; Score 260; DB 6; L 92.3%; Pred. No. 1.2e-09; iive 0; Mismatches 0;
Score 260; DB 5;
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
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TELEPHONE: (703) 243-6333
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Sequence 4, Application US/10227353

Sequence 4. Application US/10227353

GENERAL INFORMATION:

APPLICANT: CLARE, JEFFREY J.
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95.6%;
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Best Local Similarity 92.38
Matches 48; Conservative
Query Match 95.6
Best Local Similarity 92.3
Matches 48; Conservative
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NUMBER OF
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    SEQ ID NO 6
LENGTH: 922
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTASSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AMMINGENICA COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BORDETELIA PRAPERTISSIS, AND BORDETELIA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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ION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
ION: BRONGHISEPICA, THEIR USE IN DIAGNOSTICS, AND IN
ION: IMMUNOGENIC COMPOSITIONS
03495-0206-00000
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Pred. No. 2.8e-10;
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Pred. No. 3.3e-10;
0; Mismatches 0
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                            PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09855754B GENERAL INFORMATION:
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
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PRIOR FILING DATE: 2000-05-25
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                                          2001-05-16
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Best Local Similarity 85.7%;
Matches 48; Conservative
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82.8%;
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Best Local Similarity 82.5.
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SEQ ID NO 19
LENGTH: 58
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                                            CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-855-754B-19
                                                                                                                                                                                                                                         US-09-855-754B-18
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US-09-855-754B-6
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Gaps
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                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                          ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
TRAST
                                                                                     Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 257; DB 6;
Pred. No. 1.8e-09;
0; Mismatches 0,
                                                                                     Score 257; DB 5;
Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09855754B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TYPE: PRT ORGANISM: Bordetella parapertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             Sequence 6, Appilcation US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 922 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERISTICS
                                                                                  94.58;
82.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                    Best Local Similarity 82.8
Matches 48; Conservative
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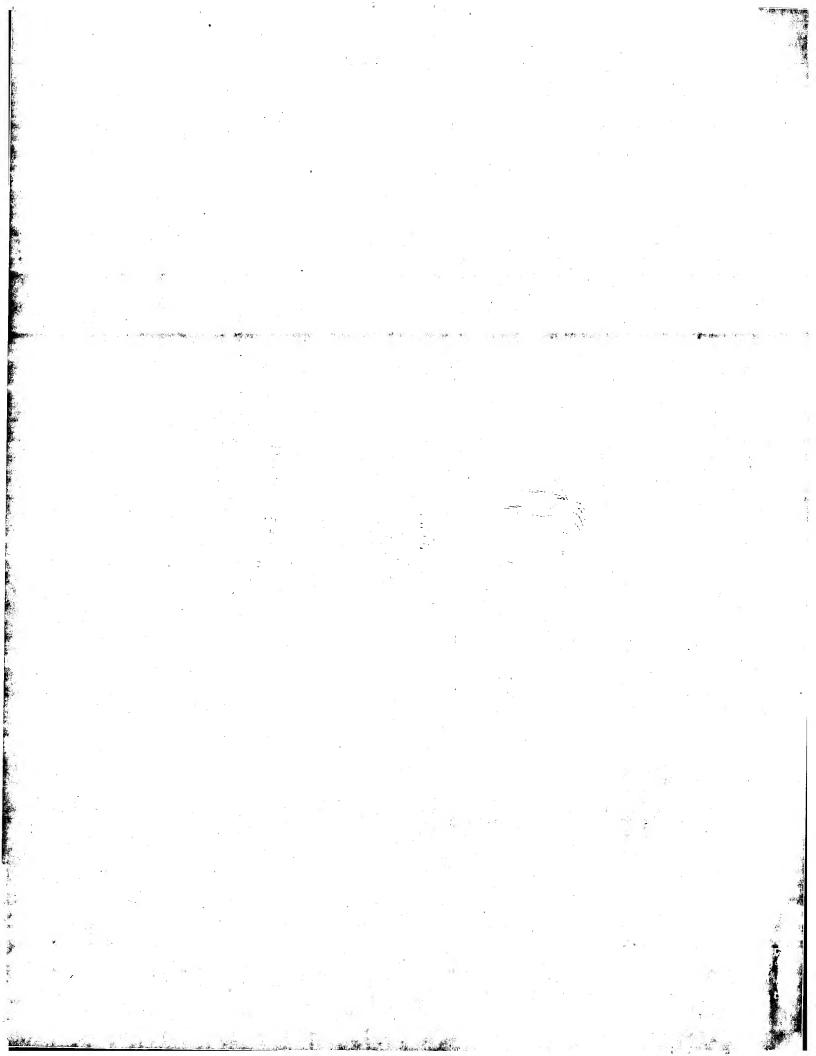
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US-09-855-754B-17
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US-09-855-754B-16
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US-09-855-754B-16
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LENGTH: 59
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POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA PRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN LIMMINOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GGISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: INMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: INMUNOCENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR TILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249; DB 5;
Pred. No. 9.9e-10;
0; Mismatches 2
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Pred. No. 1.2e-09;
0; Mismatches 2
                                         TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USI
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 0.4495-0.206-0.0000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILIKO DATE: 2001-05-16
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN Ver. 2.1
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ORGANISM: Bordetella bronchiseptica
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                          91.5%;
88.5%;
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SOFTWARE: Patentin Ver. 2.1
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Matches 46; Conserv
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Best Local Similarity
Matches 46; Conserv
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US-09-855-754B-17
                                                                                                                                                                                                                                                                               SEQ ID NO 21
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LENGTH: 54
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF DERFACTIN IN BORDEFELLA
TITLE OF INVENTION: BONDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0306-00000
CURRENT PILLING DATE: 2001-05-16
CURRENT FILING DATE: 2001-05-16
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Pred. No. 3.7e-09;
0; Mismatches 0;
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Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                0; Mismatches
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
                                                                                                                                                TYPE: PRT ORGANISM: Bordetella bronchiseptica
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PRIOR FILING DATE: 2000-05-25
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78.38;
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Best Local Similarity 88.7
Matches 47; Conservative
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SOFTWARE: PatentIn Ver.
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SOFTWARE: Patentin Ver.
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Best Local Similarity
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CURRENT APPLICATION WUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                      Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                              Query Match 82.0%; Score 223; DB 5; Length 42; Best Local Similarity 87.5%; Pred. No. 3.9e-08; Matches 42; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                               1 GAKAPPAPKPAPQPEQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23 APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Carr, Grant
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        Sequence 19, Appl 100-955 574-18

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        US-09-855-754-6
        Sequence 19, Appl 11

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        US-08-85-754-6
        Sequence 19, Appl 12

        11
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        US-08-85-754-16
        Sequence 10, Appl 13

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        US-08-85-754-17
        Sequence 17, Appl 14

        13
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        US-08-85-754-17
        Sequence 17, Appl 15

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        22.6
        US-08-85-774-17
        Sequence 17, Appl 15

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        Sequence 17, Appl 14

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        Sequence 17, Appl 14

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        T2.8
        US-09-711-577-75981
        Sequence 2, Appl 14

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        T2.8
        US-09-711-577-7698
        Sequence 11, Appl 14

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        US-09-711-577-7842
        Sequence 11, Appl 14

        23
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ALIGNMENTS

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Sequence 21, Application US/09855754

GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGEN: US/09/855,754

TITLE OF INVENTION: IMMUNGEN: US/09/855,754

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT APPLICATION NUMBER: 60/206,969

PRIOR APPLICATION NUMBER: 60/206,969

PRIOR PELLING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 21

LENGTH: S.2

LENGTH: S.2

CURRENT BATCH
ORGANISM: Bordetella bronchiseptica
US-09-855-754-21

QUETY MATCH
BEST LOCAL SIMILATITY 100.0%; Pred. NO. 3.2e-13;
MATCHES 52; CORSETVATIVE 0; MISSMATCHES 0; Indels 0; Gaps 0;
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GAKVPPAPKPAPQPGPPQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA

us-09-855-754b-21.rapm

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GENERAL INFORMATION:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BONDEFELLA PARABERTUSSIS, AND BONDEFELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 128,709/855,754
CURRENT FILLING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: LAWINGGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION UNBERS: US/09/855,754
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Length 54;
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Pred. No. 1.3e-10;
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Pred. No. 1.8e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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                                                                                                                     Sequence 22, Application US/09855754 GENERAL INFORMATION:
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92.5%;
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52; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 54
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Matches 49; Conserv
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US-09-791-537-37413
                                                                              RESULT 2
US-09-855-754-22
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POETONS OF PERTACTIN IN BORDETELLA PERTUSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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1.6e-09;
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Pred. No. 1.6e-09;
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 85698
                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 85688, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-791-537-85698
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92.5%;
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Best Local Similarity 92.5%;
Matches 49; Conservative
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Best Local Similárity 92.5°
Watches 49; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
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US-09-791-537-85698
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us-09-855-754b-21.rapm

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 125/99/855,754
CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND INTERED OF INVENTION: BRONCHISEPTICA, THERE USE IN DIAGNOSTICS, AND INTERED OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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                                                                                                                                                                                                                         Length 911;
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                                                                                                                                                                  Indels
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                                                                                                                      Score 259; DB 22;
Pred. No. 1.6e-09;
0; Mismatches 2;
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Pred. No. 1.9e-10;
0; Mismatches 2;
                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
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US-09-855-754-19
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1 Similarity 92.5%;
49; Conservative
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86.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 56
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENOTH: 58
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Best Local Similarity
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SEQ ID NO 4
LENGTH: 911
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Query Match

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APPLICANT: Debè, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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                                        Gaps
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                                      Indels
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Pred. No. 2.5e-09;
0; Mismatches 3;
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Pred. No. 2.5e-09;
0; Mismatches 3;
              Pred. No. 2.3e-10;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SED ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                     RESULT 9 (19-09-791-537-50285); Sequence 50286, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Paterilin Ver. 2.1
SEQ ID NO 6
LENGTH: 922
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US-09-791-537-50286
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US-09-855-754-20
Sequence 20, Application US/09855754
84.5%; Pre-
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ilarity 84.5%;
Conservative
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ilarity 84.5%;
Conservative
              Best Local Similarity 84.5
Matches 49; Conservative
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 49; Conserv
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LENGTH: 922
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NUMBER OF SEQ ID NOS: 24
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US-09-855-754-23
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LENGTH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIVI IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT PELING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VAIL. 201
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUS OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/99/855,754

PRIOR APPLICATION NUMBER: 60/206,969
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 1.9e-09;
1; Mismatches 3; Indels 7
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Pred. No. 5.8e-10;
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88.58;
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Similarity 81.4%;
48; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
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Best Local Similarity
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LENGTH: 59
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ORGANISM: 1
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APPLICANT: GUISO-MACIOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUGSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR PELLING DATE: 2000-05-25
PRIOR PELLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI NI BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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Pred. No. 3e-09;
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Pred. No. 4.7e-09;
1; Mismatches 1;
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bordetella bronchiseptica US-09-855-754-14
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 86.8%;
Matches 46; Conservative
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Best Local Similarity 88:9%;
Matches 48; Conservative
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SOFTWARE: Patentin Ver.
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US-60-427-194-80	US-09-724-676-92543	US-09-724-676A-92543	US-10-156-761-10081	US-10-224-999A-3465	US-10-282-122A-51472	US-10-417-886-7963	US-10-282-122A-51470	PCT-US02-36123-2812	PCT-US02-36123-2814	US-09-675-784A-12363	US-10-282-122A-48029	US-09-765-272A-160	US-10-366-683-24873	US-10-419-128-24873	US-10-282-122A-69888	US-10-282-122A-44931	US-09-724-676-51189	US-09-724-676A-51189	
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27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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APPLICANT: GUISO-MACLOUE, CANDAINE, TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED; TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS, TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS, TITLE OF INVENTION: IMMUNOSCENIC COMPOSITIONS IN DIAGNOSTICS, AND BOADDETELLA TITLE OF INVENTION: IMMUNOSCENIC COMPOSITIONS IN IMMUNOSCENIC COMPOSITIONS IN IMMUNOSCENIC COMPOSITIONS OF INVENTION: INMUNOSCENIC COMPOSITIONS OF INVENTION NUMBER: 05/206-00000 CORRENT FILING DATE: 2001-05-16 PRIOR PILING DATE: 2000-05-25 NUMBER OF SEQ TO NOS: 25 SOFTWARRE PATCHLIN Ver. 2.1

SED ID NO 21

LENGTH; 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 02,09/9855,754B
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1,arity 100.0%; Pred. No. 5.2e-13;
Conservative 0; Mismatches 0:
Sequence 21, Application US/09855754B GENERAL INFORMATION:
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-21
                                                               CAROLINE
                                                            APPLICANT: BOURSAUX-EUDE,
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Query Match
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TITLE OF INVENTION: POLYMPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYMPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMINGERIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 125/09/985,754B
CURRENT FILING DATE: 2001-05-16
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Pred. No. 1.7e-10;
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Pred. No. 2.7e-12;
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Bordetella bronchiseptica
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US-09-855-754B-22
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ilarity 92.5%;
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SOFTWARE: Patentin Ver.
NUMBER OF SEQ ID NOS: 25
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TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE R
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                 559 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
                                                                                                                                                                                                                                                                                                                      APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 911;
Length 911;
                                                                                                   1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE Milen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
Score 259; DB 5;
Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460, 269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 259; 92.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09855754B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                      Sequence 4, Application US/10227353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
  86.9%;
illarity 92.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCES:
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Matches 49; Conserv
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1 GAKVPPAPKPA----PQPGPQPPQPPQPPQP--QPQPPQPEAPAPQPPAGRELSAA
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                           Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branic
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                           Score 256; DB 5;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 256; DB 6;
Pred. No. 1.6e-09;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460, 269C
                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAWE: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                     TYPE: PRT ORGANISM: Borcetella parapertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10227353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CLARE, JEFFREY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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84.5%;
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84.5%;
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                                                                                                                                                         Best Local Similarity 84.58 Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 24
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.59
Matches 49; conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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US-10-227-353-6
                                                                                                                                           Query Match
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NIMBER: 105/09/855,754B
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYMPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND INTITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-05-16
                                                                                                                                                                                                                                                                                                                                          Gaps
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9
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                                                                                                                                                                                                                                                                                                Length 56;
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                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                         Score 257; DB 5;
Pred. No. 2.4e-10;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 256; DB 5;
Pred. No. 2.8e-10;
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FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 85.9%;
Local Similarity 84.5%;
les 49; Conservative
                                                                                                                                                                                                                                                                                         ch 86.2%;
1 Similarity 86.0%;
49; Conservative
                                                                                                             NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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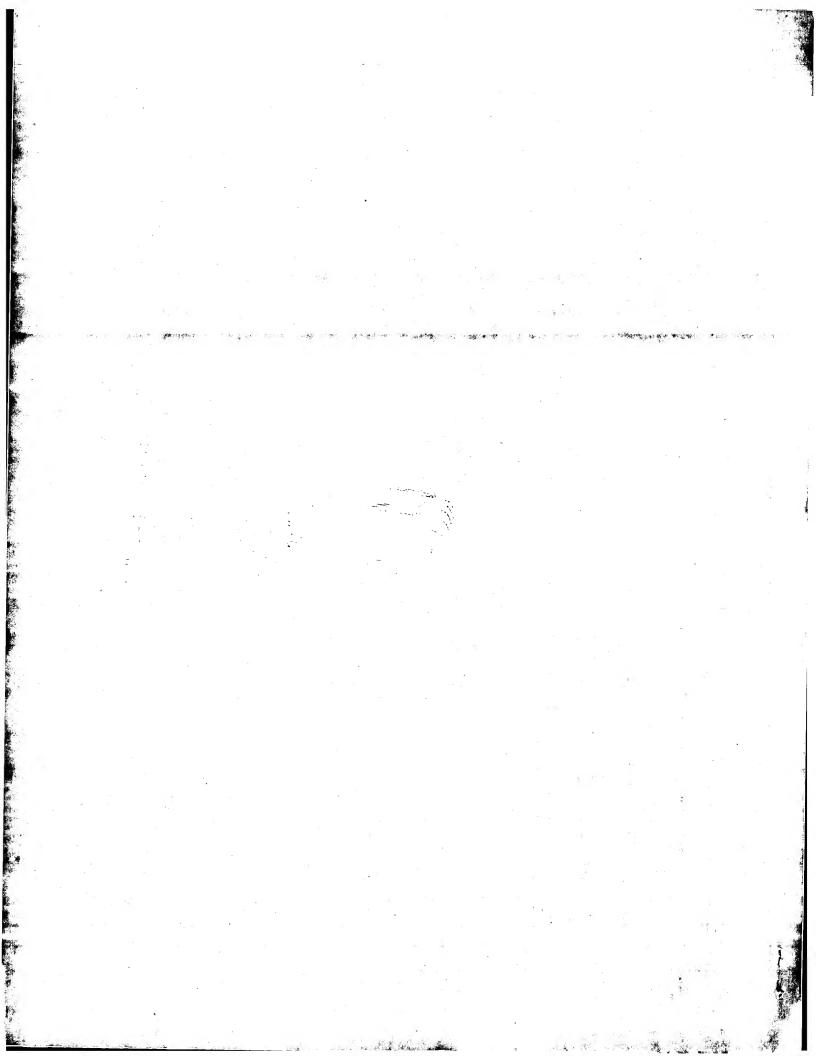
Gaps

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CURRENT FILING DATE:
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LENGTH: 52
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LENGTH: 42
                                                                                                                                                                                                TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHIEDEPLICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 00,000
CURRENT FILING DATE: 2001-05-16
PRIOR PRILICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUGSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/4855,754B
CURRENT FILING DATE: 2001-05-16
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BONDGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENE COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
81.4%; Score 242.5; DB 5; Length 59;
Best Local Similarity 81.4%; Pred. No. 2.1e-09;
Matches 48; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249; DB 5; Length 48;
Pred. No. 7e-10;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 2001-05-16
PRIOR PLLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09855754B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.6%;
88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.55
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-855-754B-16
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITILE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
GURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR PELLING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                 DB 5;
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86.8%; Pred. No. 3.4e-09;
Live 0; Mismatches 2
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                          ORGANISM: Bordetella bronchiseptica US-09-855-7548-14
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2001-05-16
                      PRIOR APPLICATION NUMBER: 60/. PRIOR FILING DATE: 2000-05-25
                                                                        NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                           Query Match 80.0 Best Local Similarity 86.8 Matches 46; Conservative
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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SOFTWARE: Patentin version 3.1
SEQ ID NO 51012
LENCTH: 768
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Pred. No. 4.5e-07;
0; Mismatches 1; Indels
                                                                              Score 217; DB 5; Length 42;
Pred. No. 7.4e-08;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  Application US/10282122A
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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NG DATE: 2000-10-23
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FILING DATE: 2000-11-27
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NG DATE: 2000-09-06
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NG DATE: 2001-02-09
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FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2001-02-16
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                                                                            Query Match 72.8%;
Best Local Similarity 78.8%;
Matches 41; Conservative
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Best Local Similarity 78.8%;
Matches 41; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
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Search completed: May 7, 2003, 17:27:51 Job time: 31.6508 secs



Sequence 37413, A Sequence 45698, A Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 75841, A Sequence 76981, A Sequence 76981, A Sequence 21274, A Sequence 21274, A Sequence 214, Appl Sequence 24, Appl Sequence 11629, Sequence 24, Appl Sequence 31, Appl Sequence 2285, Appl Sequence 22

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Database

Total number Minimum DB Maximum DB

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Run on:

Scoring table:

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APPLICANT: BORSAUX-EUDE, CAROLINE
APPLICANT: GGISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
FITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
FITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
FITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN
FILL REFERENCE: 03495-0266-0000
CURRENT FILLING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VAIL 2.1
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1 US-09-791-537-37413

1 US-09-791-537-85698

2 US-09-855-754-4

2 US-09-855-754-16

2 US-09-855-754-16

2 US-09-855-754-17

2 US-09-855-754-17

2 US-09-855-754-17

2 US-09-855-754-17

2 US-09-855-754-17

2 US-09-855-754-17

1 US-09-791-537-75691

1 US-09-791-537-1274

1 US-09-791-537-1274

1 US-09-791-537-12007

2 US-09-791-537-11629

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1 US-09-380-693A-51

1 US-09-380-693A-51

2 US-09-380-693A-51

2 US-09-380-693A-51

2 US-09-380-693A-51

2 US-09-380-693A-38

2 US-08-247-544-5

2 US-08-247-544-8

2 US-08-247-54
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llarity 100.0%; Pred. No. 8.3e-14;
Conservative 0; Mismatches 0;
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US-09-855-754-22
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    Similarity
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LENGTH: 54
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Best Local S
Matches 54
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Sequence 21, Appl
Sequence 19, Appl
Sequence 6, Appl
Sequence 6, Appli
Sequence 15, Appli
                                                                                                                                         7, 2003, 16:47:16 ; Search time 136.794 Seconds (Without alignments) 254.511 Million cell updates/sec
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                                                                                                                                                                                                                                                                          1 GAKVPPAPKPAPQPGPPQ......QPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-21
US-09-855-754-19
US-09-791-537-50286
US-09-855-754-6
US-09-855-754-15
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Listing first 45 summaries
                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Score

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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella parapertussis
US-09-855-754-6
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Local Similarity 84.5%;
hes 49; Conservative
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ilarity 84.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
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US-09-855-754-15
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03445-00000
CURRENT APPLICATION NUMBER: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                  APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA
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. No. 8.7e-11;
ismatches 5;
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Pred. No. 2.7e-12;
0; Mismatches 0;
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Pred. No. 8
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; Sequence 50286, Application US/09791537
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US-09-855-754-19
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
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                                                                                                                    Sequence 21, Application US/09855754 GENERAL INFORMATION:
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nilarity 96.3%;
Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 58
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APPLICANT: Dancer, Derek

APPLICANT: Dancer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

TITLE OF INVENTION: MTHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SEQ ID NO 50286

LENGTH: 922

TYPE:
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TITLE OF INVENTION: IMMUNOGBRIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 9.3e-10;
0; Mismatches 5;
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Pred. No. 9.3e-10;
0; Mismatches 5
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APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERPUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPELLOGIO OF STATEMENT OF STATEMENT OF STATEMENT APPLICATION NUMBER: US/09/455,754
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Pred. No. 2.7e-09;
0; Mismatches 2;
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Pred. No. 3.4e-10;
0; Mismatches 5;
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
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US-09-855-754-18
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US-09-855-754-16
; Sequence 16, Application US/09855754
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLLINE
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87.5%;
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Best Local Similarity 89.1%;
Matches 49; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY NEMBE.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 37413
LENGTH: 911
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APPLICANT: Debe, Derek
APPLICANT: Dareer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION MUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 153055
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Pred. No. 2.7e-09;
0; Mismatches 2;
                                                                                                                                                                                                                             Score 258; DB 22;
Pred. No. 2.3e-10;
0; Mismatches 2;
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Pred. No. 2.7e-09;
0; Mismatches 2;
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APPLICANT: Bionomix, Inc.
  60/206,969
                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica US-09-855-754-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica US-09-791-537-37413
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89.1%;
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1 Similarity 89.1%;
49; Conservative
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ilarity 89.1%;
Conservative
PRIOR APPLICATION NUMBER: 60/: PRIOR FILING DATE: 2000-05-25
                                           NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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Best Local
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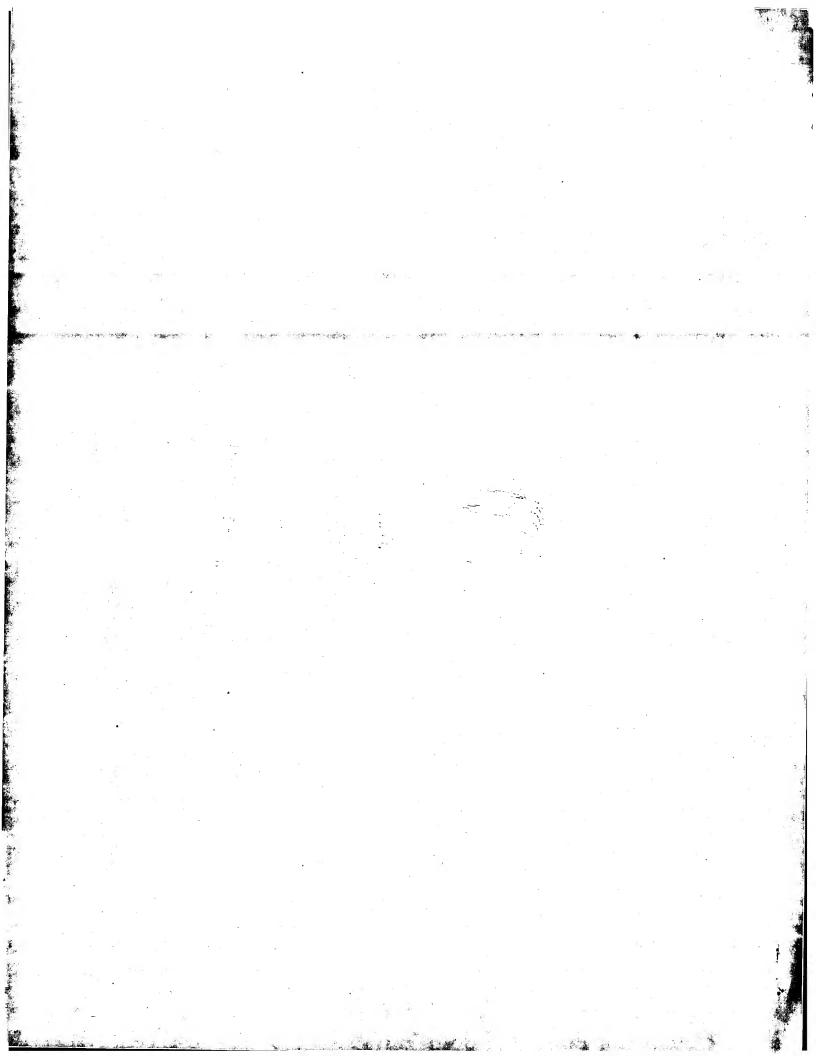
IMMUNOGENIC COMPOSITIONS

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NUMBER OF SEQ ID NOS: 24
TITLE OF INVENTION:
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US-09-855-754-23
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US-09-855-754-17
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Matches 4
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                                        APPLICANT: GUISO-MACLOUE, CANCELING
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 16
IENGTH: 59
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHELA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: ROUNGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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APPLICANT: BOURSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BORDETELIA PARABERTUSSIS, AND BORDETELIA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 9.5e-10;
1; Mismatches 3; Indels 7
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Pred. No. 1e-09;
0; Mismatches 2; Indels
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bordetella bronchiseptica US-09-855-754-16
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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                             : BOURSAUX-EUDE, CAROLINE
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81.7%;
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1 Similarity 85.2%;
46; Conservative (
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Best Local Similarity 81.73
Matches 49; Conservative
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Best Local Similarity
Matches 46; Conserv
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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FILE REFERENCE: 03495-0206-00000
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Pred. No. 7.9e-09;
1; Mismatches 1; Indels
         CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 49
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                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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85.7%;
[LE REFERENCE: 03495-0206-00
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Best Local Similarity 85.7
Matches 48; Conservative
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PRIOR FILING DATE: 2000-05
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Search completed: May 7, 2003, 17:22:08 Job time : 136.794 secs



Sequence 92543, A
Sequence 92543, A
Sequence 3465, Ap
Sequence 51472, A
Sequence 7963, Ap
Sequence 2181, Ap
Sequence 2812, Ap
Sequence 2812, Ap
Sequence 2813, Ap
Sequence 44931, Ap

7, Appl 1470, A 8, Appl 1873, A

Sequence Sequence Sequence Sequence Sequence Sequence

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Perfect score:

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Scoring table:

Searched:

Database

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APPLICANT: BOUNDAY SOUR.

APPLICANT: BOUNDAY SOUR ANALONE,

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,

TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA

TITLE OF INVENTION: BORNOHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS

FILE REFRENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/0855,754B

CURRENT PILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/206,969

REPROR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VET. 2.1
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GENERAL INFORMATION:
APPLICANT: BOURSALION:
APPLICANT: BOURSALEDE, CARCOLINE
APPLICANT: BOURSALEDE, CARCOLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND SIN BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND SIN BORDETEL
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US-60-427-194-80

US-09-724-676-92543

US-09-724-676-92543

US-10-224-999A-3465

US-10-282-122A-51472

US-10-156-761-10081

PCT-USO2-36123-2814

US-10-282-122A-44931

US-10-282-122A-44931

US-10-282-122A-51470

US-10-282-122A-51470

US-10-282-122A-51470

US-10-36-688-24873

US-10-156-761-14830

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US-10-156-761-14830

US-10-282-122A-48029

PCT-USO2-37431-155
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100.0%; Score 310; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 54; Conservative 0; Mismatches 0;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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US-09-855-7548-22
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7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
                                                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-6
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US-09-855-7548-14
US-09-855-7548-14
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APPLICANT: GUISO-MACIOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
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Pred. No. 4.2e-12;
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09855754B GENERAL INFORMATION:
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                                                                                                   ORGANISM: Bordetella bronchiseptica US-09-855-7548-21
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US-09-855-754B-6
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver.
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US-09-855-754B-19
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US-09-855-754B-6
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                                                                                          1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
                                               4.
                                                                                                                                                                                                                                              Sequence 6, Application US/10227353
GENERAL INFORMATION:
GENERAL INFORMATION:
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 922;
  Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%; Score 265; DB 6;
84.5%; Pred. No. 6.3e-10;
iive 0; Mismatches 5
Score 265; DB 5;
Pred. No. 6.3e-10;
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FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSOLY-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 243-6333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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85.5%;
nilarity 84.5%;
Conservative 0
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ADDRESSEE: Millen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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Best Local Similarity
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                          Best Local Similarity
Matches 49; Conser
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TELEFAX:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITILE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REPERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/655,754B
PRIOR PELLING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFFWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPQPGPAPAPQPPAGRELSAA 54
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
                                                                                                                                                                                                                                                                             Length 52;
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2.9e-10;
2;
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llarity 89.1%; Pred. No. 1.7e-09;
Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                      Match 83.2%; Score 258; DE Local Similarity 89.1%; Pred. No. 2.9e es 49; Conservative 0; Mismatches
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
                                     CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROMANOS, MICHAEL A. TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bordetella bronchiseptica US-09-855-7548-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09855754B GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOURSAUX-EUDE, CAROLINE
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
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nes 49; Conserv
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LENGTH: 911
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US-10-227-353-4
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Matches
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Gaps
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND STILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0306-00000
CURRENT FALLING DATE: 2006-00000
CURRENT FALLING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60,206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA 54
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 1.7e-09;
0; Mismatches 2
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Pred. No. 4.1e-10;
0; Mismatches 5
                                                                   APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGBVT INFORMATION:
REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOGOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4::05-10-227-353-4
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Sequence, 18, Application US/09855754B
SERRAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 16, Apilication US/09855754B
; GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
; APPLICANT: GUISO-MACHOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Bordetella bronchiseptica
US-09-855-754B-18
                                                                                                                                                                                                                                                                                                                    (703) 243-6333
                                                                                                                                                                                                                                                                                                                                          243-6410
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89.1%;
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Best Local Similarity 87.5%;
Matches 49; Conservative (
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INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 89.19
Matches 49; Conservative
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SOFTWARE: Patentin Ver.
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2001-05-16

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CURRENT FILING DATE:
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FITLE OF INVENTION: IMMUNICANIC COMPOSITIONS
FILL REPERENCE: 03495-0206-00000
CURRENT APPLICATION UNMBER: US/09/855,754B
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TITLE OF INVENTION: POLYEPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGSITCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGSIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
     POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKVPPAPKPAPQPGPQP-----PQP-PQPPQPPQPQPQPQPQPQPPAPGPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS RILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-16-16
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 59;
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Pred. No. 1.1e-09;
1; Mismatches 3;
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Pred. No. 1.2e-09;
0; Mismatches 2;
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-16
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Best Local Similarity 85.2%;
Matches 46; Conservative
                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.5
Best Local Similarity 81.7
Matches 49; Conservative
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US-09-855-754B-20
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                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 16
TRNGTH: 59
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APPLICANT: BOURSAUX EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REPERENCE: 03409-0206-00000
CURRENT APPLICATION NUMBER: US/09/455,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILLING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GGISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERFECTINI IN BORDETELLA PERFUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT PILING DATE: 2001-05-16
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85.7%; Pred. No. 8.5e-09;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                 Query Match 76.6%; Score 237.5; DB 5; Best Local Similarity 83.6%; Pred. No. 5.7e-09; Matches 46; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09855754B GENERAL INFORMATION:
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-14
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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SOFTWARE: PatentIn Ver. 2.1
                                                    NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 49
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Best Local Similarity 85.7
Matches 48; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 23
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US-09-855-754B-17
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Pred. No. 7.3e-07;
0; Mismatches 1; Indels 12;
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                                                                           Length 42;
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                                                                           Score 216; DB 5;
Pred. No. 1.2e-07;
0; Mismatches 1
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                               Sequence 51012, Application US/10282122A
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/206,848
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PLICATION NUMBER: 60/207,727
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NG DATE: 2000-09-06
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
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                                                                         Query Match 69.7%;
Best Local Similarity 75.9%;
Matches 41; Conservative
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Best Local Similarity 75.9%;
Matches 41; Conservative
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Forsyth, R.
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Zamudio, Carlos
Malone, Cheryl
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Wall, Daniel
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Carr, Grant
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US-10-282-122A-51012
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2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-17
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Sequence 11684, A	Sequence 48029, A	Sequence 3465, Ap	Sequence 28564, A		Sequence 51472, A	Sequence 24873, A	Sequence 24873, A	Sequence 12544, A	Sequence 9652, Ap				Sequence 92543, A		Sequence 28, Appl	Sequence 2, Appli	614	_
US-60-453-050-11684	US-10-282-122A-48029	US-10-224-999A-3465	US-10-366-683-28564	US-10-419-128-28564	US-10-282-122A-51472	US-10-366-683-24873	US-10-419-128-24873	US-10-156-761-12544	US-09-949-016-9652	US-09-949-016-6756	US-60-423-586-80	US-60-427-194-80	US-09-724-676-92543	US-09-724-676A-92543	US-09-640-419C-28	US-10-257-157-2	US-09-724-676-61497	US-09-724-676A-61497
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27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                   APPLICANT: BOURSAIX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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1jarity 100.0%; Pred. No. 1.7e-14;
Conservative 0; Mismatches 0;
; Sequence 16, Application US/09855754B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09855754B GENERAL INFORMATION:
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                                       CAROLINE
                                                                                                                                                                                                                                                           NUMBER OF SEQ 1D NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 16
LENGTH: 59
TYPE: PRT
                                   APPLICANT: BOURSAUX-EUDE,
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Best Local Similarity
Matches 59; Conserv
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PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25

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APPLICATION NUMBER: US/08/460, 269C
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                 FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                 LENGTH: 922 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     87.3%;
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ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 57; Conserv
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Matches 55; Conserv
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LENGTH: 56
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TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOSELIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CORREMY PAPLICATION NUMBER: US/09/855,754B
CURRENT FILLING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
FRIOR PLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQP-PQP-PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
                                                                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 922;
                                                                                                                                                                              Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       Indels
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                                                                                                                                                                              DB 5;
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                                                                                                                                                                                                     .1e-12;
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                                                                                                                                                                                                                       Mismatches
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Pred. No. 3.7
                                                                                                                                                                            Score 298.5;
Pred. No. 7.1
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                            ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-19
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella parapertussis
US-09-855-7548-6
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ilarity 95.0%;
Conservative
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ilarity 95.0%;
Conservative
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CORRESPONDENCE ADDRESS:
                           Patentin Ver. 2.1
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      NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
                                                                                                                                                                                                  Best Local Similarity
Matches 57; Conserv
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LENGTH: 922
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US-10-227-353-6
                                               SEQ ID NO 19
LENGTH: 58
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                                                                                          TYPE: PRT
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Matches

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APPLICANT: GUISO-MACIOE, NICOLE TITLE OF INVENTION: POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PREPACTION IN BORDETELLA PERFUSSIS, TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMBROGENIC COMPOSITIONS CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUSSIS,
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQR-PEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                       Length 922;
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                                                                                                                                                                                                                                                                                                                                                                       Score 298.5; DB 6;
Pred. No. 3.7e-11;
0; Mismatches 0;
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Pred. No. 1.2e
0; Mismatches
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*** TOPOLOGY: linear

"POECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Bordetella bronchiseptica
US-09-855-754B-18
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 6:
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US-10-227-353-4
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR PAPLICATION NUMBER: 05/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 15
LENGTH: 52
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APPLICANT: GUISO-MACLOUP, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHIELP PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIERPICA, THEIR USE IN DIAGNOSTICS, AND INTILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF PREFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
                                                                                                                                                                                                                                                                                                                                                                         Length 52;
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4.9e-10;
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Pred. No. 4.6e-11;
0; Mismatches 0;
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Pred. No. 4.9e-
0; Mismatches
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,7
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
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Sequence 15, Application US/09855754B
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica US-09-855-754B-17
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                                                                                                                                                                                                                                                                                    83.2%;
milarity 88.1%;
Conservative 0
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ilarity 85.0%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
Matches 51; Conserv
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Matches
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                  Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STRESTE: 2200 Clarendon Blvd., Suite 1400
CIT?: ARLINGTON
                                                                                                                            Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.2%; Score 267.5; DB 6;
85.0%; Pred. No. 2.7e-09;
11ve 0; Mismatches 0;
                                                                                  DB 5;
                                                                               Score 267.5; DB 5
Pred. No. 2.7e-09;
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                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
PPPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10227353
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 911 amino acids
                                                                               78.2%;
85.0%;
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Best Local Similarity 85.09
Matches 51; Conservative
                                                                               Query Match
Best Local Similarity 85.08
Matches 51; Conservative
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CURRENT FILING DATE:
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US-09-855-754B-20
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LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 20
                                                                                                                                  SEQ ID NO 21
LENGIH: 52
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA
TITLE OF INVENTION: BRONCHIELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHIEDEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/85,754B
CURRENT FILING DATE: 2001-0516
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC, COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
  POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 72.2%; Score 247; DB 5; Length 49;
Best Local Similarity 80.0%; Pred. No. 8.2e-09;
Matches 48; Conservative 0; Mismatches 0; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BORDETELLA PARAPERTUSSIS, AND BORDETELLA
BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
                            REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249.5; DB 5;
Pred. No. 6.1e-09;
1; Mismatches 3;
                                                                                                              IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYPEPTIDES CONTAINING POLYPER OF INVENTION: BORDETELLA PARAPERTUSSIS; TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS; CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: 60/206,969

PRIOR PILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 73.0%;
Best Local Similarity 81.7%;
Matches 49; Conservative
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; ORGANISM: Bord
US-09-855-754B-14
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APPLICANT: GUISO-MACLOUF, NICCLEAR APPLICANTED OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT PILLING DATE: 2001-05-16
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FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: 05/09/855,754B

PRIOR APPLICATION NUMBER: 60/206,969

PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                                                                                                                                                                                                                                 Score 242.5; DB 5;
Pred. No. 1.6e-08;
1; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-20
                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Bordetella bronchiseptica
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2001-05-16
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.4%;
Matches 48; Conservative
                PRIOR APPLICATION NUMBER: 60/2
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                                                        PRIOR FILING DATE: 2000-05-:
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.8e-05;
1; Mismatches 0; Indels 17; Gaps
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                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQPPQRPEAPAPQPPAGRELSAA 59
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                           Score 203.5; DB 5; Length 42;
Pred. No. 3.2e-06;
1; Mismatches 0; Indels 17;
                                                                                                                                                                                                                                                                                                  Sequence 51012, Application US/10282122A GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/230,347
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                             59.5%;
69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // Ramamoto, Robert
forsyth, R.
                                                                           Query Match
Best Local Similarity 69.58
Matches 41; Conservative
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Zamudio, Carlos
Malone, Cheryl
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Best Local Similarity 69.5
Matches 41; Conservative
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arr, Grant
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1 GAKAPPAPKPAPQPGPGPGP......PQRPEAPAPQPPAGRELSAA 59
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              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                           4569144 seqs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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			Description		Sequence 16, Appl	Segmence 19, Appl	Talle (CT)	Sequence 50286, A	Sequence 6 Appli	Sequence 18. Appl	radiu (or pompro)	Sequence 17, Appl	
SOMMAKIES			ID		US-09-855-754-16	US-09-855-754-19		US-09-791-537-50286	US-09-855-754-6	US-09-855-754-18		US-09-855-754-17	
			DB	1	22	22			22			22	
			Match Length DB	-	59	28		922	922	26	1	52	
	æ	Query			100.0	87.3		87.3	87.3	86.1		83.2	
			rn.		342	298.5	1	298.5	298.5	294.5		284.5	
		Result	No.		-	7	•	~	4	S	'	9	

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7 267-5 19.2 19.2 2 22 105-09-855-754-15 Sequence 15, Appl 19.2 267-5 19.2 19.2 19.2 19.2 19.2 19.2 19.2 19.2	ICATION NUMBER: 60/206,969 NG DATE: 2000-05-25 SEQ 1D NOS: 24 eatentIn Ver. 2.1 Bordetella bronchiseptica 100.0%; Score 342; DB 22; Length 59; 54milarity 100.0%; Pred. No. 6.4e-15;
7 267.5 78.2 9 8 267.5 18.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 78.2 9 9 267.5 70.3 9 9 267.5 70.3 9 9 20.3 5 59.5 9 9 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-05 NUMBER OF SEQ ID NOS: 24 SEQ ID NO 16 LENGTH: 59 TYPE: PRT ORCANISM: Bordetella bron US-09-855-754-16 QUETY MATCh Best Local Similarity 100

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERRACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGKELSAA 59

    САКАРРАРКРАРОРСРОРСРОРСРОРОРОРОРРОРРОРОРО РЕАРАРОРРАСКЕ СВАА 59

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APPLICANT: GUISO-MACLOUE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CÜRRENT APPLICATION NUMBER: US/09/855,754
  REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, BORDETELLA PARAPERTUSSIS, AND BORDETELLA BORDCHIELA THEIR USE IN DIAGNOSTICS, AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 298.5; DB 22;
Pred. No: 3.8e-11;
0; Mismatches 0;
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR U.
TITLE OF INVENTION: BRONCHISEPTICA, THEIR U.
TITLE OF INVENTION: IMMUNGENIC COMPOSITION: FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754-18
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bordetella parapertussis US-09-855-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09855754 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/09855754 GENERAL INFORMATION:
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91.7%;
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95.0%;
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SOFTWARE: PatentIn Ver.
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Best Local Similarity
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SEQ ID NO 6
LENGTH: 922
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US-09-855-754-17
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA PARAPERTUSSIS, AND BONDETICLA, PARAPERTUSSIS, AND BONDETICS, AND IN TITLE OF INVENTION: IMMUNICABLIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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Pred. No. 3.8e-11;
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Pred. No. 3.7e-
0; Mismatches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 50286
LENGTH: 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-791-537-50286; Sequence 50286, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica
                                                                                                                                     Sequence 19, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
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95.0%;
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95.0%;
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PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 95.09
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SEQ ID NO 19
LENGTH: 58
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Best Local Similarity
                                                                                                                     US-09-855-754-19
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US-09-855-754-19
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APPLICANT: Biochomix, Inc.
APPLICANT: Biochomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Darder, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 133055
SSO THARE: Patentin version 3.0
LENGTH: 911
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 04495-0206-00000
CURRENT FILING PATE: 2001-09-10
                                                                                                   9; Gaps
                                                                         1 GAKAPPAPKPAPQPGPQPGPQPGPQPGPQPPQPPQPPQR-PEAPAPQPPAGRELSAA 59
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Pred. No. 3.6e-09;
0; Mismatches 0; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 267.5; DB 22; Length 911;
Pred. No. 3.6e-09;
0; Mismatches 0; Indels 9;
                                     Indels
         85.0%; Pred. No. 3.6e tive 0; Mismatches
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PRIOR FILING DATE: 2000-05-25
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US-09-791-537-85698
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Sequence 4, Application US/09855754
GENERAL INFORMATION:
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llarity 85.0%;
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ilarity 85.0%;
Conservative
                                 51; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 4
LENGTH: 911
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Best Local Similarity
Matches 51; Conserv
         Best Local Similarity
Matches 51; Conserv
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Best Local Similarity
Matches 51; Conserv
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US-09-791-537-85698
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US-09-855-754-4
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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SEQUENCE 15, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                 Length 52;
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Pred. No. 2.6e-11;
0; Mismatches 0; Indels
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Pred. No. 3.1e-10;
0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 52
                                                                                                                                                            ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
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1 Similarity 85.0%;
51; Conservative
                                                                                                                                                                                                                            ch 83.2%;
1 Similarity 88.1%;
52; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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LENGTH: 911
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                                                                                                                                           TYPE: PRT
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                                              APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 0200-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-00500
CURRENT APPLICATION NUMBER: 103/09/9855,754
CURRENT FILING DATE: 2001-09-10
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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Pred. No. 4.5e-09;
1; Mismatches 3
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PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
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81.7%;
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SEQ ID NO 22
LENGTH: 54
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
Matches 48; Conserv
GENERAL INFORMATION:
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US-09-855-754-22
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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FILE REFERENCE: 014495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR TELLIA TELLIA DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 0201-09-10
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                                                                                                                                                                                                                                                                                                                                                                                                     70.9%; Score 242.5; DB 2
81.4%; Pred. No. 1.2e-08;
tive 1; Mismatches 3
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CORRENT FILING DATE: 2001-0-10
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                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754-20
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-BUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUISO-MACLOUF, NICOLE
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 52
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Matches 47; Conservative
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Matches 48; Conserv
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US-09-855-754-23
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LENGIH: 48
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND STILLE OF INVENTION: BROWNINGERIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT FILLING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
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/cgn2_6/ptodata/2/paa,US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa,US09_LEW_COMB.pep:*
/cgn2_6/ptodata/2/paa,US10_NEW_COMB.pep:*
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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S-10-282-122A-51012
S-09-855-754B-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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297
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Match Length DB
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Perfect score:
Sequence:
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266.
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51470, A	9652, Ap	6/56, Ap	O. Appl	92543, A	2543, A	8564, A	8564, A	48029, A	812, Ap	6157, A	814, Ap			248/3, A		84274, A							REPEATED			NI														Gaps (
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APPLICANT: GUISO-MALLOUF, NICCLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYEPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: INMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PRIOR PAPE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.1
                                      TITLE OF INVENTION: POLYPEPTINES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: POLYPEPTINES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE REPERRACE: 03495-0206-00000
CURRENT FILING DATE: 2001-05-16
PRIOR PRILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEO ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 1.4e-11;
0; Mismatches 0
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Pred. No. 1.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-855-754B-6
; Sequence 6, Application US/09855754B
; GENERAL INFORMATION:
; APPLICANT: BOURSAUX-EUDE, CAROLINE
; APPLICANT: POUTE OF THE OF TH
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Best Local Similarity 89.7%;
Matches 52; Conservative
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92.9%;
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LENGTH: 58
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LENGTH: 56
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Milen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGFON
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 297; DB 6; 100.0%; Pred. No. 1.2e-11;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Score 297; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lebovitz, Richard M. REGISTRATION WUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
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                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 4
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Best Local Similarity
Matches 52; Conserve
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US-10-227-353-4
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Length 56;

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Length 58;

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RESULT 9
US-09-855-754B-16
; Sequence 16, Application US/09855754B
; GENERAL INFORMATION:
                                                            Sequence 17, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.2%;
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85.0%;
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Best Local Similarity 85.0%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.2
Matches | 51; Conservative
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SOFTWARE: PatchtIn Ver. 2.1
SEQ ID NO 16
                                                                                                                    GUISO-MACLOUF,
                                                                                                APPLICANT: BOURSAUX-EUDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-855-754B-17
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US-09-855-754B-14
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                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQPPQPPQRDELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                              Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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APPLICATION NUMBER: US/10/227,353 FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 284; DB 6;
Pred. No. 7.9e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                          Score 284; DB 5;
Pred. No. 7.9e-11;
0; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: LEBOVILE, RICHARD M.
REGISTRATION NUMBER: 37,067
; FILE REFERENCE: 03495-0206-00000
; CURRENT APPLICATION NUMBER: US/09/855,754B
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PALENTIN VEr. 2.1
; SOFTWARE: PALENTIN VER. 2.1
; SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 243-6333
                                                                                                                                                                            ; ORGANISM: Bordetella parapertussis US-09-855-7548-6
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-227-353-6; Sequence 6, Application US/10227353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 922 amino acids
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1larity 89.7%;
Conservative
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Best Local Similarity 89.7%;
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKAPPAPKPAPQPGPQPG-
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nes 52; Conserv
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Matches
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS, TITLE OF INVENTION: BORDETELLA PRAPERTUGSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: RANDOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 8.6e-11;
0; Mismatches 0
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Pred. No. 1.5e-10;
0; Mismatches 0
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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SEQ ID NO 23
LENGTH: 42
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,

TITLE OF INVENTION: BORDETELLA THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS

FILE REPERENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754B

PRIOR APPLICATION NUMBER: 00/206,969

PRIOR FILING DATE: 2001-05-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NOS: 25

LENGRARE: PATENTING PATE: 2001-05-25

SEQ ID NOS: 25

LENGRANE: PATENTING PATE: 2001-05-25

LENGRANE: PATENTING PATE: 2001-05-25

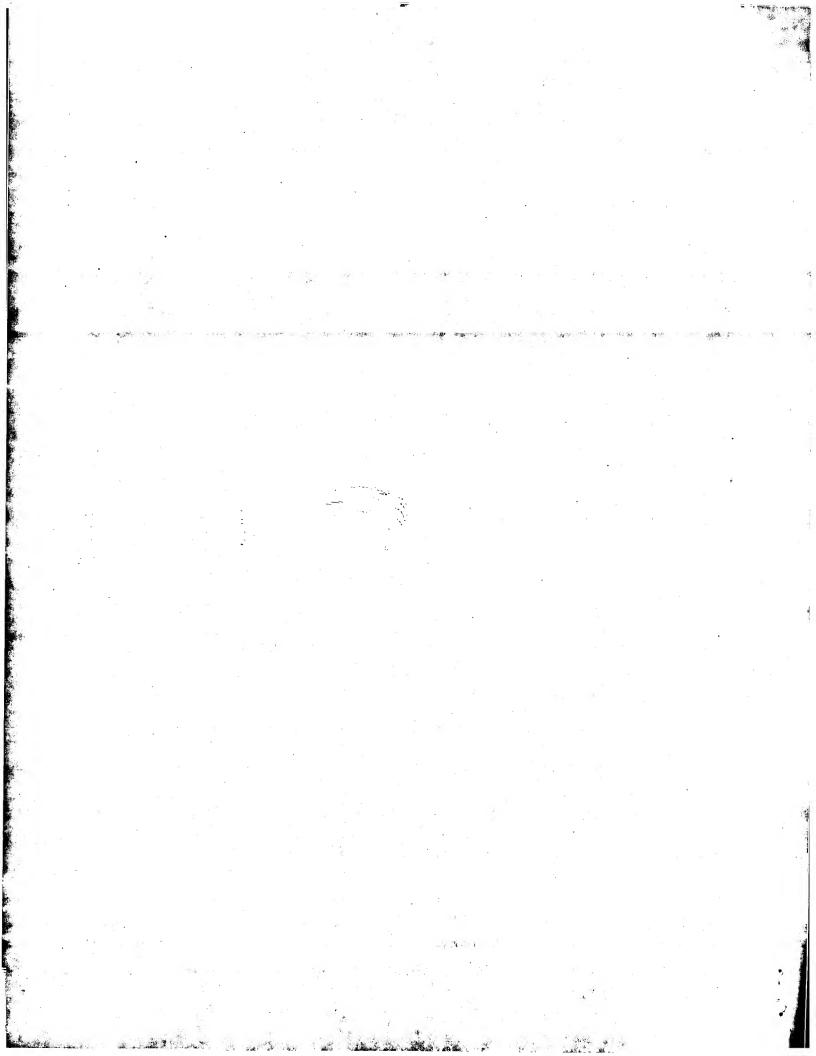
LENGRANE: PATENTING PATE: 2001-05-25

LENGRANE: PATENTING PATE: 2001-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNICABLIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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US-09-855-754B-21
: Sequence 21. Application US/09855754B
: Sequence 21. Application US/09855754B
: Sequence 21. Application:
: APPLICANT: BOURSAUX-EUDE, CAROLINE
: APPLICANT: BURSAUX-EUDE, NICOLE
: TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
: TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
: TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
: TITLE OF INVENTION: IMMUGGENIC COMPOSITIONS
: FILE REFERENCE: 03495-0206-00000
: CURRENT APPLICATION NUMBER: US/09/855,754B
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Pred. No. 4e-10;
0; Mismatches 0; Indels
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Pred. No. 1.6e-10;
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US-09-855-754B-20
Sequence 20, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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94.2%;
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92.3%;
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 92.35
Matches 48; Conservative
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Matches 49; Conserv
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PRITIE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGRNIC COMPOSITIONS
TITLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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Best Local Similarity 89.1%; Pred. No. 5.7e-10;
Matches 49; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                 Score 259; DB 5;
Pred. No. 4.9e-10;
0; Mismatches 2
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CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOURSAUX-EUDE, CAROLINE
2001-05-16
                                                                                                                                                                                                                                                                                                    87.2%;
92.5%;
CURRENT FILING DATE: 2001-05 PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 2000-05-25
                                                                               NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 52
                                                                                                                                                                                                                                                                                              Query Match 87.29
Best Local Similarity 92.59
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOURSAUX-EUDE,
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SOFTWARE: Patentin Ver.
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; ORGANISM: Bord
US-09-855-754B-22
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Search completed: May 7, 2003, 17:27:47
Job time : 31.6508 secs
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                                                                                                                         Gaps
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SOFTWARE: Patentin version 3.1
SEQ ID NO 51012
LENGTH: 768
                                                                           Query Match 71.4%; Score 212; DB 5; Length 42; Best Local Similarity 78.8%; Pred. No. 3.7e-07; Matches 41; Conservative 0; Mismatches 1; Indels 10;
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78.8%; Pred. No. 2.2e-06;
Live 0; Mismatches 1; Indels
                                                                                                                                                           1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                   Application US/10282122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 2000-10-23
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Bordetella pertussis
US-10-282-122A-51012
                                                                                                                                                                                                                                                                                                                                         : Wang, Liangsu
: Zamudio, Carlos
: Malone, Cheryl
: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 78.8
Matches 41; Conservative
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Sequence Sequence Sequence Sequence

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Scoring table:

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Minimum DB seq Maximum DB seq

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUGRANY-EUDE, CAROLINE
APPLICANT: BOUGRANY-EUDE, NICOLE
TITLE OF INVENTION: POLYREPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/085, 754
CURRENT APPLICATION NUMBER: 06/206, 969
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIL VET: 2.1
SEQ ID NO 15
LENGTH: 52
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1 US-09-791-537-50286
2 US-09-855-754-6
2 US-09-855-754-10
2 US-09-855-754-11
2 US-09-855-754-11
2 US-09-855-754-12
2 US-09-855-754-13
2 US-09-855-754-22
2 US-09-855-754-22
2 US-09-855-754-22
2 US-09-855-754-22
2 US-09-855-754-22
2 US-09-91-537-75841
1 US-09-791-537-75841
1 US-09-791-537-78841
1 US-09-791-537-71207
2 US-09-791-537-71207
2 US-09-791-537-711629
2 US-09-791-537-711629
2 US-09-791-537-711629
2 US-09-791-537-711629
2 US-09-791-537-711629
2 US-09-791-537-784-3
2 US-09-855-754-5
2 US-09-855-754-6
2 US-09-855-754-6
2 US-09-247-544-8
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US-09-417-507-22218

US-09-417-507-22218

US-60-412-418-2285

US-60-412-418-2285

US-60-312-40235

US-60-324-631-40235

PCT-US01-08631-40236

PCT-US01-08631-40236

PCT-US01-08631-40236

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100.0%; Score 297; DB 22;
Best Local Similarity 100.0%; Pred. No. 5.3e-13;
Matches 52; Conservative 0; Mismatches 0;
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US-09-855-754-15
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                                                                       Sequence 15, Appl
Sequence 37413, A
Sequence 85698, A
Sequence 4, Appli
Sequence 18, Appli
Sequence 19, Appl
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254.511 Million cell updates/sec
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                                                                                                                                                           7, 2003, 16:47:16; Search time 131.727 Seconds
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(cgn2_6/ptodata/1/paa/US06_COMB.pep:*
(cgn2_6/ptodata/1/paa/US08_COMB.pep:*
(cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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20_CGn2_6/ptodata/1/paa/US093_COMB.pep:*
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20_CGn2_6/ptodata/1/paa/US093_COMB.pep:*
20_CGn2_6/ptodata/1/paa/US092_COMB.pep:*
                       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-791-537-37413
US-09-791-537-85698
US-09-855-754-4
US-09-855-754-19
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                                                                                                                                                                                                                                                                                                                                                                                                               4569144 seqs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Score

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297 297 297 297 285 285

Sequence 23, Appl Sequence 75841 A Sequence 76981, A Sequence 76981, A Sequence 21244, A Sequence 21444, A Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 5, Appl Sequence 6, Appl Sequence 2218, A Sequence 2218, A Sequence 2285, Ap Sequence 2285, Ap Sequence 2285, Ap Sequence 2285, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 2285, Ap Sequence 22817, Appl Sequence 22815, Appl Se

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FILE REFERENCE: 03492-0206-00000
CURRENT PELLING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 3.6e-12;
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                  CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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FILE REFERENCE: 03495-0206-00000
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Best Local Similarity 92.9%;
Matches 52; Conservative
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PRIOR APPLICATION NUMBER: 60/3
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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US-09-855-754-18
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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Deseph
TITLE OF INVENTION: HEREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                    APPLICANT: Danzer, JOSEPh
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERRNCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 37413
LENGTH: 911
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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100.0%; Pred. No. 6.5e-12;
tive 0; Mismatches 0;
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                                                                                                                                                     Sequence 37413, Application US/09791537 GENERAL INFORMATION: APPLICANT: Blonomix, Inc.
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US-09-791-537-85698
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Best Local Similarity
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US-09-791-537-85698
                                                                                                           RESULT 2
US-09-791-537-37413
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LENGTH: 911
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APPLICANT: GUISO-MALLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BROWHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT PRILING DATE: 2001-09-10
                                                                                                                                                                                                     APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PREGIONS OF PERPACTIN IN BORDETELIA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
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                              564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
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Pred. No. 5.5e-11;
0; Mismatches 0;
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Pred. No. 2.9e-11;
0; Mismatches 0
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CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ 1D NOS: 24
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-08-75
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                                                                                                                                    Sequence 17, Application US/09855754 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: BOUISAUX: EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
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96.2%;
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ljarity 85.0%;
Conservative (
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 51; Conserv
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Best Local Simijarity
Matches 51; Conserv
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US-09-855-754-16
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LENGTH: 59
TYPE: PRT
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LENGTH: 52
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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VEFSION 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGLISSPITICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
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                                                                                                                                      Length 58;
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Pred. No. 4.9e-11;
0; Mismatches 0;
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Pred. No. 4.9e-11;
0; Mismatches 0;
                                                                                                                                 Score 284; DB 22;
Pred. No. 4.3e-12;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                US-09-791-537-50286; Sequence 50286, Application US/09791537; GENERAL INFORMATION:
                                                              ) ORGANISM: Bordetella bronchiseptica US-09-855-754-19
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; ORGANISM: Bordetella parapertussis
US-09-791-537-50286
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ORGANISM: Bordetella parapertussis
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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89.78;
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Best Local Similarity 89.7%;
Matches 52; Conservative
                                                                                                                               95.6%;
ilarity 89.7%;
Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 922
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LENGTH: 922
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SEQ ID NO 19
LENGTH: 58
                                              TYPE: PRT
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TITLE OF INVENTION:
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US-09-855-754-23
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LENGIH: 54
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LENGTH: 52
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                                                              APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
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                                                                                                                  TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
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APPLICANT: GUISO-MACLOUP. NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITIE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-12
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Pred. No. 1.5e-10;
0; Mismatches 0; Indels
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Pred. No. 5.5e
0; Mismatches
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US-09-855-754-14
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94.2%;
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SOFTWARE: PatentIn Ver. 2.1
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                               BOURSAUX-EUDE,
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Matches 48; Conserv
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Best Local Similarity
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US-09-855-754-20
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOCEMIC COMPOSITIONS
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llarity 92.5%; Pred. No. 1.8e-10;
Conservative 0; Mismatches 2; Indels
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IMMUNOGENIC COMPOSITIONS
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CURRENT APPLICATION NUMBER: 0S/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                        FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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                                                                                                             PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1.
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US-09-855-754-21
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
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US-09-855-754-22
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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Sequence 15, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSANCEUDE, CAROLINE
APPLICANT: BOURSANCEUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS,
TITLE OF INVENTION: BRONCHISEPPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICANTON NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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(g012_6/ptodata/2/paa/USO7_NEW_COMB.pep:*)
(g012_6/ptodata/2/paa/USO8_NEW_COMB.pep:*)
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(g012_6/ptodata/2/paa/USIO_NEW_COMB.pep:*)
(g012_6/ptodata/2/paa/USIO_NEW_COMB.pep:*)
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-4

US-09-855-7548-18

US-09-855-7548-19

US-09-855-7548-19

US-09-855-7548-19

US-09-855-7548-20

US-09-855-7548-20

US-09-855-7548-21

US-09-855-7548
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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GENERAL INFORMATION:
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TAPLICAWT: BOUNGRANK EUDE, CAROLINE
APPLICAWT: BOUNGRANK EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
TITLE OF INVENTION UNMBER: US/09/855,754B
CURRENT PILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                  Sequence 84280, A Sequence 84277, A Sequence 84277, A Sequence 84279, A Sequence 84276, A Sequence 10833, A Sequence 10833, A Sequence 9554, A Sequence 9554, A Sequence 6756, Ap Sequence 6756, Ap
                                                                     Sequence 84278,
Sequence 84278,
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                                                      Sequence
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                                           US-09-724-676-84274
US-09-724-676-84274
US-09-724-676A-84278
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US-09-724-676A-84287
US-09-724-676A-84277
US-09-724-676-84277
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; Pred. No. 1.3e-11;
0; Mismatches 0;
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-09-949-016-10853
-10-227-353-8
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US-09-855-754B-14
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FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
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US-09-855-754B-19
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LENGTH: 56
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TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERFUSSIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CLARE, JEFFREY J.
RPLICANT: CLARE, MICHAEL A.
ITTLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 911;
                                                                                                                                                                                                                                                                             Length 52;
                                                                                                                                                                                                                                                         1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAKAPPAPKPAPQPGPQPG---PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Millen, White, Zelano & Branio
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                        DB 5;
                                                                                                                                                                                           5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.5e-10;
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No. 4.5
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                                                                                                                                                                        Score 266.5;
Pred. No. 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/855,754B CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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ADDRESSEE: Millen, White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bordetella bronchiseptica
                                                                                                     ORGANISM: Bordetella bronchiseptica US-09-855-754B-15
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10227353 GENERAL INFORMATION:
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                                                                                                                                                                        95.9%;
94.2%;
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illarity 94.2%;
Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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  NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
Matches 49; Conserv
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Matches 49; Conserv
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LENGTH: 911
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US-10-227-353-4
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                                                                                    TYPE: PRT
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 911;
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Pred. No. 4.5e-10;
0; Mismatches 0
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Pred. No. 1.1e-10;
0; Mismatches 0
APPLICATION NUMBER: US/08/460, 269C FILING DATE: 02-Jun-1995
                                                                                     NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEG ID NOS: 25
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear

MOLECTLE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09855754B
                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAROLINE
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                                                                                                                                                                                                                                                                                                                                        LENGTH: 911 amino acids
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                                                        ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.1%;
Best Local Similarity 87.5%;
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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Best Local Similarity 94.2
Matches 49; Conservative
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APPLICANT: BOURSAUX-EUDE,
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NUMBER OF SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE
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US-09-855-754B-20
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US-09-855-754B-17
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FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION UNMERS: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 922;
                                                                                                                                                                                                                                             Length 58;
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..2e-10;
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                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No. 7.1
                                                                                                                                                                                                                                         Score 263.5;
Pred. No. 1.
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                               ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,969
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US-10-227-353-6
; Sequence 6, Application US/10227353
; GENERAL INFORMATION:
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84.5%;
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Best Local Similarity 84.5%;
Matches 49; Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                        NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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APPLICANT: GUISO-MACLOUF
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COUNTRY: USA
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Best Local Similarity
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GEQUENCE 20, Application US/09055754B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARABERTUSSIS, AND BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAREE PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/10/227,353
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Pred. No. 7.1e-10;
0; Mismatches 0;
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Pred. No. 1.5e-10;
0; Mismatches 0;
                                                                                                                             APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                            (703) 243-6333
703) 243-6410
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PRIOR FILING DATE: 2000-05-25
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ORGANISM: Bordetella bronchiseptica
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                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                    FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 922 amino acids TYPE; amino acid
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84.5%;
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98.0%;
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INFORMATION FOR SEQ ID NO: 6:
SECHENCE .....
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Best Local Similarity 98.0°
Matches 48; Conservative
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Best Local Similarity 84.5
Matches 49; Conservative
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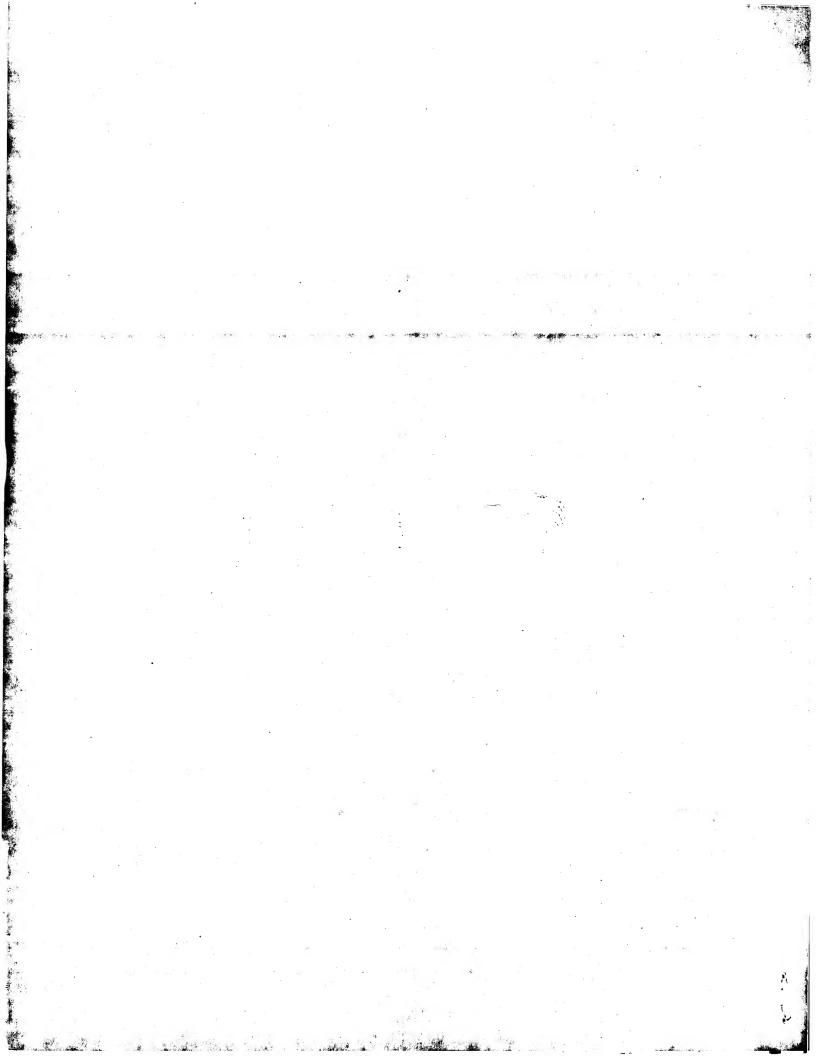
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US-09-855-754B-22
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LENGTH: 42
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPRENCUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-05-25
NUMBER OF SED ID NOS: 25
SOFTWARE: PATENTIN VEY: 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 7.9e-10;
0; Mismatches 0
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Pred. No. 1.4e-09;
0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bordetella bronchiseptica
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90.6%;
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80.0%;
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SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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US-09-855-754B-16
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LENGTH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONDHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0266-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 4.6e-09;
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83.6%; Pred. No. 5.5e-09;
live 0; Mismatches 2
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09855754B
GENERAL INFORMATION:
PPPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-21
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APPLICANT: BOURSAUX-EUDE, CAROLINE
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ORGANISM: Bordetella bronchiseptica
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86.8%;
CURRENT FILING DATE: 2001-05-
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 86.8 Matches 46; Conservative
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SOFTWARE: PatentIn Ver.
SEQ ID NO 21
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SOFTWARE: Patentin Ver. ;
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SOFTWARE: Patentin Ver
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Best Local Similarity
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US-09-855-754B-23
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51012
LENCTH: 768
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                                                                                Score 213.5; DB 5; Length 42;
Pred. No. 1.6e-07;
0; Mismatches 1; Indels
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Pred. No. 9.9e-07;
0; Mismatches 1; Indels
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                                                                                                                                                                   1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 49
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FILE REFERENCE: ELLTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                 Sequence 51012, Application US/10282122A GENERAL INFORMATION:
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RR APPLICATION NUMBER: 60/206,848
RR PILING DATE: 2000-05-23
RR APPLICATION NUMBER: 60/207,727
RR FILING DATE: 2000-05-26
RR PELLING DATE: 2000-05-06
RR FILING DATE: 2000-09-06
RR FILING DATE: 2000-03-06
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-23
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/257,931
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US-10-282-122A-51012
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Zamudlo, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Best Local Similarity 83.7%;
Matches 41; Conservative
                                                                                Ouery Match 76.8%;
Best Local Similarity 83.7%;
Matches 41; Conservative
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Forsyth, R.
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Trawick, John
Carr, Grant
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US-10-282-122A-51012
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Search completed: May 7, 2003, 17:27:46 Job time: 29.8825 secs



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US-09-855-754B-12
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                              SEQ ID NO 9
LENGTH: 56
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: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7448-10
US-10-282-122A-51012
US-09-855-7548-11
US-09-855-7548-13
US-09-855-7548-13
US-09-855-7548-6
US-09-855-7548-6
US-09-855-7548-6
US-09-855-7548-6
US-09-855-7548-8
US-09-855-7548-4
US-10-227-353-4
PCT-USO2-18256-52
PCT-USO2-18256-52
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PCT-US02-18256-46
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PCT-US02-18256-12
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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Sequence 72630, A Sequence 72631, A Sequence 72628, A Sequence 72628, A Sequence 72629, A Sequence 13303, A Sequence 13303, A Sequence 72627, A Sequence 72627, A Sequence 72627, A Sequence 8494, App Sequ
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US-09-724-676-72632
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ALIGNMENTS

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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PREPACTION IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONCHISLE PARAPERTUSSIS, AND IN TITLE OF INVENTION: BRONCHISLE PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
TITLE OF INVENTION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR PILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATCHILN VET. 2.1
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GENERAL INFORMATION:
APPLICANT: BOUKSAUX-EUDE, CAROLINE
APPLICANT: BOUKSAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTICAS PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BRONGHISELA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-9
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PRIOR FILING DATE: 2000-05-25
Sequence 9, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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Sequence

PCT-US02-18256-43

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SEQ ID NO 51012
LENGTH: 768
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US-09-855-754B-11
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LENGIH: 61
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TITLE OF INVENTION: POLYEPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERRACTIN IN BORDETELLA FERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: ROUGHSEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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                                                                                                                                                              Gaps
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Pred. No. 1.9e-20;
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CURRENT APPLICATION NUMBER: US/10/282,122A
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PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09855754B GENERAL INFORMATION:
                                                              ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-12
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Best Local Similarity 92.9%;
Matches 52; Conservative
                                                                                                                               94.5%;
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Forsyth, R.
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 56
                                                                                                                                                                53; Conservative
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
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                                                                                                                                Query Match
Best Local Similarity
Matches 53; Conserv
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US-09-855-754B-10
             SOFTWARE: POSE SEQ ID NO 12
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERFACTUI IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPETER PARAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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Pred. No. 1.9e-18;
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R FILING DATE: 2000-05-26
R APPLICATION NUMBER: 60/230,335
R FILING DATE: 2000-09-06
R APPLICATION NUMBER: 60/230,347
R FILING DATE: 2000-09-09
R APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R APPLICATION NUMBER: 60/257,931
R FILING DATE: 2000-12-22
RR APPLICATION NUMBER: 60/267,636
RR FILING DATE: 2001-20-09
RR RAPPLICATION NUMBER: 60/269,308
R FILING DATE: 2001-02-16
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PRIOR APPLICATION WNDER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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; ORGANISM: Bordetella pertussis
US-10-282-122A-51012
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Conservative
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Best Local Similarity
Matches 52; Conserv
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOSITICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REPERENCE; 03495-0206-00000
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Pred. No. 4.4e-17;
1; Mismatches 1;
                                               Score 271; DB 6;
Pred. No. 1.9e-17;
1; Mismatches 4
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Pred. No. 1.2e-
2; Mismatches
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-13
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                                               Query Match 88.0%;
Best Local Similarity 91.1%;
Matches 51; (Conservative )
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l Similarity 80.4%;
45; Conservative
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1 Similarity 87.5%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOURSAUX-EUDE,
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SOFTWARE: Patentin Ver. 2
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Best Local Similarity
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Best Local Similarity
Matches 45; Conserv
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US-10-227-353-2
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CIRLE REPRENCE: 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754B

CURRENT FILING DATE: 2001-05-16

PRICE REPRENCE: 0301-05-16

PRICE REPRENCE: 0301-05-16
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TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 910;
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ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 274; DB 5;
Pred. No. 9.9e-18;
1; Mismatches 4,
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FILING DATE: 02-Jun-1995
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                     Application US/09855754B
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                                                                                               GUISO-MACLOUF, NICOLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Bordetella pertussis
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91.1%;
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COMPUTER READABLE FORM:
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NUMBER OF SEQ ID NOS: 25
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Best Local Similarity 91.1<sup>1</sup>
Matches 51; Conservative
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                                               GENERAL INFORMATION
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Local Similarity
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Matches 42; Conserv
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US-09-855-754B-4
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LENGIH: 911
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Matches
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTION IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 922;
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SOFTWARE: Patentin Release #1.0, Version #1.30
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ADDRESSEE: Millen, White, Zelano & Branio
STREET: 2200 Clarendon Blvd., Suite 1400
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FILING DATE: 02-Jun-1995
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APPLICATION NUMBER: US/10/227,353
FILLING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
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Pred. No. 1.8
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REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
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03) 243-6410
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MEDIUM TYPE: Floppy disk
                                                                                                            Sequence 6, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bordetella parapertussis
                                                                                                                                                        CAROLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.2%;
Best Local Similarity 80.4%;
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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SOFTWARE: Patentin Ver. 2.1
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                                                                         RESULT 10
US-09-855-754B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
LENGTH: 922
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSELIC COMPOSITIONS.
FILE REFERENCE: 03495-0206-00000
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TITLE OF INVENTION: POLYMPETIDES CONTAINING POLYMORPHISMS OF THE REPEA
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISDETICA, THETR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISDETICA, THETR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03409-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                   1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
                                                                                                                                                                                                                                                                                                                        1 ORATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                      Length 922;
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                                                                                                                                                                                                      DB 6;
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illarity 75.0%; Pred. No. 3.8e-13;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                74.2%; Score 228.5; DB 6 80.4%; Pred. No. 1.8e-13; iive 2; Mismatches 4
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09855754B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                              Conservative
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SOFTWARE: Patentin Ver.
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APPLICANT: Don. N. Roth
APPLICANT: Randolph V. Lewis
APPLICANT: The University of Wyoming
TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
FILE REFERENCE: UWYO 02-004
CURRENT APPLICATION NUMBER: PCT/US02/18256
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 60/296,184
                                                   Gaps
                                                                                                                        254 QRATIRRGDAPAGGAVPGGAV------PGGFGPLLDGWYGVDVSDSTVDLAQ 299
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                                                     10;
                                                                                             1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                     Sequence 4, Application US/10227353
GENERAL INFORMATION:
GENERAL INFORMATION:
ROMANOS, MICHARL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.8%; Score 212; DB 6; Length 911; Best Local Similarity 75.0%; Pred. No. 6.3e-12; Matches 42; Conservative 2; Mismatches 2; Indels
       Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
  Score 212; DB 5;
Pred. No. 6.3e-12;
2; Mismatches 2;
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FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
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TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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  ch 68.8%;
1 Similarity 75.0%;
42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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Query Match
Best Local Similarity
Matches 42; Conserva
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US-10-227-353-4
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sequence 50286, A Sequence 6, Appl1 Sequence 17, Appl Sequence 17, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 7698, A Sequence 7698, A Sequence 111629, Sequence 2, Appl Sequence 11, Appl Sequence 21, Appl Sequence 2285, App
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTION IN BORDETELLA PERPUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILLING DATE: 2001-09-10
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ 1D NOS: 24
SOFTWARE: PATENTING DATE: 2000-05-25
NUMBER OF SEQ 1D NOS: 24
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US-09-855-754-19
US-09-857-754-19
US-09-857-754-6
US-09-857-754-6
US-09-857-754-10
US-09-857-754-10
US-09-857-754-10
US-09-857-754-11
US-09-857-754-22
US-09-857-754-23
US-08-857-754-23
US-08-9857-754-23
US-08-791-537-76881
US-09-791-537-76881
US-09-791-537-711629
US-09-85-754-5
US-09-85-754-5
US-09-85-754-5
US-09-86-0337-11
US-09-791-537-711629
US-09-380-693A-50
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ilarity 100.0%; Pred. No. 6.4e-12;
Conservative 0; Mismatches 0;
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US-09-855-754-14
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GENERAL INFORMATION:
APPILCANT: BOUSSAUX-EUDE, CAROLINE
APPILCANT: GUISO-MACLOUE, NICOLE
    Query Match
Best Local Similarity
Matches 49; Conserv
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LENGTH: 49
TYPE: PRT
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177.5
173.5
156.5
155.5
136.1
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131
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    Sequence 14, Appl
Sequence 15, Appl
Sequence 37413, A
Sequence 85698, A
Sequence 4, Appli
Sequence 18, Appli
                                                                                                                                                      ; Search time 124.128 Seconds
(without alignments)
254.511 Million cell updates/sec
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1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
                     GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-754-15
US-09-791-537-37413
US-09-791-537-85698
US-09-855-754-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Minimum DB seq Maximum DB seq

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Searched:

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Sequence:

Scoring table:

Sequence 40235, Sequence 2916,

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278 266.5 266.5 266.5 266.5 266.5

Result

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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOSINC COMPOSITIONS FILE REFERENCE: 03495-0206-00000

CURRENT APPLICATION UNBERR: US/09/855,754
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94.2%; Pred. No. 4.9e-10;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                            Score 266.5; DB 2
Pred. No. 4.9e-10;
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                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF ENQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 85698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-791-537-85698
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09855754 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
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PRIOR FILING DATE: 2000-03
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Matches 49; Conserv
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US-09-855-754-4
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APPLICANT: Blonomix, Inc.
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                 APPLICANT: GUISO-MACLOE, CARNLINE
APPLICANT: GUISO-MACLOE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFORMENT IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMNOGENIC COMPOSITIONS
GURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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Pred. No. 4.9e-10;
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Pred. No. 4e-11
0; Mismatches
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                                                                                                                                           Sequence 15, Application US/09855754 GENERAL INFORMATION:
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I Similarity 94.2%;
49; Conservative
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ilarity 94.2%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 52
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
                                                                                                                                                                                  APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUF
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Best Local Similarity
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nes 49; Conserv
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US-09-791-537-85698
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                                                                                                                    US-09-855-754-15
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US-09-855-754-15
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APPLICANT: GGISO-MCLUE, CAROLINE
TITLE OF INVENTION: POLYBEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYBEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OE INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER: 06/206,969
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GENERAL INFORMATION:
APPLICANT: BOUGANA: BOUGANA:
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: DANDINGERIC COMPOSITIONS
FILE REFERENCE: 014.95-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2000.05-25
PRIOR FILING DATE: 2000-05-25
      1 GAKAPPARKPAPQPGPQPG------PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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Pred. No. 8.1e-11;
0; Mismatches 0;
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Pred. No. 7.9e-10;
0; Mismatches 0;
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US-09-855-754-6
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US-09-855-754-17
; Sequence 17, Application US/09855754
                                                                                                                              Sequence 6, Application US/09855754
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
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Best Local Similarity 84.5%;
Matches 49; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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LENGTH: 922
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: WETHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR FILLING DATE: 2000-05-25
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Pred. No. 7.9e-10;
0; Mismatches 0; 1
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Pred. No. 7e-11;
0; Mismatches 0;
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Pred. No. 5.8e-
0; Mismatches
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                                       ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
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US-09-855-754-19
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1 Similarity 84.5%;
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ilarity 87.5%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 58
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Matches 49; Conserv
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US-09-791-537-50286
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LENGTH: 922
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SEQ ID NO 18
LENGTH: 56
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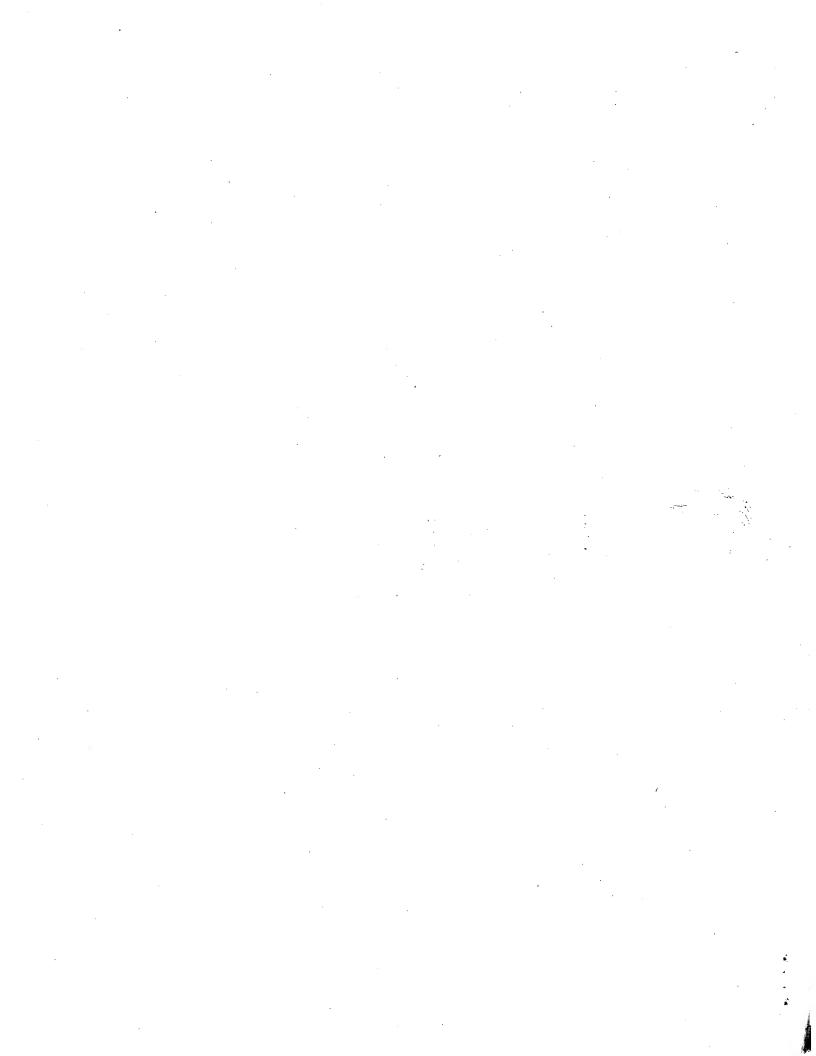
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US-09-855-754-23
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: PGLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARABERTUSSIS, AND BORDEFELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
CURRENT APPLICATION NUMBER: US/09/855,754
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Pred. No. 9.2e-10;
0; Mismatches 0; Indels
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Pred. No. 4.8e-10;
0; Mismatches 0
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
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Best Local Similarity
Matches 48; Conserv
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Best Local Similarity
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US-09-855-754-16
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LENGIH: 59
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LENGTH: 52
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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FILE REFERENCE: 03495-0206-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP-----PQRQPEAPAPQPPAGRELSAA 49
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                                                                                                                                                                                                                                                                                                                                                                                              Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP----PQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                         Score 238.5; DB 22; Length
Pred. No. .3.1e-09;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 237.5; DB 22; Ilarity 83.6%; Pred. No. 3.7e-09; Conservative 0; Mismatches 2;
        IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITION
; FILE REFERENCE: 03495-0206-00000
; CURRENT APPLICATION NUMBER: 05/09/855,754
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/26,969
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 21
; LENGTH: 52
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CURRENT FILING DATE: 2001-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bordetella bronchiseptica US-09-855-754-22
                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-855-754-22; Sequence 22, Application US/09855754; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09855754 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUISO-MACLOUF, NICOLE
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ilarity 86.8%;
Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOURSAUX-EUDE,
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Matches 46; Conserv
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GENERAL INFORMATION:

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BOUGSAUX:

APPLICANT: BOUGSAUX:

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED:

TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,

TITLE OF INVENTION: BRONGTHELA PREPRINGSIS, AND BORDETELLA

TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS:

FILE REPERENCE:

CURRENT APPLICATION NUMBER: 05/20/465,754

CURRENT PILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATCHIL VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 56;
                US-09-791-537-78243
US-09-791-537-31274
US-09-791-537-313443
US-09-855-754-11
US-09-873-111629
US-09-873-7111629
US-09-791-537-91868
US-09-791-537-98868
US-09-791-537-75841
US-09-791-537-76968
US-09-791-537-76968
US-09-791-537-4603
US-09-791-537-4603
US-09-791-537-4603
US-09-791-537-4603
US-09-791-537-4603
US-09-791-537-4660
US-09-791-537-4660
US-09-791-537-4560
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2.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANIŚM: Bordetella bronchiseptica
US-09-855-754-9
Similarity
                                                                                                                                                                                                                 SEQ ID NO 9
LENGTH: 56
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Best Local Si
Matches 56
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Sequence 4640, Ap
Sequence 12, Appl
Sequence 12, Appl
Sequence 112007,
Sequence 78242, A
                                                                                                                           7, 2003, 16:47:16 ; Search time 141.86 Seconds (without alignments) 254.511 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                  1 QRATIRRGDAPAGGGVPGGA......PVLDGWYGVDVSGSTVELAQ
                                                                                                                                                                                                                                                                                                                                                                                              4569144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

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6: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USO9_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USO9_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/USO9_COMB.pep:*
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6/ptodata/1/paa/US094_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US099_COMB.pep:*
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ptodata/1/paa/US101_COMB.pep:*
ptodata/1/paa/US102_COMB.pep:*
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                5.1.4_p5_4578
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-855-754-9
US-09-791-537-4640
US-09-791-537-4644
US-09-855-754-12
US-09-791-537-112007
US-09-791-537-78242
                                                                                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      4569144 seqs, 644733110 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                GenCore version
Copyright (c) 1993 - 2003
                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum Match 10
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308
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/cgn2_6/
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160
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Match
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308 308 308 291 291

Score

50286, A 6, Appli 8, Appli 4547, Ap 4540, Ap 4562, Ap 4573, Ap

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Total number Minimum DB : Maximum DB :

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Perfect score: Sequence: Scoring table:

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Run on:

31601, A 98868, A 76981, A 13, Appl 75841, A 76968, A

1, Appl 11629, , Appli

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7824, Application US/09791537

Sequence 7824, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Desph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILER REFERENCE: 251/210
CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 910;
                                                                                                                                                                                                                                                                                                  Length 56;
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                                                                                                                                                                                                                                                                                                  Score 291; DB 22;
Pred. No. 1.2e-22;
1; Mismatches 2;
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No. 6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112007, Application US/09791537, GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
              CURRENT APPLICATION NUMBER: US/09/855,7
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
LENGTH: 56
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Pred.
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US-09-855-754-12
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SEQ ID NO 112007
LENGTH: 910
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SEQ ID NO 78242
LENGTH: 907
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94.68;
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Best Local Similarity 94.69
Matches 53; Conservative
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US-09-791-537-78242
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Best Local Similarity
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US-09-791-537-112007
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US-09-791-537-78242
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                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Debe, Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERRINCE: 261/210
CURRENT FAPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001.02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 4644
LENGTH: 161
                                                                                                                                                                                                            APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: DATACH, JOSEPh
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PAPLICATION UNDER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTING APTE: 2001-02-22
SOFTWARE: PATENTING APTE: 2001-02-22
SOFTWARE: PATENTING APTE: 2001-02-22
LEBUTH: 160
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US-09-855-754-12
IS-09-865-754-12
| Sequence 12, Application US/09855754
| General information:
| Applicant: Boursaux-Eude, Caroline
| Applicant: Boursaux-Eude, Nicole
| TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
| TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
| TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Length 161;
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100.0%; Score 308; DB 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-24;
Matches 56; Conservative 0; Mismatches 0;
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1 Similarity 100.0%; Pred. No. 6.3e-24;
56; Conservative 0; Mismatches 0;
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                                                                                                                                       Sequence 4640, Application US/09791537 GENERAL INFORMATION:
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US-09-791-537-4644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica US-09-791-537-4640
                                                                                                                                                                                          APPLICANT: Bionomix, Inc.
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                                                                                                  RESULT 2
US-09-791-537-4640
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US-09-791-537-4644
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Sequence 33443, Application US/09791537
GENERAL INFORMATION:
APPLICANT: BAONOMIX, Inc.
APPLICANT: Debe, Derek
APPLICANT: METHODS OF USE THEREOF
FILLE OF INVENTION: METHODS OF USE THEREOF
FILLE REPERBNOE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALEGILIN VETSION 3.0
SEQ ID NO 33443
                                       APPLICANT: DEDGE, USEEN
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 26/1201
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATEUTIN VERSION 3.0
SOFTWARE: PATEUTIN VERSION 3.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EDDE, CAROLINE
APPLICANT: BOURSAUX-EDDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONOGENERAL COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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Pred. No. 2.5e-20;
1; Mismatches 3;
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Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella pertussis
US-09-791-537-21274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bordetella pertussis
US-09-791-537-33443
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92.9%;
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Best Local Similarity 92.98;
Matches 52; Conservative
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Best Local Similarity 92.99
Matches 52; Conservative
       APPLICANT: Bionomix, Inc
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GENERAL INFORMATION:
APPLICAWT: BOUNGRANT-EUDE, CAROLINE:
APPLICAWT: BOUNGRANT-EUDE, CAROLINE:
APPLICAWT: BOUNGRANT-EUDE, CAROLINE:
APPLICAWT: GUISO-MACCIOUF, NICOLE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: INMUNOSERICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: INMUNOSERICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: INMUNOSERIC COMPOSITIONS
TITLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR PILIAG DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 10
LENGTH: 56
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                                                                        254 QRATIRRGDAPAGGGVPGGAVPGGRAVPGFFGPGFGPVLDGWYGVDVSGSSVELAQ 309
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                                               1 QRATIRRGDAPAGGCVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ 56
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    Indels
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Pred. No. 1.3e-21;
1; Mismatches 3;
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Pred. No. 1e-20;
1; Mismatches
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APPLICANT BLONOMIX, INC.
APPLICANT Debe, Derek
APPLICANT Debe, Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 7343
  Mismatches
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; Sequence 21274, Application US/09791537
; GENERAL INFORMATION:
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ORGANISM: Bordetella bronchiseptica
  1;
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US-09-791-537-78243
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11 Similarity 92.9%;
52; Conservative
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92.9%;
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  Conservative
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Best Local Similarity
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53;
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  Matches
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Length 910;

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APPLICANT: BLOOMLY, Inc.
APPLICANT: BLOOMLY, Inc.
APPLICANT: BLOOMLY, Inc.
APPLICANT: Debc, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 QRATIRRGDALAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 275
                                                                                                                                                         1 QRATIRRGDAPAGGGVPGGAVPGGFDPGGFGPGGFGPVLDGWYGVDVSGSTVELAQ
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Pred. No. 1.6e-19;
1; Mismatches 4; Indels
                                       Score 274; DB 22;
Pred. No. 1.3e-19;
1; Mismatches 4;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 98868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98868, Application US/09791537 GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                 Sequence 31601, Application US/09791537 GENERAL INFORMATION:
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; ORGANISM: Bordetella pertussis
US-09-791-537-98868
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Best Local Similarity 91.1%;
Matches 51; Conservative
                                     Query Match 89.0%;
Best Local Similarity 91.1%;
Matches 51; Conservative
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US-09-791-537-31601
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Job time: 142.86 secs
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US-09-855-754-5
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Best Local S:
Matches 51
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APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 93495-00000
CURRENT APPLICATION NUMBER: 2004-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 QRATIRRGDAPAGGAVPGGAVPGGFGPGGFGPGFGPGFGPVLDGWYGVDVSGSSVELA 313
                                                                                                                                                         Gaps
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                                                                                                            Length 61;
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                                                                                                                                                      Indels
                                                                                                          DB 22;
                                                                                                          Score 278.5; DB 22;
Pred. No. 2.6e-21;
1; Mismatches 2;
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Pred. No. 4.6e-
1; Mismatches
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Sequence 111629, Application US/09791537
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-25
                                            ; ORGANISM: Bordetella bronchiseptica US-09-855-754-11
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US-09-791-537-111629
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                                                                                                          90.4%;
illarity 86.9%;
Conservative
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Best Local Similarity 86.9%;
Matches 53; Conservative
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                                                                                                                             Best Local Similarity
Matches 53; Conserv
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LENGTH: 915
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Gaps

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APPLICANT: Debe, Derek
APPLICANT: Denee, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                Length 910;
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Pred. No. 2.7e-19;
1; Mismatches 4;
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Sequence 6, Application US/09855754B
GENERAL INFORMATION:
APPLICANT: BOUNGAUX-EUDE, CAROLINE
APPLICANT: BOUNGAUX-EUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MOUNGERIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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US-09-855-754B-6
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1 QRATIRRGDAPAGGAVPGGA......PLLDGWYGVDVSDSTVDLAQ
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1: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*
              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-855-7548-10
US-09-855-7548-13
US-09-855-7548-8
US-09-855-7548-4
US-10-227-533-4
US-10-227-533-4
US-09-855-7548-9
US-09-855-7548-12
US-09-855-7548-12
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US-10-057-498-24021
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US-10-310-154-508
PCT-US02-18256-52
PCT-US02-18256-46
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Sequence 7 Application US/09855754B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOUGRAUX-BUDE, CAROLINE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
FRIOR PELICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 7
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  Sequence 27635, A Sequence 31381, A Sequence 31381, A Sequence 38, Appl Sequence 28, Appl Sequence 28, Appl Sequence 11200, Ap Sequence 1200, Ap Sequence 30130, A Sequence 12130, A Sequence 19336, A Sequence 10088, A
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US-10-366-683-27635
US-10-419-128-27635
US-10-366-683-31381
US-10-319-128-31381
US-10-311-096-28
US-10-341-097-28
US-10-141-097-28
US-10-141-097-28
US-10-141-1200
US-10-276-774-2507
US-10-276-774-2507
US-10-276-774-2507
US-10-276-683-30130
US-10-128-30130
US-10-128-30130
US-10-16-761-1210
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Similarity 100.0%; Pred. No. 2.1e-20;
51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bordetella bronchiseptica
US-09-855-7548-7
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US-10-282-122A-51012
; Sequence 51012, Application US/10282122A
; GENERAL INFORMATION:
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ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09855754B
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754B-5
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Best Local Similarity 83.9%;
Matches 47; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                            91.4%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                48; Conservative
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APPLICANT: BOURSAUX-EUDE,
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Best Local Similarity
Matches 48; Conserv
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US-09-855-754B-10
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ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 304
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                                                                                                                                             Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 272; DB 6; 100.0%; Pred. No. 3.7e-19;
                                                                                                                                                 Score 272; DB 5;
Pred. No. 3.7e-19;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION UNDER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067 , REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-227-353-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/09855754B; GENERAL INFORMATION:
                                                                        ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-7548-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 6:
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US-10-227-353-6
Sequence 6, Application US/10227353
, GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 100.
Matches 51; Conservative
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Best Local Similarity 100.0
Matches 51; Conservative
                  SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
NUMBER OF SEQ ID NOS: 25
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US-09-855-754B-5
                                      SEQ ID NO 6
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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TITLE OF INVENTION: POLYCY, THE REF
TITLE OF INVENTION: POLYCY OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARABERUCSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE: IN DIAGNOSTICS, AND ITLLE OF INVENTION: BRONCHISEPTICA, THEIR USE: IN DIAGNOSTICS, AND ITLLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTIN NOS: 22
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QRATIRRGDAPAGGAVPGGAVPGGRVPGFFGPGFGPGFGPVLDGWYGVDVSGSSVELAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QRATIRRGDAPAGGAVPGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
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Pred. No. 8.2e-17;
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Pred. No. 2.6e-17;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PELLING DATE: 2000-05-25
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Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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Gaps

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Indels

Mismatches

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85.5%;
90.2%;
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90.2%;
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-05-25
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Best Local Similarity 90.2
Matches 46; Conservative
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 90.2*
Matches 46; Conservative
Conservative
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45;
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Matches
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms File Reference: ELITRA.034A
CURRENT APPLICATION NUMBER: 0S/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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Pred. No. 3.5e-16;
3; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 66/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
REMBARDING DATE: 2001-02-16
RUMBER OF SEQ ID NOS: 78614
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                     NE FILING DATE: 2000-03-21

OR APPLICATION NUMBER: 60/206,848

OR FILING DATE: 2000-05-23

OR RELING DATE: 2000-05-23

OR PELICATION NUMBER: 60/207,727

OR FILING DATE: 2000-09-06

OR APPLICATION NUMBER: 60/230,335

OR APPLICATION NUMBER: 60/230,347

OR FILING DATE: 2000-09-09

OR RELING DATE: 2000-10-23

OR APPLICATION NUMBER: 60/242,578

OR APPLICATION NUMBER: 60/242,578

OR APPLICATION NUMBER: 60/253,625

OR RELING DATE: 2000-11-27

OR RELING DATE: 2000-11-27

OR RELING DATE: 2000-11-27
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Bordetella bronchiseptica
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ORGANISM: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.9%;
Matches 47; Conservative
                     Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-282-122A-51012
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Length 51;

Score 241; DB 5; Pred. No. 2.6e-17

88.6%; 88.2%;

Query Match Best Local Similarity

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APPLICANT: GUISGO-MACLOUF, NICCLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDEFELLA PRICESIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MONUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/99/855,754B
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2001-05-16
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 25
SEQ ID NOS: 25
SEQ ID NOS: 26
TENERAL APPLICATION OF 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: MANUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-000000
CURRENT APPLICATION NUMBER: US/09/855,754B
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   51
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1 ORATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                              1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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Pred. No. 1.7e-16;
0; Mismatches 0;
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Pred. No. 3.3e-15;
0; Mismatches 0;
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US-09-855-754B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND FITLE OF INVENTION: IMMUNOGENIC COMPOSTITION:
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TITLE OF INVENTION: POLYBEPTIDES CONTAINING POLYMORPHISMS OF THE
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
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80.4%; Pred. No. 5.2e-16;
                   APPLICATION NUMBER: US/10/227,353
FILING DATE: 26-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY AGENT INFORMATION:
NAME: Lebovitz, Richard M.
RECISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754B
CURRENT FILING DATE: 2001-05-16
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                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09855754B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                LENGTH: 910 amino acids TYPE: amino acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                        TELEFAX: (703) 243
INFORMATION FOR SEQ ID NO: 2
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SOFTWARE: Patentin Ver.
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Matches 45; Conserv
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Matches 46; Conserv
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US-09-855-754B-12
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                                                                                                               ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QRATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                            ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 232.5; DB 6
Pred. No. 3.3e-15;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/227,353 FILING DATE: 26-Aug-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

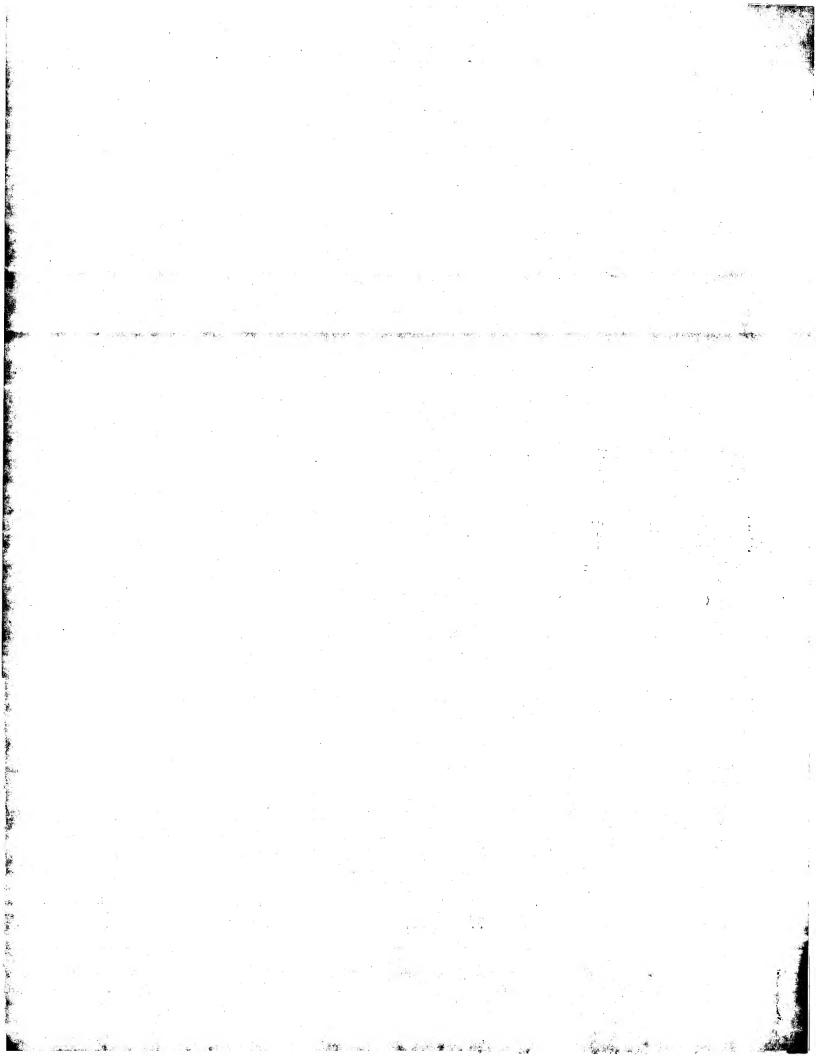
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-227-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lebovitz, Richard M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                                                                                                                                                                                                                                                                                                                                                                            : Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10227353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 911 amino acids
                                         Sequence 4, Application US/10227353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CLARE, JEFFREY
                                                                                       APPLICANT: CLARE, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%;
90.2%;
                                                                                                                                                                                NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.2<sup>3</sup>
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
                                                                                                                                                                                                                                                                                                                        COUNTRY:
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US-10-227-353-2
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BONDETELLA PARABETUSSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-00500
CURRENT APPLICATION NUMBER: 2005-00000
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DON A. Roth
APPLICANT: DON A. Roth
APPLICANT: Randolph V. Lewis
APPLICANT: The University of Wyoming
TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
FILE REFERENCE: UNYO 02-004
CURRENT APPLICATION NUMBER: PCT/US02/18256
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 60/296,184
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRONCHISEPTICS, THEIR USE IN DIAGNOSTICS, AND IN IMMUNGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QRATIRRGDAPAGGAVPGGAV----PGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ 51
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                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                       Score 228.5; DB 5.
Pred. No. 5.2e-16;
3; Mismatches 3.
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Pred. No. 1e-15;
3; Mismatches
                                                                  US/09/855,754B
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                                                                                       CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PATENTIN VOY: 2.1
                                                                                                                                                                                                                                                                  ) ORGANISM: Bordetella bronchiseptica US-09-855-7548-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09855754B GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Bordetella bronchiseptica
                                        FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/05
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.1%;
73.8%;
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Best Local Similarity 80.4%;
Matches 45; Conservative
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.1
Best Local Similarity 73.8
Matches 45; Conservative
  INVENTION:
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                                                                                                                                                                                                SEQ ID NO 12
LENGTH: 56
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LENGTH: 61
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Gaps
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                                                                                                                                                                                                  Length 171;
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                                                                                                                         ; FEATURE;
; OTHER INFORMATION: synthetic spider silk protein repeat
PCT-US02-18256-45
                                                                                                                                                                                              30.1%; Score 82; DB 1;
60.0%; Pred. No. 0.74;
tive 3; Mismatches
               NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                            Search completed: May 7, 2003, 17:27:44 Job time: 32.0613 secs
                                                                                                                                                                                                                                                                                          88 GGSGPGGYGPGGAGPGGSGPGGYGP 112
                                                                                                                                                                                                                                                                     8 GDAPAGGAVPGGAVPGGFGP 32
                                                                                                        ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                            Query Match
Best Local Similarity 60.0%
Matches 15; Conservative
                                                 SEQ ID NO 45
LENGTH: 171
                                                                                       PRT
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Sequence 5, Appli Sequence 10, Appl Sequence 21274, A Sequence 21274, A Sequence 13, Appl Sequence 78242, A Sequence 78242, A Sequence 78242, A Sequence 4547, Ap Sequence 4547, Ap Sequence 4547, Ap Sequence 4568, Ap Sequence 4568, Ap Sequence 4568, Ap Sequence 37413, Ap Sequence 37413, Ap Sequence 37413, Ap Sequence 37413, Ap Sequence 3688, Ap Sequence 9568, Ap Sequence 9569, Appli Sequence 97, Appli Sequence 97, Appli Sequence 97, Appli Sequence 97, Appli Sequence 12, Appli Sequence 4640, Ap

11, Appl 111629,

Sequence 7 Sequence 7 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2

Sequence 2 Sequence 4 Sequence 2 Sequence 1 Sequence 5 Sequence 5 Sequence 1

ALIGNMENTS

76981,

4640, Ap 4644, Ap 112007,

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ORATIRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
US-09-855-754-10
US-09-915-37-754-10
US-09-915-37-21274
US-09-791-537-21274
US-09-791-537-3443
US-09-791-537-75841
US-09-791-537-75841
US-09-791-537-75841
US-09-791-537-75842
US-09-791-537-75842
US-09-791-537-75842
US-09-791-537-4540
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4560
US-09-791-537-4640
US-09-791-537-6981
   Similarity
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                                                                                                              Query Match
Best Local S
Matches 51
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Sequence 4609, Ap
Sequence 4603, Ap
Sequence 4519, Ap
Sequence 50286, A
Sequence 6, Appli
                                                                                                       ; Search time 129.194 Seconds
  (without alignments)
254.511 Million cell updates/sec
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                                                                                                                                                                                       272
1 QRATIRRGDAPAGGAVPGGA......PLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pending_Patents_AA_Main:*

1: \cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: \cgn2_6/ptodata/1/paa/S06_COMB.pep:*

3: \cgn2_6/ptodata/1/paa/US01_COMB.pep:*

4: \cgn2_6/ptodata/1/paa/US01_COMB.pep:*

5: \cgn2_6/ptodata/1/paa/US01_COMB.pep:*

6: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

7: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

9: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

10: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

11: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

12: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

13: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

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14: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

15: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

16: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

17: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

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19: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

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27: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*

27: \cgn2_6/ptodata/1/paa/US09_COMB.pep:*
               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-754-7
US-09-791-537-4609
US-09-791-537-4603
US-09-791-537-4519
US-09-791-537-50286
US-09-855-754-6
                                                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 4569144 seqs, 644733110 residues
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                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum I
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: BOURSAUX-EUDE, NICOLE

TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERFUSSIS,

TITLE OF INVENTION: BORNCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN

TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS

TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS

FILE REFERENCE; 03495-0206-00000

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT PILING DAIE: 2000-09-10

PRIOR FILING DAIE: 2000-05-25

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 7

LENGTH: 51

SEQ ID NO 7

LENGTH: 51

SED ID NO 7
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Llarity 100.0%; Pred. No. 1.6e-22;
Conservative 0; Mismatches 0;
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US-09-855-754-7
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APPLICANT: Balonomia, inc.
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILIANG DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOGTWARE: Patentin version 3.0
SEQ ID NO 50286
LENGTH: 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
THEIR REFERENCE: 03495-0306-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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100.0%; Pred. No. 4.1e-21;
iive 0; Mismatches 0;
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No. 4.1e-21;
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illarity 100.0%; Pred. No. 5.6e-22;
Conservative 0; Mismatches 0;
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Pred.
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                 ORGANISM: Bordetella bronchiseptica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bordetella parapertussis
US-09-791-537-50286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5-09-855-754-6; Sequence 6, Application US/09855754; Sequence 1, Application SAPPLICANT: APPLICANT: GUISO-MACLOUF, NICOLE APPLICANT: GUISO-MACLOUF, NICOLE
2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                     NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 4519
LENGTH: 160
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51; Conservative
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; ORGANISM: Bordetella
US-09-855-754-6
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Best Local Similarity
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LENGTH: 922
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Best Local
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APPLICANT: BLONOMIX, INC.
APPLICANT: BLONOMIX, INC.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Derek
APPLICANT: Dabe, OB-erek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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100.0%; Score 272; DB 21;
Best Local Similarity 100.0%; Pred. No. 5.6e-22;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272; DB 21;
Pred. No. 5.6e-22;
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GENERAL INFORMATION:
APPLICANT: BLOOMAIX, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
APPLICANT: THREE DIMENSIONAL STRUCT
TITLE OF INVENTION: METHODS OF USE THEREOF
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CURRENT APPLICATION NUMBER: US/09/791,537
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                                                                                                                                        Sequence 4609, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-791-537-4603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella bronchiseptica
US-09-791-537-4609
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100.0%;
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Best Local Similarity
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US-09-791-537-4603
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LENGTH: 159
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LENGTH: 158
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Sequence 21274, Application US/09791537 GENERAL INFORMATION:
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APPLICANT: Bionomix, Inc.
                                                  Application US/09791537
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US-09-791-537-21274
                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella pertussis
US-09-791-537-78243
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.8%;
Best Local Similarity 83.9%;
Matches 47; Conservative
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Best Local Similarity 83.99
Matches 47; Conservative
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                                                                                                APPLICANT: Bioriomix, Inc.
                                                  Sequence 78243, Appl GENERAL INFORMATION:
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US-09-791-537-21274
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LENGTH: 910
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND INTELLA OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOSENTIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CORRET PAPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPPTCA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/085,754
CURRENT FILLING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VET. 2.1
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                                           1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
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    0; Indels
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85.7%; Pred. No. 1.6e-18;
1ive 3; Mismatches 0; 1
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Pred. No. 4.2e-19;
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  Mismatches
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ORGANISM: Bordetella pertussis
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83.9%;
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Best Local Similarity 83.9%
Matches 47; Conservative
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Matches 48; Conservative
Conservative
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51;
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APPLICANT: Debe, Derek, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: HREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFRENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPREBLOCE; 261/210
CURRENT MAPPLICATION NUMBER: US/09/791,537
CURRENT PILLING IDATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 78243
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ORATIRRGDAPAGGAVPGGAV-----PGGFGPLLDGWYGVDVSDSTVDLAQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ORATIRRCDAPAGGAVPGGAV----PGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.8%; Score 241.5; DB 2
83.9%; Pred. No. 9.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                    3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 241.5;
Pred. No. 3.7
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SEQ ID NO 33443

254 QRATIRRGDAPAGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 304

LENGTH: 910

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 76968
LENGTH: 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78242, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix.
APPLICANT: Debc, Derek
APPLICANT: STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOGTWARE: Patentin Version 3.0
SEQ ID NO 78242
LENGTH: 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 QRATIRRGDAPAGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QRATIRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 87.3%; Score 237.5; DB 21; Best Local Similarity 82.1%; Pred. No. 2.7e-17; Matches 46; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 241; DB 21;
Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                  ; Sequence 76968, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7, 2003, 17:21:51
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-791-537-76968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Bordetella pertussis US-09-791-537-78242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.6%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Conservative
                                                                                                                                                  APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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GENERAL INFORMATION:
Sequence 75841, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bonomia, Inc.
APPLICANT: Debe, Derek
APPLICANT: Sel/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICANTON: NOWER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/085,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOIL 2.1
                                                                                                                                                  Gaps
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                                                                                               DB 21; Length 910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 51;
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                                                                                                                                               Indels
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Best Local Similarity 88.2%; Pred. No. 4.3e-19;
Matches 45; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%; Score 241; DB 21;
88.2%; Pred. No. 1.1e-17;
                                                                                               Score 241.5; DB 2
Pred. No. 9.7e-18;
3; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bordetella bronchiseptica US-09-855-754-13
                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09855754 GENERAL INFORMATION:
APPLICANT: BOUNSAUX EUDE, CAROLINE
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-791-537-33443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella pertussis US-09-791-537-75841
                                                                                            Query Match 88.8%;
Best Local Similarity 83.9%;
Matches 47; Conservative
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Matches 45; Conserv
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US-09-791-537-75841
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LENGTH: 905
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Gaps

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Indels

51

Gaps

5;

Indels

DB 21; Length 907;

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:31:49 ; Search time 5.24361 Seconds (Without alignments) 427.133 Million cell updates/sec Мау Run on:

US-09-855-754B-22 310 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 54 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

													-															•						
	Description	P24328 bordetella		_			P21260 owenia fusi	Q92794 homo sapien	_		P40602 arabidopsis	Q9fpq6 chlamydomon				P23093 plasmodium	_	O70324 mus musculu	P51111 rattus norv	P09791 trypanosoma	_	Q64467 mus musculu	P41467 autographa	P08469 trypanosoma	Q06084 trypanosoma	_		P42858 homo sapien	_	mus muscul	Q05860 mus musculu	P08001 sus scrofa	Q9p2y4 homo sapien	P41479 autographa
SUMMARIES	QI	PERT_BORPA	PERT_BORBR	PERT_BORPE	TEGU_HSV11	SSGP_VOLCA	YPRO_OWEFU	MOZ_HUMAN	EBN2_EBV	APG_BRANA	APG_ARATH	GP1_CHLRE	Y066_NPVOP	ACRO_RABIT	CSP_PLABE	CSP_PLABA	EXLP_TOBAC	MOT8_MOUSE	HD_RAT	PARB_TRYBB	MEFD_MOUSE	G3PT_MOUSE	Y066_NPVAC	PAR1_TRYBB	PARC_TRYBB	RFX1_HUMAN	GDA3_WHEAT	HD_HUMAN	TONB_NEIGO	FM14_MOUSE	FMN1_MOUSE	ACRO_PIG	Z219_HUMAN	Y091_NPVAC
	DB	-	ч	П	П	-	-	7	ч	1	7	П	П	ч		Н	Н	7	-	7	-	-	-	-	Н	7	Ч	П	Н	-		П	П	-
	Query Match Length	922	911	910	3164	485	141	2004	487	449	534	522	875	431	339	347	426	265	3110	129	514	440	808	143	145	979	282	3144	283	1206	1468	415	722	224
æ	Query Match	85.5	83.2	69.7	50.8	49.4	48.7	48.1	47.7	47.6	46.1	45.3	45.2	45.0	44.4	44.4	44.2	44.0	43.7	43.4	•	42.9	42.9	42.7	42.7		42.6	42.3	42.1	42.1		41.8	41.8	41.3
	Score	265	258	216	157.5	153	151	149	148	147.5	143	140.5	140	139.5	137.5	137.5	137	136.5	135.5	134.5	133.5	133	133	132.5	132.5	132.5	132	131	130.5	130.5	130.5	129.5	129.5	128
	Result No.	-	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

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09pr99 ureaplasma 099014 trichoderma P78621 emericella P05142 mus musculu P02831 mus musculu P1023 homo sapien P42859 mus musculu P06470 hordeum vul 013164 homo sapien P58840 homo sapien P58840 homo sapien
YO46_UREPA KPC1_TRIRE SEPA_EMENI SEPA_EMENI SEROLUMAN HXA3_MOUSE HXA3_MOUSE HORL_HORVU MKO7_HUMAN MKO7_HUMAN BRC4_HUMAN ACRL_HUMAN ACRL_HUMAN
791 1139 1790 261 261 443 421 3119 3119 21362 2362
44444444 100000000 10000000000000000000
126.5 126.5 126.5 125.5 125.5 124.5
W W W W W W W W W W W W W W W W W W W

ALIGNMENTS

RESULT 1 PERT_BORPA STANDARD; PRT; 922 AA.	P24328; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update)	JUN-2002 (Rel. 41, tactin precursor (O	PRN. Bordetella parapertussis	Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;	bornecella. NCBI_TaxID=519;	[1] SEQUENCE FROM N.A.	STRAIN=CN2591;	Fubmed=20414/6; 5., Novotny P., Charles I.G.;	"F./U pertactin, an outer-membrane protein irom Bordetella parapertussis: cloning, nucleotide sequence and surface expression in	•	THE TREE OF THE STREET THAT THAT BINDS TO EUKARYOTIC CELLS; A PROCESS	MEDIATED BY THE R-G-D SEQUENCE, PERTACTIN MAY HAVE A ROLE IN PACTERIAL ADHESTON, AND THIS DIAV A POIR IN UTBILENCE			SS-PROT entry is copyright. It is produced throu	between the Swiss Institute of Bioinformatics and the EMBL outstation -	ng as its conter	modified and this statement is not removed. Usage by and for commercial	or send an email to license(1sb-sib.ch).	EMBL; X54547; CAAS8419.1; EMBL; A26124; CAA01786.1;	PIR; S15204; S15204. PIR: S14659: S14659	rPro; IPR004899;	InterPro; IPR003992; pertactin. InterPro; IPR003991: pertactin vir.	3212; Pertac	PRINTS; PRO1482; PERTACTIN. PRINTS; PR01484; PRTACINFAMLY.	membrane; S	SIGNAL 1 34 POTENTIAL. CHAIN 35 922 P 95	35 647	PROPEP 648 922 POTENTIAL. SITE 260 262 CELL ATTACHMENT SITE (INVOLVED IN	
SUL RT_			N SO			RP RP	22.2			RT		ខ្លួ	ဗ္ဗ								 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		X 20		žä		EE		FF	
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                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Gen. Microbiol. 138:1697-1705(1992).
-I- PUNCTION. AGGLUGITHOGEN THAT. BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBGINIT: MONOMER.
-1- SUBGELLULAR LOCATION: Outer membrane.
-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
                                                                                                                                                                                                                               (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
                                                                                                                                                                                                             1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
               LINES). 4 \times 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide, sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella bronchiseptica.";
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERTACTIN (P.68).
POTENTIAL.
CELL ATTACHMENT SITE (INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                    DB 1; Length 922;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                              Pertactin precursor (Outer membrane protein P.68) (P.94)
                                                                                                                                             85.5%; Score 2bɔ; Lī;
84.5%; Pred. No. 6.4e-10;
tive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                      911 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 35-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A47675; A47665.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003991; pertactin.
InterPro; IPR003991; pertactin.
Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTURAMIX.
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92407514; PubMed-1527510;
                                                                                                                     MM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X54815; CAA38584.1; -. EMBL; A19180; CAA01453.1; -.
                                                                                                                     95178
                                                                                                                                                                1 Similarity 84.5
49; Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                            290
270
280
285
                                                                                                                     922 AA;
                              266
266
271
276
281
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CN7531;
                                                                                                                                                                                                                                                                                                                   PERT_BORBR
Q03035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella.
                                                                                                                     SEQUENCE
                                                                                                                                                    Query Match
                                                                                                                                                                     Local
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                            DOMAIN
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                                                                         REPEAT
                                                            REPEAT
                                                                                          REPEAT
                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                      PERT_BORBR
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                        RESULT 2
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96196517; PubMed-8609998; Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.; Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.; Nature of Bordetella pertussis virulence factor P.69 pertactin."; Nature 381:90-92(1996).
-!- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M., Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                             SITE (POTENTIAL).
REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=92407514; PubMed=1527510;
Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.;
"Cloning, nucleotide sequence and heterologous expression of the
protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                           Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PROMPORE OF PROMPORE (P. 1992)
                                                                                                                                                                                                                                                                                                        Score 258; DB 1; Length 91
Pred. No. 1.7e-09;
0; Mismatches 2; Indels
                                                                                                                                                                                 280 3 (APPROXIMATE).
501 7 X 3 AA REPEATS OF P-Q-P.
93995 MW; 3078DF6EC2D987A1 CRC64;
                                                   CELL ATTACHMENT
3 X 5 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                LINES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 264 AND 332.
MEDLINE-92407514; PubMed-1527510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89264462; PubMed-2542937;
                                                                                                                                                                                                                                                                                                           83.2%;
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                                                                                                                                                                                                                                              911 AA;
                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=520;
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P14283;
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                       DOMAIN
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DB 1; Length 3164;
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                      Score 157.5; DB 1;
Pred. No. 0.0041;
2; Mismatches 6;
                                                                                                                                                                                                                                                                   P21997;
01-A0G-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-COT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Sulfation; Hydroxylation.
DOMAIN 228 340 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=f, Nagariensis / HK10;
MEDLINE=90094551; PubMed=2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; | X51616; CAA35953.1; -.
                   Ouery Match 50.8%;
Best Local Similarity 72.3%;
Matches 34; Conservative
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                  Volvox carteri
                                                                                                                                                                                                                                  SSGP_VOLCA
ID SSGP_VOLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-88274327; PubMed-2839594; MGGOCO D.J., Dolan A., Frame M.C., MGGOCO D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., MGNAD D., Perry L.J., Scott J.E., Taylor P.; "The complete DNA sequence of the long unique region in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                           LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                 CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 216; DB 1; Length 910;
Pred. No. 5.3e-07;
0; Mismatches 1; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                   (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                           PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                                                                                 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein U136).
                                                                                                                                           membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                  POTENTIAL
               InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR005210; Herpes_UL36.
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                                                                           Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             93452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X14112; CAA32311.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
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281
286
579
910 AA;
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P10220;
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).
-!- FUNCTION; THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
LINSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C32 STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carter!: molecular structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- PTM: A.CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical proline-rich protein (Fragment).
Owenia fusiformis.
Eukaryota; Métazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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49.4%; Score 153; DB 1; Length 485;
Best Local Similarity 57.1%; Pred. No. 0.002;
Matches 24; Conservative 1; Mismatches 17; Indels
                                                                                                                 Indels
                                                                   PAPKPAPQPGPQP-PQP-PQP-PQPQPQPQPQPEAPAPQPPAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 295 POLY-PRO.
435 AA; 50436 MW; A52216400A031421 CRC64;
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EBN2_EBV P12978;
                                                                                                                                                                                                                                                                                           SEQUENCE
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; "The translocation t(8;16)(pl1;pl3) of acute myeloid leukaemia fuses
                                  SEQUENCE FROM N.A.
MEDLINE=90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bakalara n., Collet J., Planells R., Thouveny Y., Fontes M.;
Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Blochem. Blophys. Res. Commun. 166:66-73(1990).
PIR; B34043; B34043.
Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                         Score 151; DB 1; Length 141;
Pred. No. 0.0011;
0; Mismatches 20; Indels
                                                                                                                                                                                                  15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                             5 РРАРКРАРОРОРОРРОРРОРРОРОРОРОРОРОРОРОРАСК 49
                                                                                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                   PRT; 2004 AA
                                                                                                                                                                POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001386; Histone_H1/H5.
Interpro; IPR002717; MOZ_SAS.
Interpro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96376968; Pubmed-8782817;
Sabellida; Owenfidae; Owenia.
NCBI_TaxID=6347;
                                                                                                                                                                                                                           48.78;
                                                                                                                                                                                                                                         55.68;
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Genew; HGNC:13013; ZNF220.
                                                                                                                                                                                                                                         Best Local Similarity 55.6 Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                     141 AA;
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Q92794;
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NON_TER
SEQUENCE
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DOMAIN
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MOZ_HUMAN
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Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
-i- PIM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Virol. 65:2545-2554(1991).
-!- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petti L., Sample C., Kieff E.; "Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins."; Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BREAKPOINT FOR TRANSLOCATION TO FORM MOZ-CBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91202599; PubMed-1850028;
Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
PROSITE; PSO1359; ZF_PHD_1; 1.
PROSITE; PSSO016; ZF_PHD_2; 2.
Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epstein-barr virus (strain B95-8) (Human herpesvirus 4). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9FFBBAC3792854BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1651 PPPPPPQPQPPPPPQPQPPPPPQQPQQPQQPQQPQPPPP 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 РАРКРАРОРСРОРРОРРОРРОРРОР 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score 149; DB 1;
Pred. No. 0.0094;
1; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                 GLN/PRO-RICH
                                                                                                                                                                            C2HC-TYPE.
POLY-GLU.
                                                                                                                                                                                                                                                     POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
POLY-GLU.
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MEDLINE=84270667; PubMed=6087149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004 AA; 225054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.0 Matches 27; Conservative
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                                                                                                                                                                                                                                                                          1078
                                                                         Nuclear protein.
ZN_FING 206
ZN_FING 259
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DB 1; Length 449;

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                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridipiantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-i- DEVELOPMENTAL. STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A., Draper J., Scott R.; Gametophytic and sporophytic expression of an anther-specific Arabidopsis thanlana gene."; Plant J. 3:111-120(1993).
                                                                                                                                                                                                     Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                     POLY-PRO.
6 X 2 AA TANDEM REPEATS OF R-G.
DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                          th 47.7%; Score 148; DB 1; Length 487; Similarity 53.2%; Pred. No. 0.0039; 25; Conservative 1; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          4 VPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRE 50
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9EFB6A3AB28EEA15 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch)
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PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                              EMBL; V01555; CAA24877.1; ALT_INIT.
TRANSFAC; T01618; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                            52544 MW;
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                                                                                                                                                                                                                        Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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345 35
487 AA; 5
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428
449 AA;
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                                                                                                                                                                                                                                                                            SEQUENCE
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ACT_SITE
SEQUENCE
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Theologis A. Ecker J. R., Palm C.J., Federspiel N.A., Kaul S., White O. Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chun M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y., Hunter J.L., Johkins J., Johnson-Hopson C., Khan S., Khaykin E., Kin C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B., Langil-Hooper S., Lee A., Lee J.M., Lez C.A., Li J.H., Li Y.-P., Militscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I., Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.K., Shin P., Stuthwick A.M.,
                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Anter-specific proline-rich protein APG precursor.
APG OR AT1G26130 OR T20H2.9.
Arabidopsis thallana (Mouse-ear cress)
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                  Gaps
                                                                                                      ----EAPAP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES. CAUTION: Ref. 2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. Columbia;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davia R.W., Ecker J.R., Theologis A.;
Submitteed (SEP-2001) to the BMBL/Genbank/DDBJ databases.
-I-TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL
TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-I-DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING
MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING
MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.W., Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROW N.A.
MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar.
Draper J., Scott R.;
"Game/cophytic and sporophytic expression of an anther-specific
Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
                                              Indels
                                                                                      -dÖdÖdÖdÖdÖddÖdd------
    Score 147.5; DB 1;
Pred. No. 0.0039;
1; Mismatches 12;
                                                                                                                                                                                                                                                                                                          534 AA.
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MEDLINE-21016719; PubMed-11130712;
      47.68;
                                                                                 KVPPAPKPAPQPGPQPPQPPQ-
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                                            Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                               Q9LNT8;
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBL_TaxID=3702;
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                                                                                                                                                                 44 QPP 46
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                                          28;
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P40602; OS
Query Match
Best Local
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                                                                                                                                                                                    ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glycosylated polyproline II rods-with-kinks as a structural motif in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                GPI_CHLRE STANDARD; PRT; 555 AA.
G9FRG6, 003927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J., Goodenough U.W.;
                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                             3 KVPPAPKPAPKPAPQPGPQP-----PQPPQPPQPPQPQPQPQPQPEAPAPQPP 46
                                                                                                                                                                                                                                                              Score 143; DB 1; Length 534;
Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                               S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: Associates with GP2 and GP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant hydroxyproline-rich glycoproteins.";
Blochemistry 40:2978-2987(2001).
                                                                                           EMBL, X60377; CAA42925.1; -
EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AX058847; AAL24235.1; -
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21159092; Pubmed=11258910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonadaceae; Chlamydomonas NCBI_raxID=3055;
                                                                                                                                                                                                                                          58007 MW;
                                                                                                                                                                                                                                                              46.18;
52.98;
 model prediction.
                                                                                                                                                                                                                                                                               27; Conservative
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141
325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3, gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                             VEGETATIVE CELL WALL PROTEIN GP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%; Score 140.5; DB 1; Length 555; 54.3%; Pred. No. 0.012; 1ve 4; Mismatches 14; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y066_NPVOP STANDARD; PRT; 875 AA.
983949; 065364; 010323;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the orgyla pseudotsugata multinucleocapsid polyhedrosis virus genome."; Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;
             as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ahrens C.H., Rohrmann G.F.;
"The DNA polymerase and helicase genes of a baculovirus of pseudosugata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication.";
Virology 210:372-382(1995).
-1- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VPPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPGAPA--PQPPA 47
non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                          InterPro; IPR003882; Pistil extensin. PRINTS; PR01217; PRICHEXTENSN. PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                     SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; PubMed-8609478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54219 MW;
                                                                                                                                                                                                                                                                                                                Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 54.3 es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     399
455
493
                                                                                                                                                                                                                                                                                                     Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 4
493 4
555 AA;
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CSP_PLABE
P06915;
                                                                                          DOMAIN
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DISULFID
DISULFID
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SEQUENCE
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                                 CHAIN
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entities requires a license agreement (See http://www.lsb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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STRAIN-Wew Zealand white; TISSUE-Testis;
MFDLINE-94368861; Pubmed-8086468;
MFDLINE-94368861; Pubmed-8086468;
Richardson R.T., O'Rand M.G.
Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA...;
Blochim. Blophys. Acta 1219:215-218(1994).
IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROFEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENCHS: 201.423, MENCHS SOL.423, MENCHS SOL.423, MENCHS SOL.423, MENCHS SOL.423, MENCHS SOL.423, MENCH SOL.423,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 PPPPQPFYPYCQYWPQQPPQPPDQPQQPQPPQQPPQQPPQQPPQQPPQQPPQ39
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKP-----APQPGPQPPQPPQPP-QPPQPQPQPQPQPQPEAPAPQPP 46
                                                                                                                                                                                                                                                                                                Score 140; DB 1; Length 875;
Pred. No. 0.018;
1; Mismatches 13; Indels '
                                                                                                                                                                                                                                                         F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                 POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                              DOMAIN 86 91 P
SEQUENCE 875 AA; 98603 MW;
                                                                                                                                                                                                                                                                                                            45.28;
                                                                                 EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U05204; AAA61630.1; -.
                                                                                                                                       EMBL; D45397; BAA08236.1; -. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, 01-FEB-1996 (Rel. 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus
                                                                                                                                                                                                Hypothetical protein.
DOMAIN 86 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFIDE BONDS.
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P48038;
                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                   Matches
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 Gaps
 VERTEBRATE HOST).

-!- MISCELLAREOUS: THE C-TERMINAL RECION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.
-!- SIMILARIEY: CONTAINS 1 TSP TYPE-1 DOMAIN.
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CHARGE RELAK SYSTEM (BY SIMILARITY).
 (BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
 ۲;
 DB 1; Length 431;
 plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 6 PAPKPAPQPGPQPPQ-----PPQPPQPPQPQPQPQPQPEAPAPQPPA 47
 Query Match
45.0%; Score 139.5; DB 1; Length
Best Local Similarity 51.0%; Pred. No. 0.011;
Matches 25; Conservative 1; Mismatches 16; Indels
 INTERCHAIN (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SI
CHARGE RELAY SYSTEM (BY SI
CHARGE RELAY SYSTEM (BY SI
1C015A4E0BCOC668 CRC64;
 CIRCUMSPOROZOITE PROTEIN.
13 X 8 AA TANDEM REPEATS.
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 SERINE PROTEASE
 339 AA
 Circumsporozoite protein precursor (CS)
 PRO-RICH.
 PIR; A25083; OZZOMB.
Interpro; IPRO03067; Cromsprzoite.
Interpro; IPRO00884; TSP1.
 P_1; 1.
CRCMSPRZOITE.
 46422 MW;
 EMBL; M14135; AAA29577.1; -.
 STANDARD;
 Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPR;
SMART; SM00299; TSP1; 1.
 238
431 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=5821;
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 Gaps
 -1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
 Gaps
 Nucleic Acids Res. 18:376-376(1990).
-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE AWTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
 SEQUENCE FROM N.A.
MEDLINE-90221834; Pubmed-2183186;
Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;
"Nucleotide sequence of the Plasmodium berghei circumsporozoite
 2 AKVPPAPK---PAPQPG---PQPPQPPQPPQPPQPQPQPQPGPE-APAPQPPAG 48
 7;
 2 AKVPPAPK---PAPQPG---PQPPQPPQPPQPPQPQPQPQPE-APAPQPPAG 48
 16 X 2 AA TANDEM REPEATS OF P-Q.; E8068A6D11D9551B CRC64;
 Length 339;
 Length 347;
 Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 Score 137.5; DB 1; Leus...
Pred. No. 0.013;
 Indels
 13 X 8 AA REPEATS.
17 X 2 AA REPEATS OF P-Q.
0EC240EE35681AF8 CRC64;
 CIRCUMSPOROZOITE PROTEIN.
 Score 137.5; DB 1;
Pred. No. 0.013;
 347 AA

 Mismatches

 1; Mismatches
 protein gene from the ANKA clone 2.34L.";
Nucleic Acids Res. 18:376-376(1990).
 POTENTIAL.
 PRT;
 Signal
 IPR003067; Crcmsprzoite.
 238 10
37138 MW;
 01-NOV-1991 (Rel. 20, Created)
 PR01303; CRCMSPRZOITE.
 44.48;
 37776 MW;
 falaria; Sporozoite; Repeat;
 44.48;
 EMBL; X17606; CAA35608.1; -
 Query Match
Best Local Similarity 55.6 Matches 30; Conservative
 MART; SM00209; TSP1; 1.
ROSITE; PS50092; TSP1; 1
 STANDARD;
 Conservative
 206 2
339 AA;
 HOST
 347 AA;
 Best Local Similarity
Matches 30; Conserv
 NCBI_TaxID=5823
 CSP_PLABA
P23093;
DOMAIN
SEQUENCE
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 Query Match
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194 ANDPPPPNPNDPAPPQGNNNPQPQPRPQPQPQPQPQPQPQPQPQPQPQPG 247

Search completed: May 7, 2003, 16:48:15 Job time : 6.24361 secs

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 Q9k5g1 bordetella
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 7, 2003, 16:38:52; Search time 27.598 Seconds (without alignments) 403.166 Million cell updates/sec
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 54
 Description
 09alp3 | 09alp3 | 09alq0 | 09k5g7 | 09alp5 | 09k5b7 | 09k5b5 | 09k
 099199 | 091462 | 099859 | 0998192 | 0998593 | 0998593 | 0998593 | 0998595 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 | 0988591 |
 671580
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 671580 segs, 206047115 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 09ALP3
09ALQ0
09K5G7
09ALP5
09K5H5
09L4E2
09K5G9
 Q9ALQ2
Q9K5H3
Q9K5G5
Q9K5H1
 Q9ALP7
 sp_vertebrate:*
sp_unclassified:*
 sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_organelle:*
sp_phage:*
sp_plant:*
 sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
 US-09-855-754B-22
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 sp_rodent:*
 Query
Match Length DB
 sp_virus:*
 SPTREMBL_21:*
 Perfect score:
 Score
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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| 09alq4 bordetella<br>09k5h9 bordetella<br>09k5h7 bordetella<br>09k1y1 bordetella<br>09k1y0 bordetella<br>09ahp0 bordetella<br>09aix8 bordetella | Q953mB bordetella Q956nD bordetella Q956nD bordetella Q956nD bordetella Q9511 bordetella Q9119B bordetella Q9119B bordetella Q9119B bordetella Q9129B pordetella Q9129B pordetella Q9139B pordetella Q9139B pordetella Q9130B pordetella | Q69088<br>Q8w158<br>Q13305<br>Q96v12<br>Q9u115<br>Q8t1y6 | ; 107 AA.<br>ed)<br>sequence update)<br>annotation update)                                   | (Alcaligenes bronchisepticus). beta subdivision; Alcaligenaceae;  0899896; Regions of Pertactin in Bordetella pertussis, and Bordetella bronchiseptica."; ; ct_sup. ct_sup.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | AOA339BFF0EABBC6 CRC64;<br>COTE 310; DB 2; Length 107;<br>red. No. 2.9e-19;<br>Mismatches 0; Indels 0; Gaps 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|-------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Q9ALQ4<br>Q9K5H9<br>Q9K5H7<br>Q9KJY1<br>Q9KJY0<br>Q9AHP0<br>Q9AHP0                                                                              | 0953M8<br>0956N1<br>00956N1<br>0091143<br>0091198<br>009129<br>001823<br>001823<br>001823<br>001823<br>001823<br>001823                                                                                                                                                                                                                                                                                                                                                                                                                                    | Q69088<br>Q8W158<br>Q13305<br>Q9GVJ2<br>Q9ULL5<br>Q8T1Y6 | PRT;<br>Created)<br>Last sequ                                                                | Alcaligene sta subdiv sta subdiv 399896; sgions of artussis,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Score 3 Pred. N                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 44444444                                                                                                                                        | 9055 2<br>9005 2<br>9005 2<br>9007 2<br>9007 2<br>9007 2<br>9008 3<br>11994 11<br>9008 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 54330                                                    | t),                                                                                          | iseptica<br>acteria;<br>PubMed=1<br>Guiso N.<br>Repeated<br>ella para<br>:4815-481<br>AB76449.1<br>99; Perta<br>rtactin;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 217; PRICHEXTENSN<br>1 107 107<br>07 AA; 11073 MW;<br>1101.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; 100.0%; |
| VVVVVVVV<br>900000                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | -W-W-W-W-W                                               | FRELI<br>PRELI<br>20 (Trew<br>22 (Trew<br>(P.168)                                            | a bronch Proteoba 10-518; 10-518; 11: 3389; 11: 3389; 12: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13: 3389; 13 | PR01217; P<br>107<br>107 AA;<br>Similarity<br>4; Conser                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                 | 216<br>216<br>216<br>216<br>216<br>216<br>216<br>216<br>216<br>216                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                          | LT 1<br>23<br>29K5G1<br>09K5G1;<br>01-0CT-2000<br>01-0CT-2000<br>01-UDN-2002<br>Pertactin (P | Bordetella bronchiseptica<br>Bacteria, Proteobacteria,<br>Bordetella.<br>NCBI_TaxID=518;<br>NCBI_TaxID=518;<br>SEQUENCE FROM N.A.<br>STRAIN=SEI;<br>MEDLINR=2035989; PubMed=<br>Boursaux-Eude C., Guiso N<br>"Polymorphism of Repeated<br>pertussis, Bordetella par<br>Infect: Immun. 68:4815-48<br>EMBL, AJ250095; CAB76449.<br>InterPro; IPRO04899; Pert<br>InterPro; IPRO04899; Pert<br>InterPro; IPRO04899; Pert<br>Pfam; PF03212; Pertactin;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PRINTS; PR<br>NON_TER<br>NON_TER<br>SEQUENCE<br>uery Match<br>est Local Si<br>atches 54;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 4 4 4 4 4 4<br>10 10 10 10                               | SUL<br>KSG                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | DR PRIN<br>FT NON_<br>SQ SEQUI<br>Query Me<br>Best Loc<br>Matches                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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164 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQP----PQPQPQPEAPAPQPPAGRELSAA 213
 1 GAKVPPAPKPAPQPPQPPQPPQPPQPQPQPQPQPPQPPAPPQPPAGRELSAA 54
 Length 304;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 1 GAKVPPAPKPAPQPPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 Length 231;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 STRAIN-MBORD591;
MEDLINE-21117018; PubMed-11179374;
Register K.B.;
Royal Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL; AY007267; AAG38443.1; InterPro; IPR003992; pertactin.
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001). EMERE, ANO/072777, AAG38453.1; InterPro; IPR004899; Pertactin. InterPro; IPR004899; Pertact_sup. InterPro; IPR002965; P_rich_extensn.
 0; Indels
 Indels
 23930 MW; 5FB281B95E74678C CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
Query Match
90.2%; Score 279.5; DB 2;
Best Local Similarity 94.4%; Pred. No. 2.3e-16;
Matches 51; Conservative 0; Mismatches 0;
 Score 274; DB 2;
Pred. No. 5.2e-16;
 88.4%; Sco...
92.6%; Pred. No. J...
0; Mismatches
 256 AA
 PRT;
 STRAIN-PV6;
MEDLINE-21117018; PubMed=11179374;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN
 Pfam; PF03212; Pertactin; 1.
 Local Similarity 92.6
Les 50; Conservative
 PRELIMINARY;
 PRELIMINARY;
 231
 Pertactin (Fragment).
 NON_TER 1
NON_TER 231 5
SEQUENCE 231 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 NCBI_TaxID=518;
 Register K.B.;
 Bordetella.
 Query Match
 09ALQ0
 Matches
 RESULT 5
 RESULT 4
 Q9ALP3
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 NX OC ON DETAIL
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 Poursaux Eude C., Guiso N.;

"Polymorphism of Repeated Regions of Pertactin in Bordetella pertuasis, Bordetella parapertussis, and Bordetella bronchiseptica."; princet. Immun. 68:4815.4817(2000).

EMBL: AJ250092; CAB76446.1; ...

InterPro; IPR004899; Pertact_sup.

InterPro; IPR002995; Prich_extensn.

Pfam; PF03212; Pertactin; 1.

PRINTS; PR01217; PRICHEXTENSN.
 Gaps
 1 GAKVPPAPKPAPQPGPPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 54
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Score 287; DB 2; Length 107;
Pred. No. 2.3e-17;
0; Mismatches 0; Indels
 Register K.B.; "Novel Genetic and Phenotypic Heterogeneity in Bordetella
 31759 MW; 3B120CB158FD7474 CRC64;
 107 AA; 11076 MW; C32F321161C9E400 CRC64;
 09ALP7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 304 AA
 107 AA.
 bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AV007273; AAG38449.1;
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin.vir.
Interpro; IPR004899; Pertact.sup.
Interpro; IPR002965; prich_extensn.
 PRT;
 STRAIN-MBORD901;
MEDLINE-21117018; PubMed-11179374;
 PRT;
 MEDLINE-20359389; PubMed-10899896;
 Pfam; PF03212; Pertactin; 1.
PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 PRINTS; PR01484; PRTACTNFAMLY.
NON_TER 1 1
NON_TER 304
SEQUENCE 304 AA; 31759 MW;
 92.68;
 Pertactin (P.68) (Fragment).
 52; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pertactin (Fragment)
 304 AA;
 Query Match
Best Local Similarity
Matches 52; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 NCBI_TaxID=518;
 STRAIN-286;
 NON_TER
SEQUENCE
 Q9K5G4;
 Q9ALP7
 09K5G4
 RESULT O
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Gaps

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RESULT 6 Q9K5G7

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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immus. 68:4815-4817(2000).
EMBL; AJ2500E1; CAB76435.1;
-Interpro; IPR004899; Pertact.gup.
Interpro; IPR002965; P.rich.extensn.
 1 GARAPPAEKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQPPAGRELSAA 72
 1 GAKVPPAFKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
 Length 347;
 Length 107;
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001),
 Indels
 Indels
 36015 MW; D9A4B719E54842EB CRC64;
 167 AA; 11036 MW; 1AC13209D0238107 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P 68) (Fragment).
 Last sequence update)
Last annotation update)
 Ouery Match 83.5%; Score 259; DB 2; L
Best Local Similarity 88.9%; Pred. No. 1.3e-14;
Matches 48; Conservative 0; Mismatches 0;
 Ouery Match
Best Local Similarity 89.1%; Pred. No. 5.8e-15;
Matches 49; Conservative 0; Mismatches 2;
 107 AA
 (TremBlrel. 17, Created)
(TremBlrel. 17, Last seq
(TremBlrel. 21, Last ann
 EMBL, |AY007275, AAG38451.1;
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR004899; pertact_sup.
InterPro; IPR002965; P_rich_extensn.
 MEDLINE-21117018; PubMed-11179374;
 MEDLINE-20359389; Pubmed-10899896;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01484; PRTACTNFAMLY.
 PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
 PRELIMINARY;
 347
 107
 347 AA;
 SEQUENCE FROM N.A.
 Bordetella.
NCBI_TaxID=518;
 01-JUN-2001
01-JUN-2001
01-JUN-2002
 NON_TER
NON_TER
SEQUENCE
 NON_TER
SEQUENCE
 Q9K5H5
 Q9ALP9
 RESULT 8
 RESULT 9
 09K5H5
 Q9ALP9
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 Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).

EMBL; AJ250089; CAB76443.1;
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002865; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
 Gaps
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 54
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 54
 1 GAKVPPAPKPAPQPGPPQPPQPPQPPQPQPQPQPQPPAPPQPPAGRELSAA
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Length 111;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Length 256;
 1; Indels
 5; Indels
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 SEQUENCE 111 AA; 11453 MW; 9B67012D3B9AEECA CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
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 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 1.6e-15;
 111 AA
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 PRT;
 PRT:
 MEDLINE-20359389; PubMed-10899896;
 InterPro; IPR002965; Prich_exterpro; IPR03215; Pertactin; 1. PRINTS; PR01482; PERTACTIN; 1. PRINTS; PR01217; PRICHEXTENSN. NON_TER 1 1 1 NON_TER 256 A8; 26277 MW; 6
 Ouery Match 85.5%;
Best Local Similarity 84.5%;
Matches 49; Conservative
 Best Local Similarity 90.73
Matches 49; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pertactin (Fragment)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-ST. LOUIS;
 Bordetella.
NCBI_TaxID-518;
 NCBI_TaxID=518;
 Bordetella.
 Query Match
 Q9K5G7
 Q9ALP5
 Q9ALP5
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RESULT 7 Q9ALP5

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Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL: AJ250087; CAB76441.1;
-InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Priof_extensn.
PF03212; Pertactin; 1.
 Nationally (New Journal) Strainting Strainti
 1 GAKVPPAPKPAPKPAPQPGPQP-PQP-PQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 111;
 Pertactin (Fragment).

Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

Bordetella.
 82.6%; Score 256; DB 2; Length 122; 87.5%; Pred. No. 9.4e-15; Live 0; Mismatches 5; Indels
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Last sequence update)
Last annotation update)
 82.6%; Score 256; DB 2; Le
87.5%; Pred. No. 8.7e-15;
Live 0; Mismatches 5;
 122 AA.
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 MEDLINE=20359389; PubMed=10899896;
 PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Pertactin (P.68) (Fragment).
 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
 Best Local Similarity 87.5
Matches 49; Conservative
 Query Match 82.6
Best Local Similarity 87.5
Matches 49; Conservative
 PRELIMINARY;
 PRELIMINARY;
 122
 SEQUENCE FROM N.A. STRAIN-16039;
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 NCBI_TaxID=518;
 Pfam; PF0321
 STRAIN-BBCH
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 "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AJ45927; CABB2515.1; InterPro; IPR003992; pertactin.

InterPro; IPR003991; pertactin.

InterPro; IPR003991; pertactin.vir.
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 King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.,
Mooi F.R.;
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 4:
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 83.2%; Score 258; DB 2; Length 911;
89.1%; Pred. No. 3.4e-14;
ive 0; Mismatches 2; Indels
 / Match 83.2%; Score 258; DB 2; Length 200; Local Similarity 89.1%; Pred. No. 9.7e-15; nes 49; Conservative 0; Mismatches 2; Indels
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Novel Genetic and Phenotypic Heterogeneity in Bordetella
 PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTNFAMLY.
SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
 200 200
200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 911 AA
 bronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007271. AAG38447.1; -
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact.up.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
 MEDLINE-21117018; PubMed=11179374;
Register K.B.;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
 49; Conservative
 PRELIMINARY;
 Pertactin (Fragment)
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 NCBI_TaxID=518;
 Bordetella.
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 STRAIN-B14;
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11'5 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
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 Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella bronchiseptica.";

Infect. Immun. 68:4815-4817(2000).

EMBL; AJ250083; CAB76437:1; -.

InterPro; IPR0024899; Pertact_sup.

InterPro; IPR002965; Prich_extensn.

Pfam; PF03212; Pertactin; I.
 Gaps
 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPQPQPQPQPGPEAPAPQPPAGRELSAA 54
 ;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID-518;
 Score 256; DB 2; Length 252;
Pred. No. 1.7e-14;
0; Mismatches 5; Indels
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella
 252
26107 MW; 368C142508D77057 CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Last sequence update)
Last annotation update)
 115 AA.
 252 AA.
 Dronchiseptica Pertactin.";
Infect. Immun. 69:1917-1921(2001).
EMBL: ANON7265, ASG38441.1;
InterPro; IPR004992; Pertactin.
InterPro; IPR004899; Pertact.
InterPro; IPR004899; Prich_extensn.
 01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
 PRT;
 STRAIN-ATCC19395;
MEDLINE-21117018; PubMed-11179374;
 MEDLINE=20359389; PubMed=10899896;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 PRINTS; PR01217; PRICHEXTENSN
 Pfam; PF03212; Pertactin; 1.
 Pertactin (P.68) (Fragment).
 ch 82.6%;
1 Similarity 87.5%;
49; Conservative
 PRELIMINARY;
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Best Local Similarity
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SEQUENCE 252 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Bordetella.
NCBI_TaxID=518;
 Register K.B.;
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Q9K5H3;
 Matches
 RESULT 14
Q9K5H3
 RESULT 13
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 Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immut. 68:4815-4817(2000).
EMBL; AJ250091; CAB76445.1;
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002965; Priof_extensn.
PF03212; Pertactin; I.
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 1 GAKVPPAPKPPAPQPGPQP-----PQP-PQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
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 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 23 GAKAPPAPKPAPQPGPQPPQPPQPP-----PQRQPEAPAPQPPAGRELSAA 70
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Length 105;
 Indels
 NON_TER 1 1
NON_TER 1.05 1.05
SEQUENCE 1.05 AA; 1.0884 MW; 813F1422271962B2 CRC64;
 09K5G5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
81.9%; Score 254; DB 2; L/81.7%; Pred: No. 1.3e-14; Wiematches 5;
 80.0%; Score 248; DB 2; L
85.2%; Pred. No. 3.8e-14;
Live 0; Mismatches 2;
 105 AA.
 PRT;
 Search completed: May 7, 2003, 16:53:17
Job time: 28.598 secs
 MEDLINE-20355389; PubMed-10899896;
 PRINTS; PR01217; PRICHEXTENSN.
 Query Match
Best Local Similarity 81.79
Matches 49; Conservative
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 4, A
Sequence 18,
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/cgn2_6/ptodata/2/pubpaa/0809_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 65-272-160
 US-09-855-754-21
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 SUMMARIES
 Post-processing: Minimum Match 0%
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 Query
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| 0 US-09-904-987-7 | 0 US-09-764-864-967 | US-10-171-384-3   | US-09-976-740-47  | 2 US-10-023-529-47 | 2 US-10-023-523-47 | US-10-067-457-5   | US-09-298-523B-61 | US-09-298-523B-1  | US-09-298-523B-60 | US-09-298-523B-8  | 0 US-09-823-240-2 | 2 US-10-042-417-32 | US-09-298-523B-62 | US-09-298-523B-2  | 0 US-09-815-242-11345 | US-09-976-740-43  | 2 US-10-023-529-43 | 2 US-10-023-523-43 | 0 US-09-791-171-70 | US-09-789-054A-10 | 0 US-09-910-087-21 | 0 US-09-864-761-34988 | 0 US-09-864-761-36844 | US-10-020-215-2   | 0 US-09-823-240-9 |  |
| ~                 | ĭ,                  | 6                 | 6                 | 12                 | 12                 | -                 | 6                 | -                 | 6                 | 6                 | 7                 | 12                 | 6                 | 6                 | 7                     | б<br>Ж            | 3                  | 3                  | 10                 | 6                 | 70                 | ;<br>_                | 1                     | 6                 | <u>-</u>          |  |
| 1543              | 316                 | 82.               | 22(               | 22(                | 22(                | 86.               | 9                 | 69                | 926               | 43                | 80                | 19.                | 70.               | 70.               | 35                    | 236               | 23                 | 238                | 99                 | 29                | 200                | 17                    | 17.                   | 127               | 9                 |  |
| 42.3              | 41.8                | 41.8              | 41.6              | 41.6               | 41.6               | 41.3              | 40.6              | 40.6              | 40.6              | 40.5              | 40.5              | 39.8               | 39.4              | 39.4              | 38.9                  | 38.7              | 38.7               | 38.7               | 38.1               | 37.7              | 37.7               | 37.6                  | 37.6                  | 37.6              | 37.4              |  |
| <br>131           | 129.5               | 129.5             | 129               | 129                | 129                | 128               | 126               | 126               | 126               | 125.5             | 125.5             | 123.5              | 122               | 122               | 120.5                 | 120               | 120                | 120                | 118                | 1117              | 1117               | 116.5                 | 116.5                 | 116.5             | 116               |  |
| 20                | 21                  | 22                | 23                | 24                 | 25                 | 26                | 27                | 28                | 29                | 30                | 31                | 32                 | 33                | 34                | 35                    | 36                | 37                 | 38                 | 39                 | 40                | 41                 | 42                    | 43                    | 44                | 45                |  |

## ALIGNMENTS

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVERTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVERTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMONGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2010-09-10
PRIOR PAPPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 APPLICANT: BOURSAUX-BUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
 Gaps
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 54
 54
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA
 Length 54;
 Indels
 Query Match

100.0%; Score 310; DB 9;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 54; Conservative 0; Mismatches 0;
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-22
 Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 Sequence 21, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 NOS: 24
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver.
RESULT 1
US-09-855-754-22
 RESULT 2
US-09-855-754-21
 SEQ ID NO 22
LENGTH: 54
 TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/855,754
 US-09-855-754-15
 US-09-855-754-4
 SEQ ID NO 15
 Query Match
 Best Local
 Matches
 Matches
 RESULT 5
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 APPLICANT: GUISO-MACLOUF, NICCLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 0.9459-0.206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 APPLICANT: BOUTSATX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
 Gaps
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPPQPQPPQPPQPPAGRELSAA 54
 BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IMMUNOGENIC COMPOSITIONS
 REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
 5
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 52;
 Length 58;
 Score 265; DB 9; Length 58
Pred. No. 6.2e-12;
0; Mismatches 5; Indels
 Indels
 Score 287; DB 9;
Pred. No. 1.9e-13;
 0; Mismatches
TITLE OF INVENTION: REGIONS OF PERTACTIN IN TITLE OF INVENTION: BORDETELLA PRARBERTUSSI TITLE OF INVENTION: BRONCHISEPTICA, THEIR UTITLE OF INVENTION: IMMUNGENIC COMPOSITION; FILE REFERENCE: 03495-0206-00000; CURRENT PELICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
 PRIOR APPLICATION NUMBER: 60/206,969
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-19
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
 Sequence 19, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Sequence 6, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 TITLE OF INVENTION: BRONCHISEPTITIEE OF INVENTION: IMMUNOGENIC FILE REFERENCE: 03495-0206-00000
 ch 92.6%;
1 Similarity 96.3%;
52; Conservative
 sh 85.5%;
L Similarity 84.5%;
49; Conservative
 2000-05-25
 NUMBER OF SEQ ID NOS: 24
 PatentIn Ver.
 Query Match
Best Local Similarity
 Best Local Similarity
Matches 49; Conserv
 PRIOR FILING DATE:
 US-09-855-754-19
 US-09-855-754-6
 SEQ ID NO 21
LENGTH: 52
 ID NO 19
 Query Match
 TYPE: PRT
 TYPE: PRT
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 TITLE OF INVENTION REGIONS OF PERTACTINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTITLE OF INVENTION: IMMUNCERNIC COMPOSITIONS PILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR FILING DATE: 2000-05-25
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: RECIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
FILLE REFERENCE: 03495-0206-00000
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPGPEAPAPQPPAGRELSAA 54
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 Score 265; DB 9; Length 922;
Pred. No. 5.8e-11;
0; Mismatches 5; Indels
 Length 52;
 Score 258; DB 9;
Pred. No. 1.7e-11;
 0; Mismatches
 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 2001-09-10
PRIOR PAPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 922
 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
 ; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-855-754-6
 Sequence 15, Application US/09855754 Publication No. US20020192237A1
 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Sequence 4, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 GUISO-MACLOUF, NICOLE
 83.2%;
89.1%;
 ch
1 Similarity 84.5%;
49; Conservative
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
 49; Conservative
 SEQ ID NOS: 24
 Query Match
Best Local Similarity
 Similarity
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Gaps

us-09-855-754b-22.rapb

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 120,709/9855,754
CURRENT FILING DATE: 2001-09-10
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
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 ;
6
 1 GAKVPPAEKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 49;
 Length 59;
 Length 48;
 Indels
 Indels
 Score 249.5; DB 9;
Pred. No. 6.7e-11;
1; Mismatches 3;
 DB 9;
 Score 248; DB 9; I
Pred. No. 7.2e-11;
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Best Local Similarity 83.6%; Pred. No. 3.6e-10;
Matches 46; Conservative 0; Mismatches 2
 0; Mismatches
 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILLING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOY: 2.1
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-20
 7206,969
) ORGANISM: Borcetella bronchiseptica
US-09-855-754-14
 Sequence 20, Aprlication US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
APPLICANT: BOURSAUX FULDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
 Sequence 14, Application US/09855754 Publication No. | US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
 80.0%;
85.2%;
 Query Match
Best Local Similarity 81.7%;
Matches 49; Conservative
 Ouery Match
Best Local Similarity 85.23
Matches 46; Conservative
 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
 US-09-855-754-16
 US-09-855-754-14
 SEO ID NO 20
 TYPE: PRT
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLIVEPTIDES CONTAINING POLIMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BONDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BONDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
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 Length 911;
 Length 56;
 Score 256; DB 9; Length by Pred. No. 2.4e-11;
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Pred. No. 1.7e-10;
0; Mismatches 2;
 0; Mismatches
 TYPE: PRT ORGANISM: Bordetella bronchiseptica
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US-09-855-754-18
 60/206,969
 PRIOR APPLICATION NUMBER: 60/206,969
 ORGANISM: Bordetella bronchiseptica
 Sequence 16, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 US-09-855-754-18
; Sequence 18, Application US/09855754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLF
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Query Match 82.6%;
Best Local Similarity 87.5%;
Matches 49; Conservative
 Query Match 83.2%;
Best Local Similarity 89.1%;
Matches 49; Conservative
 PRIOR FILING DATE: 2000-05-25
 1000-05-25
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
 NUMBER OF SEQ ID NOT. NUMBER OF SEQ ID NOT. 2. SEQ ID NO 16
SEQ ID NO 16
ENGTH: 59
 PRIOR APPLICATION NUMBER:
 RESULT 8
US-09-855-754-16
 US-09-855-754-4
 SEQ ID NO 18
LENGTH: 56
 TYPE: PRT
 LENGTH:
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Gaps

Gaps

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RESULT 15
US-10-001-873-50
 US-09-855-754-24
 SEQ ID NO 5
LENGTH: 910
 US-09-855-754-5
 LENGIH: 39
 TYPE: PRT
 TYPE: PRT
 SOFTWARE:
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 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AND BRONGHISEPPICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
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 TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARABERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BROWCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NAME: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 54
 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS TITLE OF INVENTION: BONDETELLA PARAPERTENSIS, AND BORDETELLA TITLE OF INVENTION: BONDETHISE OF THEIR USE IN DIAGNOSTICS, AN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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 1 GAKVPPAPKPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 ----POPOPEAPAPOPPAGRELSAA 42
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 Length 52;
 Length 42;
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 Indels
 Score 235; DB 9;
Pred. No. 5.6e-10;
1; Mismatches 1
 Score 216; DB 9;
Pred. No. 8.7e-09;
0; Mismatches 1
 CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-23
 Sequence 17, Application US/09855754
Publication No. US20020192237A1
GENERAL INFORMATION:
 Sequence 23, Application US/09855754 Publication No. US20020192237A1
 CAROLINE
 GUISO-MACLOUF, NICOLE
 69.7%;
75.9%;
 Query Match 75.8%;
Best Local Similarity 85.7%;
Matches 48; Conservative
 PatentIn Ver. 2.1
 Conservative
 APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUF
 NUMBER OF SEQ ID NOS: 24
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
 Query Match
Best Local Similarity
Matches 41; Conserv
 GENERAL INFORMATION
 US-09-855-754-17
 US-09-855-754-23
 SEQ ID NO 17
LENGTH: 52
 SEQ ID NO 23
 TYPE: PRT
 TYPE: PRT
 LENGTH
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
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 ----PQPQPEAPAPQPPAGRELSAA 39
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 39;
 DB 9;
 Query Match 63.1%; Score 195.5; DB 9
Best Local Similarity 70.4%; Pred. No. 1.9e-07;
Matches 38; Conservative 0; Mismatches 1
 Score 216; DB
Pred. No. 1.1e
0; Mismatches
 CURRENT APPLICATION NUMBER: US/09/855,754 CURRENT FILING DATE: 2001-09-10
 FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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PRIOR FILING DATE: 2000-05-25
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
 Sequence 24, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOUSSAUX EUDE, CAROLINE
 Sequence 50, Application US/10001873 Patent No. US20020160388A1
 CAROLINE
Sequence 5, Application US/09855754
Publication No. US20020192237A1
 APPLICANT: GUISO-MACLOUF, NICOLE
 ; ORGANISM: Bordetella pertussis US-09-855-754-5
 69.7%;
75.9%;
 PatentIn Ver, 2.1
 41; Conservative
 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
 1 GAKAPPAPKPAPQPGPOP
 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE,
 NUMBER OF SEQ ID NOS: 24
 NUMBER OF SEQ ID NOS:
 Query Match
Best Local Similarity
Matches 41; Conserv
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us-09-855-754b-22.rapb
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APPLICANT: Recipon, Reverse APPLICANT: Recipon, Reverse APPLICANT: Recipon, Reverse APPLICANT: Chen, Sel-Yu APPLICANT: Chen, Sel-Yu APPLICANT: Liu, Chenghua APPLICANT: Liu, Chenghua APPLICANT: Luu, Chenghua APPLICANT: Luu, Chenghua APPLICANT: Luu, Chenghua APPLICANT: Luu, Chenghua APPLICANT: Luu Compositions and Methods Relating to Lung Specific Genes and Prot FILE REFERENCE: DEX-0275

CURRENT APPLICATION NUMBER: US/10/001,873

CURRENT FILING DATE: 2000-11-20

PRIOR PELLING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/252,496

PRIOR APPLICANT: NUMBER: 60/252,496

PRIOR APPLICANT: DI NOS: 55

SOFTWARE: Patentin version 3.1

SEQ ID NO 50

LENGTH: 1134

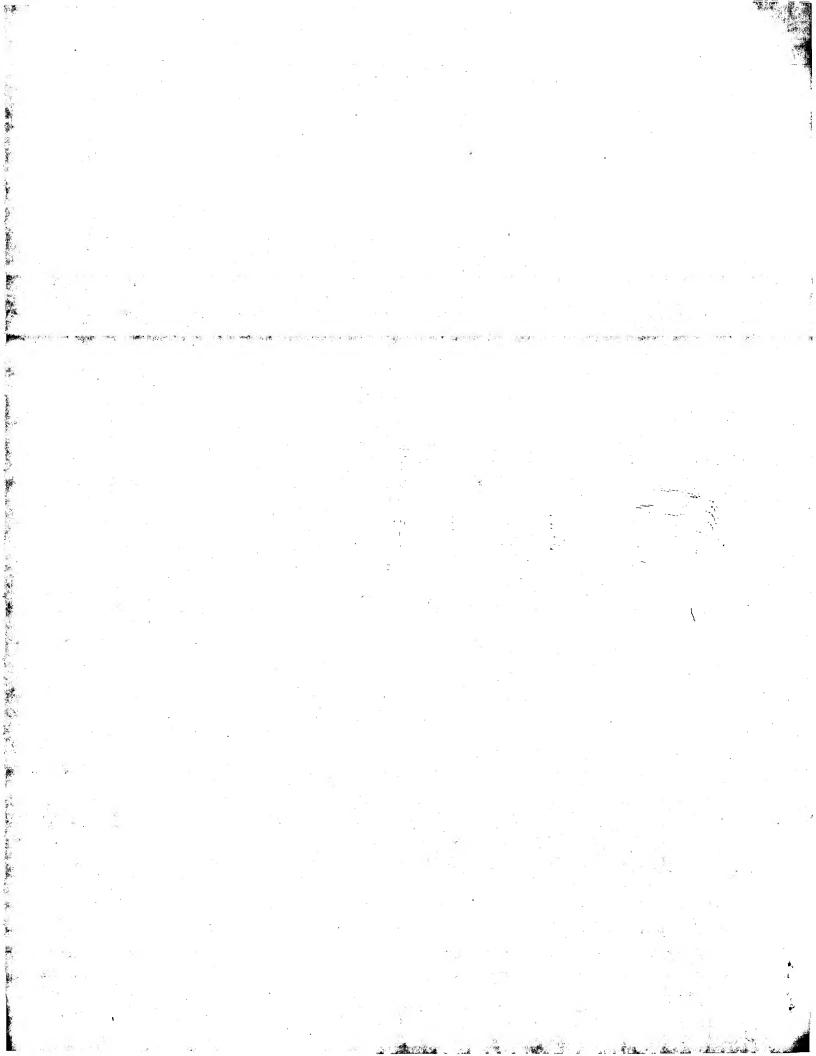
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TYPE: PRT

TYPE: PRT

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US-10-001-873-50
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 310
1 GAKVPPAPKPAPQPGPQPPQ.....QPQPEAPAPQPPAGRELSAA 54
 Description
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283224 seqs, 96134422 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 A47675
A32560
JC2301
T14355
WMBEH6
T10798
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 A34043
 r48814
 US-09-855-754B-22
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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153
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140.5
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| 1.       | 33                                       | 137                                                            | 1 4 4 4<br>1 4 6 6<br>1 4 6 6                          | 1749               | 1000                   | 022058<br>JQ1696<br>S75138                                                                                                                                                       | circumsporozoite p<br>pistil extensin-li<br>hypothetical prote |
|          | υ ω ω<br>4. α. α.                        |                                                                | 3.43                                                   | 129<br>129<br>645  | 700                    | 5093/2<br>A26036<br>A71416                                                                                                                                                       | hypothetical prote<br>procyclic acidic r<br>hypothetical prote |
|          | 36                                       |                                                                |                                                        | 288<br>506         | 77                     | T17737<br>B56201                                                                                                                                                                 |                                                                |
|          | m m .                                    |                                                                |                                                        | 514<br>400         | 777                    | A56201<br>S58222                                                                                                                                                                 | transcription fact<br>PO-rich protein –                        |
|          | 4 4 4                                    |                                                                | 3.5.                                                   | 808<br>143         | 777                    | 149681<br>C72858                                                                                                                                                                 |                                                                |
|          | * **                                     |                                                                | 4 4                                                    | 145                | 77                     | A44418                                                                                                                                                                           |                                                                |
|          | 4 4<br>4 10                              |                                                                |                                                        | 979                | 7 7                    | F95013<br>A35913                                                                                                                                                                 | pneumococcal surfa<br>regulatory factor                        |
|          |                                          |                                                                |                                                        |                    |                        | ALIGNMENTS                                                                                                                                                                       |                                                                |
|          | RESULT<br>S15204                         |                                                                |                                                        |                    |                        |                                                                                                                                                                                  |                                                                |
|          | pertactin<br>N;Alterna                   | tin Bo<br>rnate na                                             | rdetella<br>mes: out                                   | er memb            | rtu                    | ssis<br>e protein P70                                                                                                                                                            |                                                                |
|          | C; Spec                                  | : 07-Apr                                                       | -1994 #8<br>15204: S                                   | paraper<br>equence | re                     |                                                                                                                                                                                  | <pre>#text_change 08-Oct-1999</pre>                            |
|          | ш. 2                                     | L.J.; Do                                                       | ugan, G.<br>5, 409                                     | ; Novotny,         | .yr.                   | P.; Charles, I.G.                                                                                                                                                                |                                                                |
| •        | A;Titl                                   | A; Title: P.70 pertactin, an o'A; Reference number: S15204; M  | pertacti<br>mber: S1                                   | 5204; N            | ute                    | outer-membrane protein from MUID:91251771; PMID:2041476                                                                                                                          | m Bordetella parapertussis: clo<br>6                           |
| . \      | A; Mole                                  | ssion: S<br>scule typ<br>dues: 1-                              | e: DNA                                                 | Ą                  |                        |                                                                                                                                                                                  |                                                                |
|          | A; Cros<br>C; Gene<br>A; Gene            | A)Cross references: EMBL:X54547;<br>C;Genetics:<br>A;Gene: prn | nces: EM                                               | BL:X545            | 47;                    | NID:939761; PIDN:CAA38419                                                                                                                                                        | 8419.1; PID:939762                                             |
|          | C; Key                                   | ords: me                                                       | membrane protein                                       | rotein             |                        |                                                                                                                                                                                  |                                                                |
|          | Query Ma<br>Best Loc                     | J.E                                                            | th<br>Similarity                                       |                    | 85.5%;                 | Score 265; DB 2;<br>Pred. No. 7.8e-11;                                                                                                                                           | 922;                                                           |
|          | Matc                                     |                                                                | ; conse                                                | Conservative       |                        | U; Mismatches 5;                                                                                                                                                                 |                                                                |
|          | d<br>d                                   | 1 GAKV<br>    <br>564 GAKA                                     | PPAFKPA-<br>        <br> <br>                          | 0PGPQPG            | <u> </u>               | GAKVPPAKKAPQPGPQPPOPPOPPOPOPOPOPOPOPOPGPELSAA<br>                                                                                                                                | PAPQPPAGRELSAA 54<br>                <br>PAPQPPAGRELSAA 621    |
|          | RESULT                                   | =                                                              |                                                        |                    |                        |                                                                                                                                                                                  |                                                                |
|          | A47675<br>68K ou                         | ter memb                                                       | rane pro                                               | tein P.            | 89                     | pertactin - Bordetella                                                                                                                                                           | - Bordetella bronchiseptica                                    |
|          | C; Date                                  | 19-Dec                                                         | -1993 #8                                               | proncu<br>equence  | re                     | tica<br>vision 18-Nov-1994 #te                                                                                                                                                   | xt_change 08-Oct-1999                                          |
|          | R; L1,                                   | J., Fair                                                       | weather,                                               | N.F.;              | NOV<br>170             | otny, P.; Dougan, G.;                                                                                                                                                            | G.; Charles, I.G.                                              |
|          | A; Refe                                  | e: Cloni                                                       | ng, nucl                                               | eotide<br>7675; N  | Sed                    | uence and heterologous<br>:92407514; PMID:152751                                                                                                                                 | expression of the protective o $^{0}$                          |
|          | A; Cont<br>A; Acce<br>A; Stat            | ents: CN<br>Ssion: A<br>us: prel                               | 7331<br>47675<br>iminary                               |                    |                        |                                                                                                                                                                                  |                                                                |
|          | A; Mole<br>A; Resi<br>A; Cros<br>A; Note | cule typ<br>dues: 1-<br>is-refere                              | e: nucle<br>911 <l11<br>nces: GB<br/>ce extra</l11<br> | ic acid            |                        | A:Molecule type: nucleic acid<br>A:Residues: 1-911 < L11><br>A:Cross-referenced: A:Residues: NID:939396; PIDN:C.<br>A:Note: sequence extracted from NCBI backbone (NCBIN:113318, | PIDN:CAA38584.1; PID:939397<br>13318, NCBIP:113319)            |
|          | Query Ma<br>Best Loc<br>Matches          | tch<br>al                                                      | 7                                                      | 8<br>8<br>vati     | 13.28;<br>19.18;<br>ve | Score 258; DB 2;<br>Pred. No. 2.2e-10;<br>0; Mismatches 2;                                                                                                                       | Length 911;<br>Indels 4; Gaps 2;                               |
|          | ογ                                       | 1 GAKV                                                         | PPAPKPAP<br>                                           | QPGPQP-            | 8<br>                  | GÄKVPPAPKPAPQPGPOP-PQPPQPPQPPQPQPQPQPGAPAPQPPAGRELSAA                                                                                                                            | 54                                                             |

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RESULT 3 A32560

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R.MGGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; I J. Gen. Virol. 69, 1531-1574, 1988
A.Title: The complete DNA sequence of the long unique region in the genome of herpes A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Reference number: A30083
 A;Accession: I30085
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-3164 <MCG>
A;Residues: 1-3164 <MCG>
C;Genetics: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
C;Genetics:
 targeted to the
 EMBL: AF077000; NID: 93598973; PID: 93598974; PIDN: AAC62959.1
 A;Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699 A;Experimental source: strain HK 10; sub_apeciae Magariensis A;Note: in contrast to the other pherophorins, pherophorins is targeted to C;Keywords: extracellular matrix; glycoprotein; pheromone
 pherophorin-S - Volvox carteri
C;Species: Volvox carteri
C;Dape; 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10798
R;Godl, K; Hallamn, A.; Wenzl, S.; Sumper, M.
R;Godl, K; Hallamn, A.; Wenzl, S.; Sumper, M.
A;Title: Differential targetting of closely related ECM-glycoproteins: The FA;Reference number: 217154; MUID:97162277; PMID:9009264
A;Accession: T10798
A;Accession: T10798
 C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
C;Accession: I30085
 Gaps
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 Gaps
 A.Cross-references: EMBL:AF077000; NID:93598973; PID:93598974; Plun:AMNUOL
A.Experimental source: brain
C.Genetics:
A.Gene: PTP-TD14
C.Function:
A.Description: may be involved in regulating Ha-ras-dependent cell growt
C.Keywords: phosphoric monoester hydrolase
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 5
 4
 Length 3164;
 Length 1494;
 Length 599;
 1 GAKVPPAPKPAPQPGPQPPQPPQP-PQP-PQPQPQPQPQPEAP--APQP 45
 Indels
 6 PAPKPAPQPGPQP-PQP-PQP-PQP-PQPQPQPQPEAPAPQPPAG
 Score 154; DB 2; Le
Pred. No. 0.00094;
1; Mismatches 17;
 9
 DB 1;
 ;Superfamily: varicella-zoster virus gene 22 protein
 5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОР
 Score 162; DB 2;
Pred. No. 0.00058;
3; Mismatches 10
 Score 157.5; DB Pred. No. 0.002; 2; Mismatches
 UL36 protein - human herpesvirus 1 (strain 17)
 Query Match
Best Local Similarity 57.1%;
Matches 24; Conservative
 50.8%;
ilarity 72.3%;
Conservative
 52.3%;
ilarity 65.3%;
Conservative
A; Residues: 1-1494 <CAO>
 A; Molecule type: mRNA
A; Residues: 1-599 <GOD>
 Best Local Similarity
Matches 34; Conserv
 Query Match
Best Local Similarity
Matches 32; Conserv
 Query Match
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 Nypothetical 47.8K protein - Pneumocystis carinii
N'Alternate names: ORF-3
C:Species: Pneumocystis carinii
C:Species: Pneumocystis carinii
C:Date: 06-Jan-1995 #text_change 28-May-1999
C;Date: 06-Jan-1995 #text_change 28-May-1999
C;Date: 06-Jan-1995 #text_change 28-May-1999
C;Date: 06-Jan-1995 #text_change 28-May-1999
N'A akamura, Y.
N'A Radan, M.; Nakamura, Y.
N'A
 PI
 protein-tyrosine-phosphatase (EC 3.1.3.48) TD14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14355
R;Cao, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, K.R.; Graham, R.M.; Zhou, M. B;Cao, L.; Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase contains a BRO1-like domain and A;Reference number: 218004; MUID:98361981; PMID:9694860
A;Accession: T14355
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
 C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Dates: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Caccesion: A32560
R;Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Titles: Molecular cloning and characterization of protective outer membrane protein P.(A):Reference number: A32560; MUID:89264462; PMID:2542937
 A;Molecule type: DNA
A;Residues: 1-430 <WAD>
A;Cross-references: GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06706.1; PID:d1007278;
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 Gaps
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 PPAPKPAPQPGP-----QPPQPPQPPQPPQ-------PQPQPQPQPE-APAPQP 45
 A;Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054 A;Note: it is uncertain whether Met-1 or Met-3 is the initiator
 C; Keywords: membrane protein
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-910/Product: outer membrane protein P6.9 #status predicted <MAT>
 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP---PQRQPEAPAPQPPAGRELSAA 610
 19;
 12;
 54
 Score 171.5; DB 2; Length 430;
Pred. No. 5.3e-05;
5; Mismatches 5; Indels 19
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPGPAPPAPPAGRELSAA
 Length 910;
 Indels
 - Bordetella pertussis
 Score 216; DB 2; I
Pred. No. 1.2e-07;
); Mismatches 1;
 Pred. No. 1.26
0; Mismatches
 outer membrane protein P.69 precursor
 69.78;
75.98;
 ch 55.3%;
1 Similarity 52.5%;
32; Conservative
 41; Conservative
 Query Match
Best Local Similarity
Matches 41; Conserv
 Query Match
Best Local Similarity
 A; Residues: 1-910 <CHA>
 A; Molecule type: DNA
 318 P 318
 46 P.46
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Indels

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Length 1952;

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hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
 C.Species: Owenia| fusiformis
C.Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
 A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
 5 РРАРКРАНРОРСРОРРОРРОРРОРРОРРОРОРОРОР
 Score 151.5; DB 2;
Pred. No. 0.0034;
4; Mismatches 14;
 48.9%;
56.8%;
 Ouery Match
Best Local Similarity 55.6%;
Matches 25; Conservative
 Conservative
 A)Cross-references: GB:M32217
A;Accession: B34043
A;Molecule type: DNA
A;Residues: 59-136 cBA2>
A;Cross-references: GB:M32217
 Query Match
Best Local Similarity
Matches 25; Conserv
 A; Molecule type: DNA
A; Residues: 1-141 <BAK>
 A; Molecule type: DNA
A; Residues: 1-487 <FAR>
 A; Gene: NCSP:15E6.220
A; Molecule type: DNA
 A; Map position: 2
A; Introns: 281/3
 C;Genetics;
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 RESULT, 11
 RESULT 12
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 C; Species: Volvox carrer:
C; Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Accession: A33647, Renzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A; Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A; Reference number: A33647; MUID:90094551; PMID:2689458
 C; Species: Neurospora crassa
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C; Accession: T40804
R; Schulte, U: Algn, V: Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
 chitinase (EC 3.2.1.14) precursor - beet
C;Species: Beta vulgaris (beet)
C;Date: 28-0ct-1996 sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: S51939; S72315; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.
Plant Mol. Biol. 27, 211-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
A;Reference number: S51939; MUID:95170004; PMID:7865792
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 A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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 A; Molecule type: DNA
A; Residues: 1-439 <BER>
A; Residues: 1-639 <BER: A; Cross-references: EMBL:X79301; NID:9488730; PID:9488731
A; Note: the authors translated the codon TGC for residue 416 as Gly A; Accession: S72315
 4;
 Length 439;
 Length 485;
 PPAPKPAPQPGPQPPQP----PQPPQPPQPQPQPQPGPAPAPQPPAGR 49
 17; Indels
 hypothetical protein 15E6.220 [imported] - Neurospora crassa
 5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРОР 46
 C; Superfamily: plant chitinase homology
C; Keywords: giycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26439/Product: chitinase #status predicted <MAT>
F;183-423/Domain: plant chitinase homology <PCH>
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 Score 153; DB 2;
Pred. No. 0.00093;
1; Mismatches 17;
 sulfated surface glycoprotein 185 - Volvox carteri
 ch 49.4%;
1 Similarity 57.1%;
24; Conservative
 A; Reference number: 224541
A; Accession: T48814
A; Status: preliminary
 A; Molecule type: mRNA
A; Residues: 191-397 <BER2>
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
 A; Introns: 248/1; 300/2
 Query Match
 Query Match
 Best Local
 C; Genetics:
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C;Accession: A34043; B34043
R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized by the repetitio
A;Reference number: A90159; MUID:90147742; PMID:2105723
 nuclear protein EBNA2 - human herpesvirus 4
C;Species: |human herpesvirus 4, Epstein-Barr virus
C;Species: |human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 *Requence_revision 19-Mar-1997 *text_change 20-Jun-2000
C;Accession: S42442; S32988; S42447
R;Sample, J.; Hummel, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: A;Reference number: S42440; MUID:86259739; PMID:3460083.
 A;Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
R;Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad., Sci. U.S.A. 81, 7632-7636, 1984
A;Title: UZ region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen A;Reference number: S42447; MUID:85063846; PMID:6209719
A;Accession: S42447
 ö
 Gaps
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 Length 141;
 PPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGR 49
 Score 151; DB 2;
Pred. No. 0.00048;
0; Mismatches 20
 A;Molecule type: mRNA
A;Residues: 1-487 <SAM>
R;Farrell, p.J:
submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S32998
 A; Melecule type: DNA
A; Residues: 1-88, 'PPP', 89-487 <DAM>
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Best Local Similarity
Matches 23; Conserva
 completed: May 7
 A; Residues: 1-383 <KUR>
 A;Gene: all3916
 Query Match
 C; Genetics:
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 R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. submitted to the EMBL Data Library, August 1991
A;Description: Cloning and characterization of a proline-rich gene expressed specificall A;Reference number: S16748
 R.Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUID:93342083; PMID:8341705
 :Title: Developmental expression of tobacco pistil-specific genes encoding novel extens: Reference number: P00474; MUID:93005740; PMID:1392607
 C. Reywords: cell wall; extracellular matrix; fertilization; glycoprotein F;1-19/Domain: signal sequence *status predicted <SIG>F;20-209/Product: cysteine-rich extensin-like protein 1 *status experimental <MAT>F;146/Binding site: carbohydrate (Asn) (covalent) *status predicted
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 C;Date: 26-May-1994 *sequence_revision 26-May-1994 #text_change 01-Dec-2000 C;Accession: A48232; PQ0475; S24617 R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
 Species: Brassica napus (rape)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
A;Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
 Gaps
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 A;Molecule type: mRNA
A;Residues: 1-209 <WUA>
A;Cross-references: GBL-L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
 16;
 ó
 Length 449;
 extensin-like protein 1 precursor - common tobacco
 47.4%; Score 147; DB 2; Length 209;
ilarity 42.4%; Pred. No. 0.0012;
Conservative 6; Mismatches 12; Indels
 Length 487;
 Score 148; DB 2; Length 48
Pred. No. 0.002;
1; Mismatches 21; Indels
 Cross-references: EMBL:214020; NID:919918; PID:919919
Experimental source: stigma, style; strain Petit Havana SRI
Superfamily: glutelin
 4 VPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRE 50
 A; Cross-references: EMBL: X60376; NID: 922596; PID: 922597
 12;
 DB 2;
 Score 147.5; DB
Pred. No. 0.002;
4; Mismatches
 proline-rich protein - rape (fragment)
C; Species: Brassica napus (rape)
C; Date: 13-3n-1995 #sequence_revision
C; Accession: S1678 R; Roster, G.D.; Blundell
 47.78;
53.28;
 47.68;
 44.48;
 Query Match
Best Local Similarity 53.2%
 Conservative
 Molecule type: mRNA
Residues: 39-209 <GOL>
 Query Match
Best Local Similarity
Matches 25; Conserv
 A; Molecule type: mRNA
A; Residues: 1-449 <ROB>
 Best Local Similarity
Matches 28; Conser
 Status: preliminary
 A; Accession: S16748
 Accession: A48232
 Accession: PQ0475
 44 QPP 46
 cysteine-rich
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 A;Cross-references: GB:BA000019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179
A;Experimental source: strain PCC 7120
 Gaps
 47
-PPQPPQPQPQPQPEAPAPQPPA
 ó;
 Length 383;
 .18; Indels
 5 РРАРКРАРОРСРОРРОРРОРРОРРОРОРОРОРОРОР
 Score 146; DB 2;
Pred. No. 0.0022;
1; Mismatches 18
 7, 2003, 16:55:40
 47.1%;
54.8%;
 23; Conservative
```

### GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

protein search, using sw model OM protein - 7, 2003, 16:31:28 ; Search time 28.0579 Seconds (without alignments) 256.453 Million cell updates/sec Мау Run on:

US-09-855-754B-22 Title: Perfect score:

310 1 GAKVPPAPKPAPQPGPOPPQ..........0PQPEAPAPQPPAGRELSAA 54 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_101002:\* Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:

/gcgdata/geneseg/genesegp-emb1/AA1990. SIDS2/gcgdata/geneseq/genesegp-emb1/AA1989 /SIDS2

'gcgdata/geneseg/genesegp-emb1/AA1993 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 gcgdata/geneseq/geneseqp-embl/AA1994 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199

'gcgdata/geneseq/geneseqp-emb1/AA1996.DAT 'gcgdata/geneseg/genesegp-emb1/AA1999 .DS2/gcgdata/geneseq/geneseqp-emb1/AA1995 /gcgdata/geneseq/geneseqp-emb1/AA19

/SIDS2/gcgdata/geneseq/genesegp-emb1/AA2002.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000

# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the retal score distribution.

| and is delived by analysis of the total score distribution. | -         |
|-------------------------------------------------------------|-----------|
| score                                                       |           |
| roral                                                       | SUMMARIES |
| 9                                                           | SUM       |
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| allalysts                                                   |           |
| à                                                           |           |
| ner ran                                                     | •         |
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|        |       | *     |                 |    |          |                     |
|--------|-------|-------|-----------------|----|----------|---------------------|
| Result |       | Query |                 |    |          |                     |
| No.    | Score |       | Match Length DB | DB | ΩI       | Description         |
| 1      | 310   | 100.0 | 54              | 23 | AAE16201 | B. bronchiseptica   |
| 7      | 287   | 92.6  |                 | 23 | AAE16200 | B. bronchiseptica   |
| m      | 265   | 85.5  |                 | 23 | AAE16198 | B. bronchiseptica   |
| 4      | 265   | 85.5  |                 | 13 | AAR25578 | Bordetella parape   |
| S      | 265   | 85.5  |                 | 23 | AAE16185 | Bordetella parape   |
| 9      | 258   | 83.2  |                 | 23 | AAE16194 | B. bronchiseptica   |
| 7      | 258   | 83.2  |                 | 12 | AAR14320 | Pertactin antigen   |
| ω      | 258   | 83.2  | 911             | 13 | AAR26503 | · prn proteins. Box |
| 0      | 258   | 83.2  |                 | 23 | AAE16183 | Bordetella bronch   |
| 10     | 256   | 82.6  |                 | 23 |          | B hronchisentica    |

| Pertactin antigen B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica B. bronchiseptica |                                          | huma<br>huma<br>beet<br>poly<br>poly<br>poly                   | Human polypeptide Human polypeptide Herbicidally activ Arabidopsis thalia Novel human diagno Novel human diagno Arabidopsis thalia Arabidopsis thalia | Ser-Pro-Pro-Pro ge<br>Mouse ischaemic co<br>Plasmodium berghei<br>Sugarcane proline<br>Streptococcus pneu<br>Glutamic acid rich<br>Arabidopsis thalia<br>Arabidopsis thalia                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|-------------------------------------------------------------------------------------------------------------|------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AAR14321<br>AAE16195<br>AAE16199<br>AAE16196<br>AAE16193<br>AAE16203                                        |                                          | ABG0987<br>AAR2815<br>AAO0441<br>AAO0207<br>AAO0457<br>ABB7006 | AACOUZIL24 2 AACOUZO36 3 ABB93838 1 AAG49660 2 ABG17580 2 AAG21580 2 AAG22949                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|                                                                                                             |                                          |                                                                |                                                                                                                                                       | 76 23<br>261 23<br>272 10<br>329 23<br>1749 22<br>1252 21                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 82.3<br>80.0<br>79.8<br>76.6                                                                                | 59.7<br>553.7<br>551.0<br>50.3           |                                                                | 6 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 255<br>254<br>247.5<br>237.5                                                                                | 216<br>216<br>195.5<br>158<br>158<br>156 | 155.5<br>155.5<br>151<br>151<br>147.5                          | 143.5<br>143.141<br>140.5<br>139.5                                                                                                                    | 135 136<br>135 136<br>136 135<br>137 5<br>137 5<br>138 5 |
| 11<br>12<br>14<br>15                                                                                        | 17<br>18<br>19<br>20<br>22               | 23<br>25<br>26<br>28<br>29<br>29                               | 32<br>32<br>34<br>35<br>36<br>37                                                                                                                      | 38<br>39<br>44<br>44<br>44<br>45<br>45<br>45                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

### ALIGNMENTS

AAE16201 standard; peptide; 54 AA AAE16201; AAE16201

RESULT 1

26-MAR 2002 (first entry)

B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica.

W0200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457.

25-MAY # 2000; 2000US-206969P.

XXXXXXXXXXXXX

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

```
The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
 pertactin outer membrane protein region II
Claim 26; Fig 1c; 47pp; English.
```

;; Length 54; 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA Indels ch 100.0%; Score 310; DB 23; 1 Similarity 100.0%; Pred. No. 8.8e-17; 54; Conservative 0; Mismatches 0; Query Match Best Local Similarity 54 AA; Sednence Matches g

Gaps

AAE16200 standard; peptide; 52 AA 26-MAR-2002 (first entry) AAE16200; **AAE16200** RESULT 

bronchiseptica strain II-8 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica

WO200190143-A2 29-NOV-2001.

25-MAY-2000; 2000US-206969P 23-MAY-2001; 2001WO-EP06457

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C; WPI; 2002-097639/13. Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of

```
;;
 Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\rm II}\,.
 5
 54
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA
 Length 52;
 Indels
 .;
0
 Score 287; DB 23;
Pred. No. 4.4e-15;
0; Mismatches 0;
 AAE16198 standard; peptide; 58 AA
 Match 92.6%;
Local Similarity 96.3%;
hes 52; Conservative
 Query Match
Best Local S
Matches 52
 Sequence
 AAE16198
 RESULT
 ð
 셤
 20228
```

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. Guiso-maclouf N, Boursaux-eude C; 23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P. Bordetella bronchiseptica. (INSP ) INST PASTEUR. 29-NOV-2001.

B. bronchiseptica strain II-6 pertactin outer membrane protein region II.

26-MAR-2002 (first entry)

AAE16198;

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods 

WPI; 2002-097639/13.

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

58 AA; Sequence

4 DB 23; Length 58; Query Match 85.5%; Score 265; DB 2: Best Local Similarity 84.5%; Pred. No. 2e-13; Matches 49; Conservative 0; Mismatches

ä

54 õ

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.

Bordetella parapertussis

Reg 10n Region

Location/Qualiflers
254..304
/note= "Pertactin region I" .
764.621
/note= "Pertactin region II"

WO200190143-A2 29-NOV-2001

Bordetella parapertussis pertactin outer membrane protein, p.70.

AAE16185 standard; Protein; 922 AA.

RESULT 5 AAE16185

26-MAR-2002 (first entry)

AAE16185;

RESULT AAR2557

```
A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (#P95*) is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
 Location/Qualifiers
35..643
/label= P70
260..262
/note= "motif associated with cell-cell adhesion"
 /note= "contains 9 direct repeats of Pro-Gln-Pro" 712..714
/note= "motif associated with cell-cell adhesion"
 Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
 Whooping cough; P70 antigen; P95 precursor protein; vaccination.
 Length 922;
 266..285
/note= "contains 5 direct, tandem repeats"
 Score 265; DB 13; Length 92
Pred. No. 1.5e-12;
0; Mismatches 5; Indels
 Bordetella parapertussis P95 antigen precursor.
AAR25578 standard; Protein; 922 AA.
 Claim 1; Fig 1; 20pp; English.
 ch 85.5%;
1 Similarity 84.5%;
49; Conservative
 91WO-GB02302
 90GB-0027901
 (WELL) WELLCOME FOUND LID.
 (first entry)
 Bordetella parapertussis.
 575..612
 WPI; 1992-250033/30.
N-PSDB; AAQ26509.
 Query Match
Best Local Similarity
Matches 49; Conserv
 922 AA;
 Binding-site
 Binding-site
 23-DEC-1991;
 21-DEC-1990;
 08-JAN-1993
 WO9211292-A
 09-JUL-1992
 Charles IG;
 AAR25578;
 Sequence
 Protein
 Region
 Region
```

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

N-PSDB; AAD25442

25-MAY-2000; 2000US-206969P 23-MAY-2001; 2001WO-EP06457

(INSP ) INST PASTEUR

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Disclosure; Page 34; 47pp; English

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ä
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin attibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affility chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis
 Gaps
 621
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPQPPAPPQPPAGRELSAA
 4;
 Length 922;
 Indels
 ů,
 Score 265; DB 23;
Pred. No. 1.5e-12;
0; Mismatches 5;
 Ş
 standard; peptide; 52
 85.5%;
84.5%;
 Query Match
Best Local Similarity 84.59
Matches 49; Conservative
 922 AA;
 AAE16194
 AAE16194;
 Sequence
 AAE16194
 RESULT
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Gaps

4;

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapartussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3354-3448 (1989).
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 B. bronchiseptica; P.68; outer membrane protein; piglet; probe; atrophic rhinitis; alternative cleavage.
 Pichia microorganism transformants - for production of Bordetella pertactin antigens for whooping cough vaccines
 Score 258; DB 12;
Pred. No. 4.8e-12;
0; Mismatches 2;
 35..632
/label= P.68
266..279
/label= Repeat_region
 Location/Qualifiers
 AAR26503 standard; Protein; 911 AA.
 Disclosure; Fig 1B; 38pp; English
 (WELL) WELLCOME FOUNDATION LTD.
 repeat
 578..580
/label- repeat
 581..583
/label= repeat
 87..589
/label= repeat
 599..601
/label- repeat
 repeat
 repeat
 83.2%;
 91WO-GB00487
 (first entry)
 584..586
/label- re
 570..572
/label- re
574..576
 Bordetalla bronchiseptica
 Query Match 83.2
Best Local Similarity 89.1
Matches 49; Conservative
 'label-
 Clare JJ, Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14319.
 911 AA;
 28-MAR-1991;
 prn proteins
 02-APR-1990;
 12-MAR-1993
 WO9115571-A.
 17-0CT-1991
 Sequence
 AAR26503;
 Protein
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Pept1de
 Region
 RESULT 8
 AAR26503
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 g
 ä
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloological fluids, such as human or other animal cells, as well as bloological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
 B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Gaps
 4:
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPPQPEAPAPQPPAGRELSAA 54
 Length 52
 Indels
 Pertactin; Pichia; B. pertussis; B. parapertussis.
 83.2%; Score 258; DB 23;
89.1%; Pred. No. 6.2e-13;
tive 0; Mismatches 2;
 Location/Qualifiers
 AAR14320 standard; Protein; 911 AA
 Guiso-maclouf N, Boursaux-eude C;
 Claim 26; Fig 1c; 47pp; English.
 266..270
/label= repeat
271..275
/label= repeat
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 20-JAN-1992 (first entry)
 (first entry)
 Bordetella bronchiseptica
 Query Match
Best Local Similarity 89.1:
Matches 49; Conservative
 Bordetella bronchiseptica
 Pertactin antigen P.68.
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 52 AA;
 WO200190143-A2
26-MAR-2002
 29-NOV-2001
 AAR14320;
 Sequence
```

;;

Gaps

Indels

Peptide Peptide

AAR14320 RESULT

ð 셤

Length 911;

for

Peptide Pept1de

Region

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(outer membrane protein) or their fragments. Pertactin (PRN) is used as waccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquent to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
 B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Polypeptides, containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 The present invention relates to Bordetella bronchiseptica pertactin
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPPAPAPQPPAGRELSAA 54
 Length 911;
 83.2%; Score 258; DB 23;
89.1%; Pred. No. 4.8e-12;
iive 0; Mismatches 2;
 ΰ
 Disclosure; Page 28; 47pp; English
 Guiso-maclouf N, Boursaux-eude C;
 Ŕ
 Guiso-maclouf N. Boursaux-eude
 AAE16197 standard; peptide; 56
 23-MAY-2001; 2001WO-EP06457.
 25-MAY-2000; 2000US-206969P.
 25-MAY-2000; 2000US-206969P.
 (first entry)
 Bordetella bronchiseptica
 Best Local Similarity 89.1
Matches 49; Conservative
 (INSP) INST PASTEUR.
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
N-PSDB; AAD26440.
 WPI; 2002-097639/13.
 Sequence 911 AA;
 WO200190143-A2.
 26-MAR-2002
 29-NOV-2001
 AAE16197;
 Query Match
 RESULT 10
 AAE16197
 QQ .
ò
 5,
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.68.
 The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the entire P.94 sequence.
 Gaps
 Bordetella bronchiseptica pertactin outer membrane protein, p.68
 DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhinitis in pigs
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 83.2%; Score 258; DB 13; Length 911;
llarity 89.1%; Pred. No. 4.8e-12;
Conservative 0; Mismatches 2; Indels
 'note= "Pertactin region II"
 254..299
/note= "Pertactin region I"
559..610
 260..262
/label- RGD_tripeptide
701..703
/label- RGD_tripeptide
 Repeat_region
 Location/Qualifiers
 AAE16183 standard; Protein; 911 AA.
 Claim 1; Fig 1; 28pp; English.
 23-MAY-2001; 2001WO-EP06457
 92WO-GB00561
 91GB-0006568
 (WELL) WELLCOME FOUND LTD
 (first entry)
 Bordetella bronchiseptica
 WPI; 1992-366258/44.
N-PSDB; AAQ34566.
 Local Similarity
les 49; Conserv
 911 AA;
 WO200190143-A2
 27-MAR-1992;
 27-MAR-1991;
 26-MAR-2002
 15-0CT-1992.
 29-NOV-2001
 409217587-A
 Charles IG;
```

Sequence

Query Match

Best Loc Matches

AAE16183;

RESULT 9 **AAE16183** 

g

ò

Region Region

Key

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Gaps

4,

91WO-GB00487.

```
Pichla microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
 The 46 Xs represent amino acids missing in the specification
 Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
 Disclosure; Fig 1C; 38pp; English.
 (WELL) WELLCOME FOUNDATION LTD.
 Claim 26; Fig 1c; 47pp; English.
 Clare JJ, Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14320.
 28-MAR-1991;
 02-APR-1990;
 26-MAR-2002
 29-NOV-2001.
 Sequence
 AAE16195;
 Pichia
 RESULT 12
AAE16195
 ŏ
 g
 Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiquens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
 Gaps
 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 54
 2;
 Score 256; DB 23; Length 56;
Pred. No. 9.2e-13;
0; Mismatches 5; Indels
 The present invention relates to Bordetella bronchiseptica
 Indels
 Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
 pertactin outer membrane protein region II
 Location/Qualifiers
 Æ
 579..581
/label= ...
 26; Fig 1c; 47pp; English.
 AAR14321 standard; Protein; 922
 /label= repeat
610..612
/label= repeat
 266..270
/label= repeat
 repeat
 repeat
 repeat
 repeat
 repeat
 repeat
 repeat
 repeat
 Query Match 82.6%;
Best Local Similarity 87.5%;
Matches 49; Conservative (
 20-JAN-1992 (first entry)
 11..285
1abel=
 label re
 //1..275
//abel= re
 76..280
[abel= re
 86..588
'label= re
 575..577
'label= re
 583..585
/label= re
 592..594
'label= re
 195..597
Tabel - re
 Bordetella parapertussis
 ..600
 56 AA;
 WO9115571-A.
 AAR14321;
 Sequence
 Peptide
 Pept1de
 Peptide
 eptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Peptide
 Claim
 AAR1432
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3
 B. bronchiseptica strain II-3 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Gaps
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQP---PQPQPQPQPQPEAPAPQPPAGRELSAA
 4
 Length 922;
 Indels
 5
 Score 255; DB 12;
Pred. No. 8.2e-12;
0; Mismatches 5;
 Guiso-maclouf N, Boursaux-eude C;
 AAE16195 standard; peptide; 60 AA
 Query Match 82.3%;
Best Local Similarity 84.5%;
Matches 49; Conservative (
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 Bordetella bronchiseptica.
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
922 AA;
 WO200190143-A2.
```

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as

17-0CT-1991

and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal clais, such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. Pertactin antibody is useful for treating Bordetella infections vaccine. I 88888888888888888

60 AA; Sequence

Gaps . 9 Length 60; Indels Score 254; DB 23; Pred. No. 1.4e-12; 0; Mismatches 5; 81.9%; 81.7%; Conservative Query Match Best Local Similarity 49; Matches

'n

1 GAKVPPAPKPAPQPGPQP-----PQP-PQPPQPPQPQPQPQPEAPAPQPPAGRELSAA

RESULT 13

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AAE16199 standard; peptide; 48 AAE16199;

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(first entry) 26-MAR-2002

B. bronchiseptica strain II-7 pertactin outer membrane protein region II.

outer membrane protein; vaccine; Bordetella infection; Pertactin; PRN; outer membrane protein; vaccin therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica,

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic composition

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vectine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiqens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiqens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antiqens can be used for qualitative or quantitative determination of Bordetella in materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica present invention relates to Bordetella bronchiseptica pertactin outer membrane protein region ii. pertactin The

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Gaps

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Indels

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AAE16193 standard; peptide; 49

RESULT 15

셤

AAE16193 ID AAE1

48 AA; Seguence

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ä
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affility chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

 B. bronchiseptica strain II-4 pertactin outer membrane protein region II.

 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Gaps
 9
 1 САКУРРАРКРАРОРСРОРРОРРОРРОРРОРРОРОРОРОРОРЕАРАРОРРАСКЕТSAA 54
 Length 53;
 Length 48;
 Indels
 23;
 Score 247.5; DB 23;
Pred. No. 3.8e-12;
0; Mismatches 2;
 DB 23;
Score 248; Db 2.,
 Pred. No. 3.26
0; Mismatches
 Boursaux-eude C;
 Ź
 Claim 26; Fig 1c; 47pp; English.
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 79.8%;
87.5%;
 85.2%;
 25-MAY-2000; 2000US-206969P.
 23-MAY-2001; 2001WO-EP06457
 26-MAR-2002 (first entry)
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 Query Match 79.8
Best Local Similarity 87.5
Matches 49; Conservative
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 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 Best Local Similarity
Matches 46; Conserv
 53 AA;
 Guiso-maclouf N,
 WO200190143-A2
 29-NOV-2001
 Sequence
 AAE16196;
 Query Match
 RESULT 14
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AAE16193;
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26-MAR-2002 (first entry)

B. bronchiseptica strain II-1 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P.

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. 

49 AA; Sequence

Gaps 76.6%; Score 237.5; DB 23; Length 49; 83.6%; Pred. No. 2e-11; Live 0; Mismatches 2; Indels 7, Conservative Query Match Best Local Similarity Matches 46; Conserv

5

1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54

ò

1 GAKAPPAPKPAPQPGPQPGPQPPQPPQP-----PQRQPEAPAPQPPAGRELSAA 49 셤

Search completed: May 7, 2003, 16:47:11 Job time: 29.0579 secs

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APPLICANT: CLARE, JEFFREY
 YEAST
 Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative
 COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
 SEQUENCES:
 NUMBER OF
 US-08-460-269C-6
 RESULT 1
à
 Sequence 6, Appli
Sequence 4, Appli
Sequence 2, Appli
Patent No. 5202236
 520236
 Appl1
Appl1
 Appl
 i pp l
 ; Search time 8.92334 Seconds (without alignments) 178.054 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 Patent No.
Patent No.
 Seguence 2
 Sequence 1
 Sequence
 Sequence
Sequence
Sequence
Sequence
Sequence
 Seguence
 Sequence
 Sequence
Sequence
Sequence
Sequence
 Sequence
Sequence
 GAKVPPAPKPAPQPGPPQPPQ.......QPQPEAPAPQPPAGRELSAA
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: /cgn2_c/ptodata/1/laa/PCTUS_COMB.pep:*
: /cgn2_c/ptodata/1/laa/PCTUS_COMB.pep:*
 GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
 US-08-961-083-160
US-08-929-417-2
US-08-429-817-2
US-09-041-886-28
US-09-041-886-29
US-09-041-886-30
US-09-041-886-31
US-09-041-886-31
US-08-453-265-6
US-08-453-265-6
US-08-453-265-6
US-08-56-419-21
US-08-56-419-21
US-08-56-6419-21
US-08-56-6411-1
US-08-109-841-2
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US-08-460-6354-21
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-09-281-476-21
-09-095-443-2
 -08-460-269C-6
-08-460-269C-4
-08-460-269C-2
 Total number of hits satisfying chosen parameters:
 262574 seqs, 29422922 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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length: 2000000000
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Match Length
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3144
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3144
33
 BLOSUM62
 Minimum DB seq
Maximum DB seq
 Perfect score:
 scoring table:
 216
133.5
133
132.5
 132
131.5
131.5
131
 Score
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
 Result
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 Appl1
Appl1
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 Gaps
 Sequence 2,
Sequence 2,
Sequence 2,
Sequence 2,
 Sequence Seq
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Sequence
Sequence
 Sequence
 4
 OF HETEROLOGOUS PROTEIN IN
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-01-1995
ATTORNEY,ASENT INFORMATION:
REFERENCE/DOCKET NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELEPHONE: (703) 243-6410
 DB 4; Length 922;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
 Indels
 5;
 US-09-179-558-66
US-09-314-268-149
US-09-314-268-149
US-08-476-5098-4
US-09-227-420-4
US-08-465-746-2
US-08-467-852A-3
US-08-246-656-2
 Score 265; DB 4;
Pred. No. 4e-16;
0; Mismatches
 -08-247-491A-3
 US-08-319-795-2
US-08-468-985-2
 -08-312-949-2
-08-072-070-2
 ALIGNMENTS
 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-460-269C-6
 TITLE OF INVENTION: EXPRESSION
 Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
 TELEFAX: (703) 243-5410
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGHH: 922 amino acids
TYPE: amino acid
TOPOLOGY: linear
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 12;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 54
 Length 331;
 DB 4; Length 910;
 1; Indels
 APPLICANT: MAGGH, KATHY J.:ANDERSON, DAVID M.:STRAUSBERG, SUSAN L.:MCCANDLISS, RUSS;WEI, TENA:FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
 APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
 5 PPAP--KPAP----QPGPQPPQPPQPPQPPQPQP--QPQPEAPAPQPP
 DB 6;
 Pred. No. 4.1e-05;
1; Mismatches 15
 Score 216; DB 4
Pred. No. 7e-12;
0; Mismatches
APPLICATION NUMBER: US/08/460, 269C
 43.1%; Score 133.5; 51.0%; Pred. No. 4.1
 REFERENCE/DOCKET NUMBER: Popov-2 TELECOMMUNICATION INFORMATION:
 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOY-1986
APPLICATION NUMBER: 650,128
 NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 93,456
APPLICATION NUMBER: 933,945
 (703) 243-6410
 LENGTH: 910 amino acids
 FILING DATE: 02-Jun-19
ATTORNEY/AGENT INFORMATION:
 FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
 SEQUENCE CHARACTERISTICS
 69.7%;
 FILING DATE: 13-SEP-1984
 Query Match
Best Local Similarity 75.9°
Matches 41; Conservative
 TELEPHONE: (703)
 INFORMATION FOR SEQ ID NO:
 TYPE: amino acid
 TOPOLOGY: linear
 Conservative
 NUMBER OF SEQUENCES: 39
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 Query Match
Best Local Similarity
Matches 26; Conserva
 FELEFAX:
 5202236
 ;Patent No. 5202236
 , SEQ ID NO:37:
LENGTH: 331
 5202236-37; Patent No.
 5202236-37
 520236-3
 RESULT 5
 PROTEIN
 PROTEIN
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 Gaps
 559 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQP---PQRQPEAPAPQPPAGRELSAA 610
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRELSAA 54
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
 83.2%; Score 258; DB 4; Length 911; llarity 89.1%; Pred. No. 1.6e-15; Conservative 0; Mismatches 2; Indels
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 STREET: 2200 Clarendon Blvd., Suite 1400
 APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
 Sequence 4, Application US/08460269C
Patent No. 6197548
 Sequence 2, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 LENGTH: 911 amino acids
 ATTORNEY/AGENT INFORMATION:
 - CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS
 INFORMATION FOR SEQ ID NO: 4:
 ZIP: 22201
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 TYPE: amino acid
 CITY: ARLINGTON
 USA
 COUNTRY: USA
 Query Match
Best Local Similarity
Matches 49; Conserva
 STATE: VA
 STATE: VA
 US-08-460-269C-2
 RESULT 3
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Gaps

Gaps

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SEQUENCES:
 TOPOLOGY:
 COMPUTER:
 US-08-929-417-2
 RESULT, 8
 ò
 Gaps
 Gaps
 Sequence 160, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
 ö
 DB 4; Length 641;
 Score 133; DB 6; Length 334;
Pred. No. 4.6e-05;
1; Mismatches 20; Indels
 APPLICANT: Burnham, Martin K.
TITLE OF INVENTION: No. 5928895el IGA Fc Binding Protein
 16; Indels
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 5 РРАРКРАРДРСРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРРА 47
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
 Score 132.5; DB Pred. No. 9e-05; 5; Mismatches
 SSEE: Human Genome Sciences, Inc. T: 9410 Key West Avenue Rockville
 APPLICATION NUMBER: US/08/961,083
 ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
 Sequence 2, Application US/08929417
Patent No. 5928895
GENERAL INFORMATION:
 42.78;
52.98;
 Query Match
Best Local Similarity 51.2%;
Matches 22; Conservative
FILING DATE: 13-SEP-1984
 Query Match
Best Local Similarity 52.9
Matches 27; Conservative
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-961-083-160
 STRANDEDNESS: single
 amino acid
 STATE: Maryland
 20850
 LENGTH: 334
 ADDRESSEE:
 08-961-083-160
 COUNTRY:
 RESULT 7
US-08-929-417-2
 SEQ ID NO:3
 5202236-3
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Gaps
 .,
6
 APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER! OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
 1 GAKVPPARKPAPQPGPQP-----PQPPQPPQPPQPQPQPQPQPAPAPQ 44
 Length 351;
 Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION, NUMBER: US/08/246, 982A
FILING DATE: May 20, 1994
 13;
 Score 132; DB 2;
Pred. No. 5.8e-05;
6; Mismatches 13
 OPERATION SYSTEM: DOS
SOFTWARE: FESTSED for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/929,417
 28,354
HER: P50545
 Sequence 16, Application US/08246982A
Patent No. 5686288
 60/027,030
 REFERENCE/ĎOCKET NUMBER: PE
TELEMOMUNICÁTION INFORMATION:
TELEPHONE: 215/994-2252
TELEFAX: 215/994-2222
 42.6%;
48.1%;
 3: Diskette
IBM Compatible
 FILING DATÉ: 10-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATIÓN NUMBER: 28,
 24-SEP-1996
 351 amino acids
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acid.
 CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
 Query Match 42.6
Best Local Similarity 48.1
Matches 25; Conservative
 FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDER: 66
FILING DATE: 24-SEP-15
APPLICATION NUMBER: 60
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STRANDEDNESS: double
 COMPUTER READABLE FORM:
 CITY: C. STATE: PA COUNTRY: USA COUNTRY: USA TE: 19103-2793
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 GENERAL INFORMATION:
 MEDIUM TYPE:
 JS-08-246-982A-16
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 CITY: San Dies STATE: California COUNTRY: United St. 2IP: 92122
 STATE: Calt
 FILING DATE:
 ADDRESSEE:
 TOPOLOGY:
 US-09-041-886-29
 US-09-041-886-28
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 Gaps
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42.4%; Score 131.5; DB 1; Length 3119;
Best Local Similarity 54.0%; Pred. No. 0.00044;
Matches 27; Conservative 3; Mismatches 17; Indels 3;
 Score 131.5; DB 1; Length 3119;
Pred. No. 0.00044;
3; Mismatches 17; Indels 3:
 APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
 6 PAPKPAPQPGPPQPPQPPQPPQPQPQPQPEAPAPQP--PAGRELSA 53
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 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 Kessler, Goldstein & Fox
 NAME: Goldstein, Jorge, A.
REGISTRATION WUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 311-2600
TELEFAX: (202) 311-2540
INFORMATION FOR SEQ ID NO: 16:
 APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
 COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-453-265-16; Sequence 16, Application US/08453265; Patent No. 5693757; Patent No. 5693757;
 1: Sterne, Kessler, (
1100 New York Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
 TELECOMMUNICATION INFORMATION TELEPHONE: (202) 371-2600
 Best Local Similarity 54.08;
Matches 27; Conservation
 3119 amino acids
 SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
 ATTORNEY/AGENT INFORMATION:
 ; MOLECULE TYPE: protein US-08-246-982A-16
 CORRESPONDENCE ADDRESS:
 amino acid
 Linear
 Washington
 amino acid
 linear
 CLASSIFICATION:
 ADDRESSEE:
 FOPOLOGY:
 US-08-453-265-16
 TOPOLOGY:
 STREET:
 STATE:
 셤
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Length 513;
 TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
 6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRE 50
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides, and Methods of Use
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
 Score 131; DB 4;
Pred. No. 9.9e-05;
0; Mismatches 21;
 Sequence 29, Application US/09041886 Patent No. 6235872
; Sequence 28, Application US/09041886; Patent No. 6235872; GENERAL INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carthryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
 Query Match 42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
 TELEPHONE: (619) 535-900
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
 : 513 amino acids
amino acid
 STATE: California
COUNTRY: United States
ZIP: 92122
 MOLECULE TYPE: peptide US-09-041-886-28
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Gaps
 Gaps
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 ö
 APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
 Length 589;
 Sequence 31, Application US/09041886

Patent No. 6235372

GENERALITORNATION:
APPLICANT: Redesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
 6 PAPKPAPUPGPQPPQPPQPPQPQPQPQPQPQPEAPAPQPPAGRE 50
 41 РРРРРРРРРОПРОРРОДОРПИРОВОВРЕРРРРРРР 85
 6 PAPKPAPOPGPOPPOPPOPPOPOPOPOPOPOPOPGAPAPOPPAGRE 50
 41 РРРРРРРРОПРОРРОДАОРІЛЬОРОРРРРРРРРРРРРР
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 Score 131; DB 4;
Pred. No. 0.00011;
 Goldstein & Fox
 0; Mismatches
 0; Mismatches
 Pred. No
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 6, Application US/08246982A Patent No. 5686288
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RECISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 31:
 : Sterne, Kessler, (1100 New York Avenue
 Query Match
42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
 : 589 amino acids
amino acid
 United States
 Matches 24; Conservative
 SEQUENCE CHANACTERISTICS
 ; MOLECULE TYPE: peptide US-09-041-886-31
 CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, K
 linear
 Washington
 SILL
CITY: Su.
STATE: Callic
COUNTRY: Unit
TO 92122
 FILING DATE
 US-09-041-886-31
 TOPOLOGY:
 US-08-246-982A-6
 Patent No.
 RESULT 13
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 Db
 Gaps
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 Query Match 42.3%; Score 131; DB 4; Length 530; Best Local Similarity 53.3%; Pred. No. 0.0001; Matches 24; Conservative 0; Mismatches 21; Indels
 Score 131; DB 4; Length 552;
Pred. No. 0.00011;
 6 PAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRE 50
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell 6 Flores LLP
 STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/041,886
YSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFRAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 29:
 NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/041,886
 Sequence 30, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-901
TELEPA: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
 42.3%;
 SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
 ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
 ; MOLECULE TYPE: peptide US-09-041-886-29
 Inear
 linear
 Query Match
Best Local Similarity
 CITY: San Diego
 CLASSIFICATION:
 FILING DATE:
CLASSIFICATION:
 TOPOLOGY:
 RESULT 12
US-09-041-886-30
 TOPOLOGY:
 US-09-041-886-30
 STREET:
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Search completed: May 7, 2003, 16:57:30 Job time: 12.0142 secs.
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 Gaps
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 GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
 Score 131; DB 1; Length 3144;
Pred. No. 0.00049;
0; Mismatches 21; Indels
 6 РАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРЕАРАРОРРАСТЕ 50
 CITY: Washington
STATE: D.C.
COUTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
 SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
YITORNEY FACENE
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
 AUTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELERONE: (202) 371-2560
INFORMATION FOR SEQ ID NO: 6: SEQUENCE HARACTERISTICS:
LENGTH: 3144 amino acids
TYPE: amino acids
 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ODTWARE: PatentIn Polace
 ATTORNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTATION UNDHER: 36,203
REFERENCE/DOCKET NUMBER: 0609,
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6:
 Sequence 6, Application US/08453265 Patent No. 5693757
 Query Match
Best Local Similarity 53.3%;
Matches 24; Conservative
 SEQUENCE CHARACTERISTICS:
LENGTH: 3144 amino acids
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 amino acid
 US-08-246-982A-6
COUNTRY:
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Gaps
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 Score 131; DB 1; Length 3144; Pred. No. 0.00049; O; Mismatches 21; Indels
 6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPQPEAPAPQPPAGRE 50
 Query Match 42.3%;
Best Local Similarity 53.3%;
Matches 24; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-453-265-6
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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2003, 16:31:49; Search time 5.0494 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

US-09-855-754B-21 298 1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA 52 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|           |        | Description | Q03035 bordetella | P24328 bordetella | P14283 bordetella | P21997 volvox cart | P10220 herpes simp |            | P40603 brassica na |           | _        |            |            |           |        | Q64467 mus musculu | Q83949 orgyia pseu |           |           | Q9fpq6 chlamydomon |          | _          | PO4723 triticum ae | P41467 autographa | P10323 homo sapien | P42859 mus musculu | P22670 homo sapien | _          | P41479 autographa | P58840 homo sapien | P08001 sus scrofa | O60885 homo sapien | P09791 trypanosoma | Q9p2y4 homo sapien | Q05859 mus musculu |
|-----------|--------|-------------|-------------------|-------------------|-------------------|--------------------|--------------------|------------|--------------------|-----------|----------|------------|------------|-----------|--------|--------------------|--------------------|-----------|-----------|--------------------|----------|------------|--------------------|-------------------|--------------------|--------------------|--------------------|------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES |        | αī          | PERT_BORBR        | PERT_BORPA        | PERT_BORPE        | SSGP_VOLCA         | TEGU_HSV11         | YPRO_OWEFU | APG_BRANA          | MOZ_HUMAN | EBN2_EBV | EXLP_TOBAC | ACRO_RABIT | APG_ARATH | HD_RAT | G3PT_MOUSE         | Y066_NPVOP         | CSP_PLABE | CSP_PLABA | GP1_CHLRE          | HD_HUMAN | MOT8_MOUSE | GDA3_WHEAT         | Y066_NPVAC        | ACRO_HUMAN         | HD_MOUSE           | RFX1_HUMAN         | SEPA_EMENI | Y091_NPVAC        | ACRL_HUMAN         | ACRO_PIG          | BRD4_HUMAN         | PARB_TRYBB         | 2219_HUMAN         | FM14_MOUSE         |
|           |        | 8           | н                 | -                 | ч                 | Н                  | Н                  | -          | -                  | Н         | Н        | -          | -          | -         | -      | -                  | -                  | -         | -         |                    | -        | -          | -                  | -                 | -                  | -                  |                    | -          | ~                 | ч                  | -                 | -                  | -                  | -                  | -                  |
|           |        | Length      | 911               | 922               | 910               | 485                | 3164               | 141        | 449                | 2004      | 487      | 426        | 431        | 534       | 3110   | 440                | 875                | 339       | 347       | 555                | 3144     | 565        | 282                | 808               | 421                | 3119               | 979                | 1790       | 224               | 232                | 415               | 1362               | 129                | 722                | 1206               |
| æ         | Query  | Match       | 86.9              | 85.9              | 72.8              | 49.3               | 48.8               | 48.7       | 48.5               | 47.7      | 47.3     | •          | ٠          | 44.5      |        | •                  |                    | ٠         |           | 43.5               | ٠        | •          | 42.6               | ٠                 | 42.3               | 42.3               | 42.1               |            | •                 | 41.9               | ٠                 | 41.9               | 41.8               | 41.8               | 41.8               |
|           |        | Score       | . 259             | 256               | 217               | _                  | 145.5              | 145        | 144.5              | 142       | 141      | 133.5      | 132.5      | 132.5     | 131.5  | 131                | 131                | 129.5     | 129.5     | 129.5              | 128      | 127.5      | 127                | 127               | 126                | 126                | 125.5              | 125.5      | 125               | 125                | 125               | 125                | 124.5              | 124.5              | 124.5              |
|           | Result | S           | 7                 | 7                 | ო                 | 4                  | S                  | 9          | 7                  | 8         | 6        | 10         | 11         | 12        | 13     | 14                 | 15                 | 16        | 17        | 18                 | 19       | 20         | 21                 | 22                | 23                 | 24                 | 25                 | 26         | 27                | 28                 | 58                | 30                 | 31                 | 32                 | 33                 |

| 005860 mus musculu | P08469 trypanosoma | P14918 zea mays (m       | P02831 mus musculu<br>Oqumpf homo asotler | P05142 mus musculu<br>006432 neisseria a | P05143 mus musculu<br>Q63943 mus musculu |  |
|--------------------|--------------------|--------------------------|-------------------------------------------|------------------------------------------|------------------------------------------|--|
| FMN1_MOUSE         | PARI_TRYBB         | EXTN_MAIZE<br>KPC1 TRIRE | HXA3_MOUSE                                | PRP2_MOUSE<br>TONB_NEIGO                 | PRP3_MOUSE<br>MEFD_MOUSE                 |  |
|                    |                    |                          |                                           | רה                                       |                                          |  |
| 1468               | 143                | 267                      | 443                                       | 261                                      | 296<br>514                               |  |
| 41.8               | 4.4                | 41.4                     | 8 0 4                                     | 4.0                                      | 40.4                                     |  |
| 124.5              | 123.5              | 123.5                    | 121.5<br>  121                            | 120.5                                    | 120.5                                    |  |
| 34                 | 36                 | 38                       | 410                                       | 42                                       | 44                                       |  |

### ALIGNMENTS

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Query Match
 SEQUENCE
 REPEAT
REPEAT
 DOMAIN
 REPEAT
 DOMAIN
 PERT_BORPE
 Matches
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioliformatics and the EMEL OUTSTAILS.

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 5
 STRAIN-CN2591;
MEDLINE-91251771; PubMed-2041476;
Li L.J., Dougan G., Novotny P., Charles I.G.;
I. J.O. pertactin, an outer-membrane protein from Bordetella parapertussis: cloning, nucleotide sequence and surface expression in Escherichia coll...
 MOI. MICTODIOI. 5:409-417(1991).
-I- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
 Gaps
 SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Outer membrane.
DISERSE: MAY COMPRIBUTE TO THE DISERSE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 CELL ATTACHMENT SITE (INVOLVED IN
 3
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 52
 DB 1; Length 911;
 Bordetella parapertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Score 259; DB 1,
-4 NO. 9.8e-10;
2; Indels
 01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
 3 (APPROXIMATE).
7 X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
 P.95.
PERTACTIN (P.70).
 922 AA
 Pred. No. 9.86
0; Mismatches
 Signal; Virulence; Repeat. 34 POTENTIAL.
 POTENTIAL
 IPR003991; pertactin_vir.
 PIR; S15204; S15204.
PIR; S14659; S14659.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last ann
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTUFAMLY.
 M
 Pfam; PF03212; Pertactin; 1.
 86.9%;
92.5%;
 EMBL; X54547; CAA38419.1; -.
 EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
 93995
 Conservative
 STANDARD;
 911 AA;
 CONCENTRATIONS
 Local Similarity
 SEQUENCE FROM N.A.
701
266
266
271
271
570
 NCBI_TaxID-519;
 Outer membrane;
 PERT_BORPA
P24328;
 46;
 Bordetella
 nterPro;
 SEQUENCE
 Query Match
 CHAIN
PROPEP
SITE
 REPEAT
REPEAT
 SIGNAL
 DOMAIN
 DOMAIN
 REPEAT
 CHAIN
 PERT_BORPA
 Matches
 RESULT
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 FFFFFS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
 ;
 Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.; "Structure of Bordetella pertussis virulence factor P.69 pertactin."; Nature 381:90-92(1996).
 MEDINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
 Gaps
 -1- SUBCELLULAR LOCATION: Outer membrane.
-1- DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1- MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
 X 3 AA APPROXIMATE REPEATS OF P-Q-P. 3DF7BC58D4712478 CRC64;
 22
 X 5 AA TANDEM REPEATS OF G-A-V-P
 -I- FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.
 Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
ADHESION TO VARIOUS EUKARYOTIC CELL
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQP--QPQPPAPQPPAGRELSAA
 ;
9
 Length 922;
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Score 256; DB 1; Length 92
Pred. No. 1.5e-09;
0; Mismatches 3; Indels
 01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2007 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
 (APPROXIMATE)
 910 AA
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 Gen. Microbiol. 138:1697-1705(1992).
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 PRT;
 EMBL; J04560; AAA22980.1; ALT_SEQ.
 REVISIONS TO 264 AND 332.
MEDLINE-92407514; Pubmed-1527510;
 x
6
 MEDLINE=96196517; PubMed=8609998;
 95178 MW;
 85.98;
 84.5%;
 49; Conservative
 STANDARD;
 290
270
275
280
285
 Bordetella pertussis.
 -!- SUBUNIT: MONOMER.
 276
281
575
922 AA;
 Local Similarity
 CONCENTRATION
 NCBI_TaxID=520;
 bronchiseptica
 PRN OR OMP69A
 STRAIN=CN2992
 PERT_BORPE
P14283;
 Bordetella.
```

PRO-RICH

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228
260
2'85 AA;
 Best Local Similarity
Matches 32; Conserv
 SEQUENCE FROM N.A.
 MCBI_TaxID=10299;
 Best Local Sim
 TEGU_HSV11
P10220:
 SEQUENCE
 SEQUENCE
 Query Match
 Query Match
 Repeat.
 DOMAIN
 YPRO_OWEFU
 ø
 RESULT 5
 RESULT 6
 STT
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 g
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
 1;
 cellular compartment.";

Cell Biol. 109:3493-3501(1989),

FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONDMENT CRESCHESOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE
COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS.

RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

FTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
 Gaps
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Magariensis / HKLO;
MEDLINE-90094551; PubMed-268458;
Extl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of
 LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3067;
 CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
 10;
 5 (APPROXIMATE).
5 X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
 Length 910;
 1; Indels
 Score 217; DB 1;
Pred. No. 3.4e-07;
0; Mismatches 1,
 PERTACTIN (P.69).
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
 (APPROXIMATE).
 Outer membrane; Signal; Virulence; Repeat.
 Glycoprotein; Sulfation; Hydroxylation.
 POTENTIAL
 InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03312; Pertactin; 1.
 PRT;
 PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRIACTNFAMLY.
 93452 MW;
 72.8%;
78.8%;
 EMBL; X51616; CAA35953.1; -.
 HYDROXYPROLINE RESIDUES.
 41; Conservative
 STANDARD;
PIR; A32560; A32560.
 276
281
286
579
579
910 AA;
 Query Match
Best Local Similarity
Matches 41; Conserv
 PIR; A33647; A33647
 Volvox carteri
 SSGP_VOLCA
P21997;
 REPEAT
DOMAIN
SEQUENCE
 CHAIN
PROPEP
SITE
 DOMAIN
REPEAT
REPEAT
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 SIGNAL
 REPEAT
 CHAIN
 SSGP_VOLCA
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 Gaps
 Gaps
 MEDILINE-88274337; PubMed-2839594; McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P.; "The complete DNA sequence of the long unique region in the genome
 herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCION: TEGUNENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
 Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
 ŝ
 ö
 Length 3164;
 2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
 Length 485;
 Indels
 Indels
 295 POLY-PRO.
50436 MW; A52216400A031421 CRC64;
 PAPKPAPQPGPQP-PQP-PQP-PQPQPQPGAPAPQPPAG 46
 Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
 48.8%; Score 145.5; DB 1;
71.1%; Pred. No. 0.017;
tive 2; Mismatches 6;
 16;
 5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРЕАРАРОРР 44
 Score 147; DB 1;
Pred. No. 0.0036;
 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virlon protein UL36).
 YPRO_OWEFU STANDARD; PRT; 141 AA. P21260; P21201; Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-NOY-1995 (Rel. 32, Last annotation update) Wypothetical proline-rich protein (Fragment). Owenia fusiformis.
 PRT; 3164 AA
 1; Mismatches
 PIR; 130085; WMBEH6.
InterPro; IP3005210; Herpes_UL36.
Pfam; PF03585; Herpes_UL36; 1.
 49.38;
 EMBL; X14112; CAA32311.1; -.
 Similarity 57.5%;
 Conservative
 Conservative
 STANDARD;
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ZN_FING
 DOMAIN
 DOMAIN
 DOMAIN
 qq
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 ö
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 Gaps
 Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.; "Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.":
Blochem. Blophys. Res. Commun. 166:66-73(1990).

 -i- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.

 01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
 ö
 Score 145; DB 1; Length 141;
Pred. No. 0.002;
0; Mismatches 19; Indels
 9EFB6A3AB28EEA15 CRC64;
 15745 MW; B294E884D152BDB9 CRC64;
 H-T-H MOTIF (POTENTIAL).
 5 PPAPKPAPQPGPPQPPQPPQPPQPQPQPGPEAPAPQPPAGR 47
 48.7%; Score ... 55.8%; Pred. No. 0.00z;
 449 AA.
 BY SIMILARITY.
 POTENTIAL.
 Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
 POLY-PRO
 protein; DNA-binding.
 InterPro; IPR001087; Lipase_GDSL.
 MEDLINE-90147742; PubMed-2105723;
 Ψ.
 01-FEB-1995 (Rel. 31, Created)
 EMBL; X60376; CAA42924.1; -.
Oweniidae; Owenia
 48779
 24; Conservative
 STANDARD;
 428
 Brassica napus (Rape)
 PIR; A34043; A34043.
PIR; B34043; B34043.
 132
428
449 AA;
 141 AA;
 Best Local Similarity
Matches 24; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=6347;
 MATURATION.
 Hypothetical p
NON_TER
DOMAIN
 PIR; S16748;
 01-FEB-1995
01-NOV-1995
 APG_BRANA
P40603;
 APG OR CEX
Sabellida;
 ACT_SITE
SEQUENCE
 DNA_BIND
NON_TER
 SEQUENCE
 Query Match
 APG_BRANA
 RESULT
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 use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Gaps
 46
 67
 15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Monocytic leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 3 KVPPAPKPAPQPGPQPPQPPQ------PPQPPQPPQPQPQPPAG
 translocation; Zinc-finger; Repeat;
 15;
 Length 449;
 Indels
 DB 1;
Score 144.5; DB Pred. No. 0.0049; 3; Mismatches 1:
 PHD-TYPE 1.
PHD-TYPE 2.
 C2HC-TYPE.
POLY-GLU.
 POLY-GLU.
POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
 InterPro; IPR001386; Histone_HI/H5.
InterPro; IPR001717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Ffam; PF00628; PHD; 2.
Ffam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00549; PHD; 2.
PROSITE; PS01359; ZE_PHD_1; 1.
PROSITE; PS01359; ZE_PHD_2; 2.
Proto-oncogene; Chromosomal transloca
 SEQUENCE FROM N.A. MEDLINE-96376968; PubMed-8782817;
 3;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUN-2002 (Rel. 41, Last anno
 EMBL; U47742; AAC50662.1; -. Genew; HGNC:13013; ZNF220.
 48.5%;
 Conservative
 STANDARD;
 (Human)
 Similarity
 NCBI_TaxID=9606;
 Nuclear protein
 MIM; 601408; -
 Homo sapiens
 Query Match
Best Local Simi
Matches 28;
 MOZ_HUMAN
Q92794;
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Query Match
 SIGNAL
 REPEAT
 REPEAT
 EXLP_TOBAC
 ACRO_RABIT
 RESULT 10
 RESULT 11
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 ö
 MEDLINE-84270667; PubMed-6087149;
Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glbson T.J., Haffull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
 OF LMP-1.
-I- SUBCELLUTAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
 J. Virol. 65:2545-2554(1991).
-!- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
 Gaps
 MEDLINE-90266473; PubMed-2161130;
Petti L., Sample C., Kieff E.;
Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
 TRANSFAC; T01618; -
Transcription regulation; Activator; Nuclear protein; DNA-binding;
 BREAKPOINT FOR TRANSLOCATION TO FORM
 Cohen J.I., Wang F., Kleff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential
domains for transformation and transactivation.";
J. Virol. 65:2545-2546(1991).
 4:
 Length 2004;
 X 2 AA TANDEM REPEATS OF R-G.
DEF40D7F8ED61D1A CRC64;
 12; Indels
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
 MW; 9FFBBAC3792854BA CRC64;
 44
 5 РРАРКРАРОРСРОРРОР-РОРРОР---РОРОРОРОРЕАРАРОРР
 Score 142; DB 1;
Pred. No. 0.02;
 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
EBNA-2 nuclear protein.
 487 AA
 1; Mismatches
 GLN/PRO-RICH.
 SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
 MET-RICH
 MOZ-CBP
 PRT;
 EMBL; V01555; CAA24877.1; ALT_INIT.
 MEDLINE-91202599; PubMed-1850028;
 52544 MW;
 Similarity 61.4%;
27; Conservative
 2004 AA; 225054
 Phosphorylation; Repeat.

DOMAIN 345 356

SEQUENCE 487 AA; 5254
 STANDARD;
 -! - PTM: PHOSPHORYLATED.
 1704
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10377;
1411
1593
1643
1897
1546
 EBN2_EBV
P12978;
 SEQUENCE
 Query Match
 DOMAINS
 DOMAIN
DOMAIN
SITE
 BYRF1.
 Matches
 EBN2_EBV
 RESULT
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 ö
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 PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
 Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Nicotiana.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
51A495CC94017812 CRC64;
 ö
 Length 426;
 2 AKVPPAPRPAPRPAPGPQPPQPP-----QPPQPPQPQPQPQPEAPAPQPP 44
 Score 141; DB 1; Length 487;
 23; Indels
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPQPQPQPEAPAPQPPAGRE 48
 01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
 Interpro; IPR000419; Pollen_Ole_e_I.
Pfam; PF01199; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
 DB 1;
 Pred. No. 0.0084;
 44.8%; Score 133.5; DB 50.9%; Pred. No. 0.022; ive 1; Mismatches ...
 Ą.
 Ą
 1; Mismatches
 426
 431
 PRT;
 PRT;
 Created)
 44278 MW;
47.3%;
 EMBL; Z14019; CAA78397.1; -.
 Conservative
 STANDARD;
 Conservative
 STANDARD;
 178
310
426 AA;
 Best Local Similarity
Matches 24; Conserv
 Best Local Similarity
Matches 27; Conserv
 NCBI_TaxID-4097;
 POLLINATION.
 24;
 JQ1696;
 01-JUN-1994
 ACRO_RABIT
P48038;
 EXLP_TOBAC
 CARBOHYD
 Query Match
 CHAIN
 REPEAT
REPEAT
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 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 APG_ARATH
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 -!- CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
-!- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
 STRAIN-New Zealand white; TISSUE-Testis;
MEDLINE-9436861; Pubmed-8086468;
Richardson R.T., O'Rand M.G.;
Richardson R.T., O'Rand M.G.;
Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";
Biochim. Biophys. Acta 1219:215-218(1994).
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SINTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_LHS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine procease; Glycotchin; Zymogen; Sperm; Signal.
 ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY)
 CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
 Score 132.5; DB 1; Length 431;
Pred. No. 0.025;
); Mismatches 19; Indels 11;
 INTERCHAIN (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY)
BY SIMILARITY
BY SIMILARITY
 1C015A4E0BC0C668 CRC64;
 -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 01-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Acrosin precursor (EC 3.4.21.10).
 SERINE PROTEASE
 BY SIMILARITY.
 SIMILARITY
 SIMILARITY
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
 PRO-RICH.
 BY
Created)
 46422 MW;
 EMBL; U05204; AAA61630.1; -.
 44.58;
 DISULFIDE BONDS.
 Query Match
Best Local Similarity
Matches 25; Conserv
 431 AA;
 SEQUENCE FROM N.A.
 MEROPS; S01.223;
 4SSP; P00763;
 ACROSOME
 DOMAIN
DISULFID
 DISULFID
 DISULFID
CARBOHYD
CARBOHYD
 ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
 DISULFID
 DISULFID
 SIGNAL
 PROPEP
 CHAIN
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Theologis A., Ecker J.R., Palmo, J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palmo, J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao G., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Milischer J., Miranda M., Nguyen M., Nerman W.C., Osborne B.I.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu Utterback T., Van Aken S., Vaysberg M., Wysotskala V.S., Walker M.,

" "Sequence and analysis of chromosome I of the plant Arabidopsis
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eudlocts; Rosidae;
Surantanta II; Brassicales; Brassicaceae; Arabidopsis.
 SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES. CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 SSP consortium (Salk/Stanford/PGEC).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- TISSUE SPECIFICITY: FOUND IN SPOROPHYTIC AND GAMETOPHYTIC CELL TYPES IN THE ANTHER, ONLY IN MALE FERTILE PLANTS.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE DEVELOPMENT: HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
 MEDLINE-94004980; PubMed-8401599;
Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
 Draper J., Scott R.;
"Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
 P40602; 093214; O9LNT8;
01-FEB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anter-specific proline-rich protein APG precursor.
APG OR ATIG20130 OR T20H2.9.
534 AA
 STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed-11130712;
 Nature 408:816-820(2000).
STANDARD;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 eurosids II; Bra
NCBI_TaxID=3702;
 thaliana.";
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EMBL; X60377; CAA42925.1; -.

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2 АКУРРАРКРАРОРСРО------РРОДРРОРРОРОРОРОРОРОРОВАРАРОРРА 45

ó;

25; Conservative

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HEAT
 EMBL; U18650; AAA90987.1; ALT_SEQ.
 STRAIN-ICR Swiss; TISSUE-Testis;
MEDLINE-95254745; Pubmed-773666;
 Interpro; IPR000091; Huntingtin.
Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
 Genet. 16:179-189(1995).
 : AAC52133.1; -.
 44.18;
59.28;
 343757
 Conservative
 STANDARD;
 38
51
1411
2611
 (GAPDH)
 1408 141
2506 261
3110 AA;
 Best Local Similarity
Matches 29; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 (EČ 1.2.1.12) (G
GAPDS OR GAPD-S.
 U01022
 G3PT_MOUSE
 SEQUENCE
 Query Match
 DOMAIN
 cells.
 RESULT 14
G3PT_MOUSE
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 Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hamelster H., Epplen J.T., Rless O., F. Brothession of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
 R.L.;
Huntington's disease gene
 ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
 Gaps
 MEDLINE=94100980; PubMed=8275091;
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K.,
Strong T.V., Tagle D.A., Valdes J.M., Elmer L.W., Boehm K.,
Swaroop M., Kaatz K.W., Collins F.S., Albin R.L.;
"Widespread expression of the human and rat Huntington's disease ge
in brain and nonneural tissues.";
Nat. Genet. 5:259-265(1993).

-i- FUNCTION: WAY PLAY A ROLE IN MICROTUBULE-MEDIATED TRANSPORT OR
 01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
 7;
 DB 1; Length 534;
 Pred. No. 0.029;
3; Mismatches 12; Indels
 S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
E -> H (IN REF. 1).
BA851DC3CF7429DB CRC64;
 PPAPKPAPQPGPQPPQPPQPPQPQPQPQPQP-----EAPAPQP 43
 PRT; 3110 AA.
 Score 132.5;
 POTENTIAL.
 Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
EMBL; AC022472; AAF79900.1; ALT_SEQ.
EMBL; AY0S8847; AAL24235.1;
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
 Hum. Mol. Genet. 4:1173-1182(1995)
 MEDLINE-96133292; PubMed-8528205;
 SEQUENCE OF 1773-1926 FROM N.A.
 ž
 44.58;
 58007
 Local Similarity ... hes 24; Conservative
 STANDARD;
 Rattus norvegicus (Rat).
 35
534
211
511
77
 77
141
325
534 AA;
 development.
 SEQUENCE FROM N.A.
 TISSUE-Brain;
 ACT_SITE
ACT_SITE
CONFLICT
 CONFLICT
CONFLICT
SEQUENCE
 Query Match
 HD_RAT
P51111;
 Signal.
 during
 CHAIN
 Matches
 RESULT 13
 STATETTERS
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 3,
 Gaps
 Welch J.E., Brown P.R., O'Brien D.A., Eddy E.M.:
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-melotic spermatogenic
 -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING THE SWITCH
BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
SPERMIOGENESIS AND IN THE SPERMATOZOON.
-1- CATALYTIC ACTIVITY: D-91yceraldehyde 3-phosphate + phosphate +
NAD(+) = 3-phospho-D-91yceroyl phosphate + NADH.
-1- PATHWAY: Second phase of 91ycolysis; first step.
-1- SUBGNIT: HOMOTETRAMER (BY SIMILATY).
 + phosphate +
 Mus músculus; (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammajia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 7;
 STRAIN=CD-1, TISSUE-Testis;
MEDLINE-92273722; PubMed-1375514;
Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.;
Expression of a glyceraldehyde 3-phosphate dehydrogenase gene specific to mouse specmatogenic cells.";
Blol. Reprod. 46:869-878(1992).
 Length 3110;
 064467; 060650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific
 9 KPAPQPGPQPPQPPQPPQPQPQPQPGPAPAPQP---PAGR---ELSA 51
 18 ОРРРОРРОРРОРОРОР - РОСОРРРРР В СВРЕНИРККЕТSA 65
 Indels
 MW; 33C357E8FC141550 CRC64;
 REPEATS DOMAIN 1.
REPEATS DOMAIN 2.
REPEATS DOMAIN 3.
 DB 1;
 12;
 Score 131.5; DI
Pred. No. 0.12;
1; Mismatches
 440 AA.
 POLY-GLN.
POLY-PRO.
 POLY-THR.
POLY-GLU.
 POLY-PRO
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Search completed: May
Job time: 7.0494 secs
 replication.
 EMBL; D45397
 SEQUENCE
 Query Match
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 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 5
TISSUE SPECIFICITY: TESTIS-SPECIFIC.
DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC
GERM CELLS. LEVELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
 Gaps
 SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
 "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997),
 Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
 5 PPAPKPAPQPGPQPPQPPQ-----PPQPPQPPQPQPEAPAPQPPAGRELS 50
 10;
 01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kba protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
 Score 131; DB 1; Length 440;
Pred. No. 0.031;
1; Mismatches 17; Indels
 GLYCERALDEHYDE 3-PHOSPHATE (BY
 MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
 SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 MISSING (IN REF. 2).
L -> V (IN REF. 2).
05FF0A093D1ABD9C CRC64;
 (BY SIMILARITY
 875 AA
 CYS/PRO-RICH.
 POLY-PRO
 HSSP; P56649; IDSS.
MGD; MGI:95653; Gapds.
Interpro; IPR000173; GAP_dhdrogenase.
Pfam; PP000044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
 PRT;
 SEQUENCE OF 1-807 FROM N.A.
MEDLINE-96201426; PubMed-8609478;
 Oxidoreductase; NAD
 Gen. Virol. 77:825-837(1996)
 010323;
1 35, Created)
 Pfam, PF02800, gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
 47657 MW;
 49.18;
 EMBL; M60978; AAA53033.1; -. EMBL; U09964; AAA80276.1; -.
 44.08;
 DEHYDROGENASE FAMILY.
 27; Conservative
 STANDARD;
 283
 Nucleopolyhedrovirus.
 DURING MATURITY
 Query Match
Best Local Similarity
 440 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=164623;
 283
 Q83949; Q65364;
01-NOV-1997 (Rel
 Glycolysis;
 TOGG_NPVOP
 CONFLICT
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 Matches
 RESULT 15
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 (See http://www.isb-sib.ch/announce/
 Gaps
 Ahrens C.H., Carlson C., Rohrmann G.F.; "Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyia pseudotsugata baculovirus DNA
 14;
 5 PPAPKP------APQPGPQPPQPPQPP-QPPQ--PQPQPPQPEAPAPQPP 44
 Virology 210:372-382(1995),
-1. SIMILARITY: TO CORRESPONDING ORF IN ACMNPY AND LDMNPY.
 44.0%; Score 131; DB 1; Length 87;
51.9%; Pred. No. 0.052;
ive 1; Mismatches 11; Indels
 875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
 entities requires a license agreement (
or send an email to license@isb-sib.ch)
 POLY-PRO
 7, 2003, 16:48:14
PubMed=7618274;
 EMBL; U75930; AAC59070.1; -. EMBL; U39145; AAB04047.1; -.
 ; BAA08236.1;
 Best Local Similarity 51.9 Matches 28; Conservative
 Hypothetical protein.
 P01100; 1FOS
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us-09-855-754b-21.rspt

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Ouery Match

Ouery Match

Best Local Similarity 100.0%; Pred. No. 2.2e-18;

Matches 52; Conservative 0; Mismatches 0;
 Interpro; IPR004899; Pertact_up.
Interpro; IPR002965; P.rich_extensn.
Pfam: PF03213; Pertactin; 1.
PRINTS; PR01217; Pertactin; 1.
NON TER 107 107
SEQUENCE 107 AA; 11076 MW; C32F321
 SO FF F SO
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 g
 Q9k594 bordetella
Q9k591 bordetella
Q9alp7 bordetella
Q9alp3 bordetella
Q9alp5 bordetella
Q9alp5 bordetella
Q9k59 bordetella
Q9k59 bordetella
Q9k59 bordetella
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Q9k59 bordetella
Q9k57 bordetella
Q9k595 bordetella
Q9k595 bordetella
Q9k595 bordetella
Q9k595 bordetella
 7, 2003, 16:38:52; Search time 26.5758 Seconds (without alignments) 403.166 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 298
1 GAKVPPAPKPAPQPGPQPPQ......QPQPEAPAPQPPAGRELSAA
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 671580 seqs, 206047115 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q9ALP3
Q9ALP0
Q9ALP5
Q9K5H5
Q9ALP9
Q9L4E2
Q9K5G9
Q9KXX9
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 sp_unclassified:*
 sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_virus:*
sp_vertebrate:*
 sp_archea:*
sp_bacteria:*
sp_fung1:*
 sp_organelle:*
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-855-754B-21
 sp_rodent:*
 B
 sp_plant:*
 SPTREMBL_21:*
 sp_human:*
 sp_phage: *
 Length
 Query
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994.1
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997.2
986.9
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 Title:
Perfect score:
Sequence:
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287
280.5
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 Scoring table:
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 Database :
 Searched:
 Run on:
 Result
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|-----|----------|-----------------------------------------|----------------------------------------------------------------------------------------------|-------------------|------------|------------------|-------------------------------|------------------|----------------------------|
|     | 17       | 248.5                                   | 60<br>60<br>40<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60<br>60 | 215               | <b>~</b> c | 09ALQ4           |                               | 09alq4           | bordetella                 |
|     | 19       | 238.5                                   | 0.08                                                                                         | 105               | 9 (7       | 09K5H7           |                               | 0985h7           | bordetella                 |
|     | 20       | 238.5                                   | 90.0                                                                                         | 115               | 7          | Q9KJY1           |                               | 09k1y1           | bordetella                 |
|     | 21       | 238.5                                   | 90.0                                                                                         | 115               | 7          | Q9KJY0           |                               | 09kjy0           | bordetella                 |
| ٠.  | 25       | 238.5                                   | 90.0                                                                                         | 198               | ~          | O9AHP0           |                               | 09ahb0           | bordetella                 |
|     | 2.4      | 217                                     | 20.0                                                                                         | 90.5              | 4 C        | OSSEMS           |                               | Coeparxe         | bordetella<br>bordetella   |
|     | 25       | 217                                     | 72.8                                                                                         | 905               | 1 (1       | 09S3M8           |                               | 0983m8           | bordetella                 |
|     | 56       | 217                                     | 72.8                                                                                         | 905               | ~          | 0N9S60           |                               | 09860            | bordetella                 |
|     | 27       | 217                                     | 72.8                                                                                         | 910               | ~          | 09S6N1           |                               | Q9s6n1           | bordetella                 |
|     | 87.0     | 217                                     | 8.72                                                                                         | 910               | ~ (        | 069259           |                               | 069259           | bordetella                 |
| ٠   | 7 6      | 217                                     | 9.0                                                                                          | 0 0               | ۷ ،        | 088143           |                               | 088143           | bordetella                 |
|     | 3 5      | 1961                                    | 2.6                                                                                          | 907               | 9 (        | 069257           |                               |                  | bordetella<br>bordetella   |
|     | 32       | 196.5                                   | 6.6                                                                                          | 912               | 10         | ORRSHO           |                               |                  | bordetella                 |
|     | 33       | 162.5                                   | 54.5                                                                                         | 430               | ı m        | 001823           |                               |                  | pneumocyst1                |
|     | 34       | 158.5                                   | 53.2                                                                                         | 938               | 3          | Q96VI4           |                               |                  | pneumocysti                |
| ٠   | 35       | 157.5                                   | 52.9                                                                                         | 166               | ٣          | 09UVD0           |                               | 0pan60           | pneumocysti                |
| )   | 36       | 154.5                                   | 51.8                                                                                         | 493               | m          | 09UVD1           |                               | Q9uvd1           | pneumocyst1                |
|     | 37       | 151.5                                   | 20.8                                                                                         | 686               | Ξ;         | O9JLE9           |                               | 09j1e9           | O9jle9 rattus norv         |
|     | 200      | 2.0c1                                   |                                                                                              | 525               | 2          | QBW158           |                               | Q8w158           | brassica ol                |
|     | ה כי     | 1 4                                     | 0.0                                                                                          | 543               | n ;        | CRITIC           |                               | OBtlyb           | dictyostel1                |
|     | 2 -      | ٦,                                      | 0.0                                                                                          | 4 0<br>2 0<br>2 0 | ٦,         | OSSBM1           |                               | 1 mgs60          | O9sbml volvox cart         |
|     | † ¢      | 149                                     | 0.0                                                                                          | 200               | n :        | TOAGA            |                               | CAPA             | pneumocy                   |
|     | 4 4      | 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 0.0                                                                                          | 1217              | Ι,         | 2088302          |                               | 088902           | rattus norv                |
|     |          | ο,                                      | 0 1                                                                                          | 177               | * *        | n                |                               | CTIDED           | nomo sapien                |
|     | 4 4      | 148                                     | 4.4<br>0.0                                                                                   | 490               | 25         | Q08194<br>Q69023 |                               | Q08194<br>Q69023 | nicotiana t<br>human herpe |
|     |          |                                         |                                                                                              |                   |            |                  |                               |                  |                            |
|     |          | . :                                     |                                                                                              |                   |            | ALIGNMENTS       | MENTS                         |                  |                            |
|     |          |                                         |                                                                                              |                   |            |                  |                               |                  |                            |
| RES | RESULT 1 |                                         |                                                                                              |                   |            |                  |                               |                  |                            |
| 09K |          | _                                       |                                                                                              |                   |            |                  |                               |                  |                            |
| a   | 09K      | Q9K5G4                                  |                                                                                              | PRELIMINARY;      |            | PRT;             | 107 AA.                       |                  |                            |
| AC  | Q9K      | 564;                                    |                                                                                              |                   |            |                  |                               |                  |                            |
| DI  | 01-      | OCT-2000                                | (TrEMBLrel                                                                                   | 3Lrel.            | 15,        |                  |                               |                  |                            |
| DŢ  | 01-      | 01-OCT-2000                             |                                                                                              | Mrel.             | 15,        |                  | sequence update)              |                  |                            |
| 5 5 | -TO      | JUN-2002                                | TrE                                                                                          | Streit.           | 21,        | Last ann         | annotation update)            |                  |                            |
| N C | DEN      |                                         |                                                                                              | (Frayment         |            |                  |                               |                  |                            |
| So  | Bor      | Bordetella bronchiseptica               | bronchi                                                                                      | septic            |            | Alcaligen        | (Alcalidenes bronchisepticus) |                  |                            |
| 8   | Bac      | Bacteria: Proteobacteria:               | roteoba                                                                                      | cteria            |            | beta subdi       | subdivision: Alcalidenaceae   | . 00000          |                            |
| 8   | Bor      | Bordetella.                             |                                                                                              |                   |            |                  | mafitante (mater)             | מכפפים,          |                            |
| ŏ   | NCB      | NCBI_TaxID=518;                         | 518;                                                                                         |                   |            |                  |                               |                  |                            |
| Z.  | Ξ        |                                         |                                                                                              |                   |            |                  |                               |                  |                            |
| RP  | SEO      | SEQUENCE FROM N.A                       | OM N.A                                                                                       |                   |            |                  |                               |                  |                            |
| מ א | STR      | STRAIN=286;<br>MEDITME-20250200.        | 50200.                                                                                       | Dubloc            | 2          | 10000005         |                               |                  |                            |
| 2 2 | Bou      | FSBUX-EUC                               | 19309;                                                                                       | Guiso N           |            | ,04046,          | ,                             |                  |                            |
| RT  | Po-      | "Polymorphism of                        | Sin of F                                                                                     | Repeated Regions  | ğ          | gatons of        | Pertactin in                  | Bordetella       |                            |
| RT  | per      | tūssis, l                               | Bordete                                                                                      | alla pa           | rape       | ertussis,        | and Bordetella                | bronchisentica   | otica.":                   |
| Æ   | Inf      | ect. Imm                                | ni. 68                                                                                       | 4815-4            | 817        | 2000).           |                               |                  |                            |
| DR  | EW :     | EMBL; AJ250092; CAB76446.1;             | 092; CZ                                                                                      | AB76446           | .1;        |                  |                               |                  |                            |

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Gaps

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Indels

Length 107;

107 AA; 11076 MW; C32F321161C9E400 CRC64;

21 GAKVPFAFKPAPQPEQPPQPPQPPQPPQPQPQPQPQPGPAPAPQPPAGRELSAA 72

1 GAKVPPAFKPAPQPGPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA

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Indels

DB 2; Length 304;

RESULT 2

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146 GAKVPPAPKPAPQPGPQPPQPPQ-PQPQPQPQPQPGPAPAPQPPAGRELSAA 196
 Bordetella bronchiseptica (Alcaligenes bronchisepticus). absteria; beta subdivision; Alcaligenaceae; Bordetella. NCBL_TaxID=518;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";
Inflect. Immun. 69:1917-1921(2001).
EMBL; AX007267, AAG38443.1;
InterPro; IPR003992; pertactin.
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAQPPAGKELSAA
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA
 Novel Genetic and Phenotypic Heterogeneity in Bordetella
 Score 275; DB 2; Length 23
Pred. No. 3.4e-16;
0; Mismatches 0; Indels
 231
23930 MW; 5FB281B95E74678C CRC64;
 09ALQ0;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
 , 5e-16;
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 256 AA
94.1%; Score 280.5;
98.1%; Pred. No. 1.5e
iive 0; Mismatches
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Infect. Immun. 69:1917-1921(2001).
EMBL; AY007277; AAG38453.11.
Interpro; IPR003992; pertactin.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR004995; Prich_extensn.
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 MEDLINE=21117018; PubMed=11179374;
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PRINTS; PR01217; PRICHEXTENSN.
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96.2%;
 Pfam; PF03212; Pertactin; 1
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 51; Conservative
 PRELIMINARY;
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 231 AA;
 SEQUENCE FROM N.A.
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Matches 51; Conserv
 SEQUENCE FROM N.A.
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 Register K.B.;
 Bordetella.
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 Poursaux_Ende C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815.4817(2000).
EMBL; AJ250095; CAB76449.1;
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InterPro; IPR002965; Pirtoc_atensn.
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 52
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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 Length 107;
 Register K.B.; "Novel Genetic and Phenotypic Heterogeneity in Bordetella
 Ouery Match 96.3%; Score 287; DB 2; Length 10 Best Local Similarity 96.3%; Pred. No. 1.8e-17; Matches 52; Conservative 0; Mismatches 0; Indels
 31759 MW; 3B120CB158FD7474 CRC64;
 107 107
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 107 AA
 304 AA
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Infect. Immun. 69:1917-1921(2001).
EMBL, SAV07273; AAG38449.1; -
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InterPro; IPR003991; pertactin.-ir.
InterPro; IPR003991; pertactin.-ir.
InterPro; IPR004899; Pertact.-yr.
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 STRAIN-MBORD901;
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01-JUN-2002 (TrEMBLrel. 21, Last ann
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 0914E2;
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 191 GAKAPPAPKPAPQPGQPPQPPQP--QPQPQPQPQPQPEAPAPQPPAGRELSAA 240
 F. Wovel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";

L. Infect. Immun. 69:197-1921(2001).

E. EMBL: AV007275; AMG38451.1;

InterPro; IPR003992; pertactin.

InterPro; IPR003991; pertactin.vir.

InterPro; IPR004999; Pertactin.vir.

InterPro; IPR004999; Pertactin.vir.

R. InterPro; IPR004999; Pertactin.vir.

R. PRINTS; PR01212; Pertactin; 1.

R. PRINTS; PR01482; PRINCIN.

R. PRINTS; PR01484; PRIACTNFAMLX.
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 87.2%; Score 260; DB 2; Length 347; ilarity 92.3%; Pred. No. 8.4e-15; Conservative 0; Mismatches 0; Indels
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PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 1 1
NON_TER 256 256
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 ch 88.3%;
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48; Conservative
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Boursaux-Ende C., Guiso N.; Polymorphism of Repeated Regions of Pertactin in Bordetella pertubsis, abordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000). EMBL, #A2500B1; CAB76435.1; InterPro; IPR004899; Pertact.sup.
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 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
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 86.9%; Score 259; DB 2; Length 200; 92.5%; Pred. No. 6.5e-15; Live 0; Mismatches 2; Indels
 Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).

EMBL, AX007271, AAG38447.1; -...

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InterPro; IPR003995; Pertactin.

InterPro; IPR003965; P. Ich. Extensn.

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200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
 Last sequence update)
Last annotation update)
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92.5%; Pred. No. 3.9e-15;
tive 0; Mismatches 2;
 200 AA.
 911 AA
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Keil D.J., Fenwick B.; "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of
 42 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQP-PQRQPEAPAPQPPAGRELSAA 97
 1 GAKVPPAPKPAPQPGPQP-----PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Length 252;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 6:1917-1921(2001). EMBL; AX007265; AAG38441.1; -. InterPro; IPR003992; pertactin. InterPro; IPR004899; Pertactin. InterPro; IPR004899; Pertactin. FinterPro; IPR004995; Pertactin. FinterPro; IPR004965; Pertactin. FinterPro; IPR004965; Pertactin. InterPro; IPR044965; Pertactin. InterPro; IPR044969; Pertactin. IPR044969; Pertact
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 Submitted (10N-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF156773; AAF83397.1; -1 InterPro; IPR00489; Pertact_sup. InterPro; IPR002965; P_rich_extensn. PF03212; Pertactin; 1.
 26107 MW; 368C142508D77057 CRC64;
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122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
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86.0%; Pred. No. 6.3e-15;
iive 0; Mismatches 2.
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1-JUN-2002 (TrEMBLrel. 21,
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es 49; Conserv
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 NCBI_TaxID=518;
 NCBI_TaxID=518;
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 STRAIN=16039
 01-OCT-2000
01-JUN-2002
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MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-10899896;
MEDLINE-20359389; PubMed-1089896;
MeDLINE-20359389; PubMed-108089; Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250087; CAB76441.1; InterPro; IPR004899; Pertact_sup.
InterPro; IPR004899; Pertact_sup.
 "Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines."; Submitted (Ang-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ45927; CAB82515.1; --
InterPro; IPR003991; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR003991; pertactin.vir.
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PRINTS; PR01489; PERTACTIN:
SEQUENCE 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
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 King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.,
Mooi F.R.;
 1 GAKVPPAPKPAPKPAPQPGPQP----PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
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 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA 52
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Boursaux-Eude C., Guiso N.;

"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

EMBL; AJ250091; CAB76445.1;

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01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
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Matches 49; Conservative 0; Mismatches 2;
 Search completed: May 7, 2003, 16:53:16
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 STRAIN-CAT1;
MEDLINE-20359389; Pubmed-10899896;
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 Boursaux-Eude C., Guiso N.;

"Polymorphism of Repeated Regions of Pertactin in Bordetella

"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";

EMBL; AJ250089; CAB76443.1; ..

EMBL; AJ250089; Pertact_sup.

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Pfam; PF03212; Pertactin; I
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Polymorphism of Repeated Regions of Pertactin in Bordetella
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815.4817(2000).
EMBL; AJ250083; CAB76437.1;
InterPro; IPR004899; Pertact.sup.
InterPro; IPR002965; P_rich_extensn.
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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## GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

protein search, using sw model 1 OM protein Run on:

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7, 2003, 16:41:51; Search time 8.59284 Seconds (without alignments) 178.054 Million cell updates/sec

US-09-855-754B-21 Perfect score: Sequence:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|            | Description  | Sequence 4, Appli | 9                | ~                | 11,              | 160               | 28,              | 29,              | 30,              | 31,              | , ,              | ò               | 42,               | 21,              | 15,              | . 52(      | æ                | Patent No. 5202236 | Sequence 16, Appl | 16,              | 11,              | 8, 2             | Sequence 2, Appl1 | 7               | 99               | 7,              | 143               | 138,              |
|------------|--------------|-------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-----------------|-------------------|------------------|------------------|------------|------------------|--------------------|-------------------|------------------|------------------|------------------|-------------------|-----------------|------------------|-----------------|-------------------|-------------------|
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|            | DB           | 4                 | 4                | 4                | П                | 4                 | 4                | 4                | 4                | 4                | Н                | -               | ~                 | ٣                | 4                | 9          | ~                | 9                  | -                 |                  | 4                | 4                | 7                 | 4               | 4                | 7               | 4                 | 4                 |
|            | Match Length | 911               | 922              | 910              | 33               | 641               | 513              | 530              | 552              | 589              | 3144             | 3144            | 3144              | 3144             | 3144             | 331        | 3118             | 334                | 3119              | 3119             | 24               | 23               | 351               | 490             | 311              | 299             | 174               | 174               |
| *<br>Ouerv | atch         | 86.9              | 85.9             | 72.8             | 44.0             | 43.5              | 43.0             | 43.0             | 43.0             | 43.0             | 43.0             | 43.0            | 43.0              | 43.0             | 43.0             | 42.4       | 42.3             | 42.1               | 42.1              | 42.1             | 41.9             | 40.9             | 40.9              | 39.1            | 38.8             | 38.1            | 37.8              | 37.8              |
| 0          | Score M      | 259               | 256              | 21.7             | 131              | 129.5             | 128              | 128              | 128              | 128              | 128              | 128             | 128               | 128              | 128              | 126.5      | 126              | 125.5              | 125.5             | 125.5            | 125              | 122              |                   | 116.5           | 115.5            | 113.5           | 112.5             | 112.5             |
| Result     | NO.          | -                 | 7                | Э                | 4                | ഗ                 | 9                | 7                | 80               | 6                | 10               | 11              | 12                | 13               | 14               | 15         | 16               | 17                 | 18                | 19               | 20               | 21               | 22                | 23              | 24               | 25              | 56                | 27                |

| Sequence 143. Ann | Sequence 138. App | •                | θ,               | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | 7               | Sequence 4, Appl1 | 4                | 7               | 7               | 'n               | 7               | ω,               | 7               | 7               | 2,              |   |
|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-----------------|-------------------|------------------|-----------------|-----------------|------------------|-----------------|------------------|-----------------|-----------------|-----------------|---|
| US-09-056-556-143 | US-09-072-596-138 | US-09-142-551A-4 | US-09-142-551A-3 | US-09-095-443-2   | US-08-155-888-2   | US-09-080-897-2   | US-09-323-735-2 | US-08-348-518C-4  | US-08-476-509B-4 | US-08-465-746-2 | US-08-214-164-2 | US-08-467-852A-3 | US-08-246-636-2 | US-08-247-491A-3 | US-08-319-795-2 | US-08-468-985-2 | US-08-312-949-2 | • |
| 4                 | 4                 | 4                | 4                | 4                 | <u>س</u>          | ~                 | 4               | ٣                 | ო                | _               | -               | 7                | ~               | ~                | ~               | ~               | 6               |   |
| 174               | 174               | 370              | 396              | 1274              | 478               | 1248              | 1248            | 454               | 454              | 619             | 619             | 619              | 619             | 619              | 619             | 619             | 619             |   |
| 37.8              | 37.8              | 37.8             | 37.8             | 37.6              | 37.2              | 37.2              | 37.2            | 36.9              | 36.9             | 36.9            | 36.9            | 36.9             | 36.9            | 36.9             | 36.9            | 36.9            | 36.9            |   |
| 112.5             | 112.5             | 112.5            | 112.5            | 112               | 111               | 111               | 111             | 110               | 110              | 110             | 110             | 110              | 110             | 110              | 110             | 110             | 110             | _ |
| 28                | 59                | 30               | 31               | 32                | 33                | 34                | 32              | 36                | 37               | 38              | 39              | 40               | 41              | 42               | 43              | 44              | 45              |   |
|                   |                   |                  |                  |                   |                   |                   |                 |                   | ٠.               |                 |                 |                  |                 |                  |                 |                 |                 |   |

### ALIGNMENTS

```
Gaps
 ;
;
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
 Length 911;
 CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
 Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
CERMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 86.9%; Score 259; DB 4; I 92.5%; Pred. No. 1.8e-15; tive 0; Mismatches 2;
 SNT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
 NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
 (703) 243-6333
 Sequence 4, Aprilication US/08460269C Patent No. 6197548 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
 Query Match 86.9
Best Local Similarity 92.5
Matches 49; Conservative
 NUMBER OF SEQUENCES:
 TELEPHONE:
 CURRENT
 US-08-460-269C-4
RESULT 1
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1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 52

ŏ q Gaps

10;

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Length 910;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA
 1; Indels
 ADDRESSEE: Nixon & Vanderhye, P.C.
STREET: 1100 No. 5589384th Glebe Road, 8th Floor
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 Score 217; DB 4;
Pred. No. 7.4e-12;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
 REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
 APPLICANT: LIPSCOMBE, Martin J
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
CORRESPONDENCE ADDRESS:
 APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
 ATTORNEY AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
 Sequence 11, Application US/08237716 Patent No. 5589384
 TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 NAME: Wilson, Mary J
RECISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
 32,955
 72.8%;
78.8%;
 33 amino acids
 TYPE: amino acid
TOPOLOGY: linear
 Query Match 72.8
Best Local Similarity 78.8
Matches 41; Conservative
 703-816-4100
 NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
 TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 FILING DATE:
 COMPUTER: IBM PC OPERATING SYSTEM:
 Virginia
: USA
 CITY: Arlington
 GENERAL INFORMATION:
 US-08-237-716-11
 COUNTRY:
 STATE:
 RESULT 4
 õ
 g
 Gaps
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQP--QPQPGPEAPAPQPPAGRELSAA
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
YEAST
 Length 922;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
 Indels
 PatentIn Release #1.0, Version #1.30
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON
 Score 256; DB 4;
Pred. No. 3.3e-15;
0; Mismatches 3;
 APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995
 NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-460-269C-6
 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
 Sequence 2, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
 Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
 Floppy disk
 TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 922 amino acids TYPE: amino acid
 ATTORNEY/AGENT INFORMATION:
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS
 85.9%;
illarity 84.5%;
Conservative
 ZIP: 22201
COMPUTER READABLE FORM:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
 NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 CITY: ARLINGTON
 USA
 COUNTRY: USA
 Best_Local Similarity
Matches 49; Conserv
 IP: 22201
 US-08-460-269C-2
 Query Match
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78-09-041-886-29
Sequence 29, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
 NUMBER OF SEQUENCES: 72
CORRESPONDAÇE ADDRESS:
CORRESPONDAÇE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
 6 PAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAG-
 ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CITY: San Diego
STATE: California
COUNTRY: United States
 FILING DATE
 92122
 US-09-041-886-28
 TOPOLOGY:
 STREET:
CITY: Sa
 RESULT 7
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 Gaps
 Gaps
 GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
 10;
 DB 4; Length 641;
 /label= P69 BB05 epitope of Bordetella
pertussis sequence
 6 PAPKP-APQPGPQPPQPPQPPQPPQPQPQPEAPAPQP----PAGRELSA 51
 Query Match
44.0%; Score 131; DB 1; Length 33;
Best Local Similarity 63.2%; Pred. No. 1e-05;
Matches 24; Conservative 2; Mismatches 2; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
 43.5%; Score 129.5; DB 4 llarity 52.9%; Pred. No. 0.00019; Conservative 3; Mismatches 16
 6 РАРКРАРОРБРОРРОРРОРРОРРОРОРОРОРОРОР 43
 OTHER INFORMATION: /label = LTB sequence
 /label= hinge region
 ADDRESSEE: Human Genome Sciences, Inc. STREEF: 9410 Key West Avenue CITY: Rockville STATE: Maryland
 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
 Sequence 160, Application US/08961083
Patent No. 6159469
 ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
 641 amino acids
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 single
 ; MOLECULE TYPE: protein US-08-961-083-160
 LOCATION: 10.31
COTHER INFORMATION:
COTHER INF
 LOCATION: 4.7
OTHER INFORMATION:
 Query Match
Best Local Similarity
Matches 27; Conserve
 Region
 amino acid
 NAME/KEY: Region
 linear
 STRANDEDNESS:
 FILING DATE:
 FILING DATE:
NAME/KEY:
LOCATION:
 US-08-961-083-160
 COUNTRY:
 LENGIH:
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Indels 14; Gaps
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 Score 128; DB 4;
Pred. No. 0.00021;
1; Mismatches 15
 2626 J-L
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 28, Application US/09041886
Patent No. 6235872
 ATTORNEY/AGGNT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
 Query Match
Best Local Similarity 48.3%;
Matches 28; Conservative 1
 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INPERMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
 LENGIH: 513 amino acids
 STREET: 4370 La Jolla VCITY: San Diego
STATE: Callfornia
COUNTRY: United States
 ; MOLECULE TYPE: peptide US-09-041-886-28
 amino acid
 GENERAL INFORMATION:
 CLASSIFICATION:
```

51

```
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
COMMER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
 6 РАРКРАРОРБОРРОРРОРРОРОРОРОРОРОРОРВАРАРОРРАG--
 Score 128; DB 4;
Pred. No. 0.00023;
 : Sterne, Kessler, Goldstein & Fox
 1; Mismatches
 US/09/041,886
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 6, Application US/08246982A
Patent No. 5686288
 Sequence 31, Application US/09041886
Patent No. 6235872
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERROE/POCKET UNMBER: P-LA
TELECOMMUNCATION INFORMATION:
TELEPHONE: (619) 535-9001
 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31:
 Query Match
Best Local Similarity 48.3%;
Matches 28; Conservative
 United States
 SEQUENCE CHARACTERISTICS
 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-041-886-31
 CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, K
 CITY: San Dies STATE: California COUNTRY: United State 17P: 92122
 APPLICATION NUMBER:
 STREET: 1100 New 1
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
 GENERAL INFORMATION:
 GENERAL INFORMATION:
 FILING DATE:
 US-08-246-982A-6
 US-09-041-886-31
 RESULT 10
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 Gaps
 Gaps
 Score 128; DB 4; Length 552;
Pred. No. 0.00022;
1; Mismatches 15; Indels 14;
 DB 4; Length 530; 0.00021;
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
 Patentin Release #1.0, Version #1.25
 6 PAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAG--
 43.0%; Sco...
48.3%; Pred. No. v...
1; Mismatches 1:
 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION UNDHER: 31,815
REFERENCE/DOCKET UNDHER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
 P-LJ 2626
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 Sequence 30, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
 48.38;
 552 amino acids
 530 amino acids
 COUNTRY: United States
 Query Match 43.0 Best Local Similarity 48.3 Matches 28; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 28; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
 COMPUTER READABLE FORM:
 California
 Best_Local Similarity
Matches 28; Conserva
 amino acid
 amino acid
 San Diego
 CLASSIFICATION:
 FILING DATE:
 FILING DATE
 US-09-041-886-30
 US-09-041-886-30
 US-09-041-886-29
 LENGIH:
 STREET:
 STATE:
 Query Match
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41 PPPPPPFPPPPDLPQPPPQAQPLLPQPQPPP--PPPPPPPPPPPPPPTHRPKKELSA 96
 ---RELSA
 14;
 TITLE OF INVENTION: Mouse Model for Huntington's Disease and TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: NO : 5849995th Carolina
 Length 3144;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
 6 PAPKPAEQPGPQPPQPPQPPQPQPQPQPGPEAPAPQPPAG-
 6 раркрарурсроррорроррорроророророргарароррас
 Score 128; DB 1
Pred. No. 0.001;
1; Mismatches
 1; Mismatches
 ; Sequence 42, Application US/08457273B
; Patent No. 5849995
; GENERAL INFORMATION:
 Sequence 21, Application US/08556419C Patent No. 6093549
 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTATION NUMBER: 37,092
REFERENCE/POCKET NUMBER: 3477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
 43.0%;
 APPLICANT: Hayden, Michael
APPLICANT: Lin, Biaoyang
APPLICANT: Nasir, Jamal
 Best Local Similarity 48.3
Matches 28; Conservative
 Query Match 43.0
Best Local Similarity 48.3
Matches 28; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
; MOLECULE TYPE: protein US-08-453-265-6
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 TYPE: amino acid
STRANDEDNESS: si
 GENERAL INFORMATION:
 FILING DATE:
 US-08-457-273B-42
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 Gaps
 6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPEAPAPQPPAG------RELSA 51
 15; Indels 14;
 Sequence 6. Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacConald, Marcy E.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 Score 128; DB 1; Length 3144;
Pred. No. 0.001;
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILIG DATE: May 20, 1994
CLASSIFICATION: 435
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILIG DATE: 30-MAY-1995
CLASSIFICATION: 514
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
 1; Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME: LUDWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 43.0%;
 3144 amino acids
 ATTORNEY/AGENT INFORMATION:
 Floppy disk
 Best_Local Similarity 48.39
Matches 28; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 READABLE FORM
 20005
 amino acid
 Washington
 FILING DATE: 30 CLASSIFICATION:
 US-08-246-982A-6
 COUNTRY:
 TOPOLOGY:
 LENGTH:
 US-08-453-265-6
 Query Match
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5202236-37; Patent No.
 PROTEIN
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 Gaps
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 Indels 14;
 Score 128; DB 4; Length 3144;
Pred. No. 0.001;
1; Mismatches 15; Indels 1
 Score 128; DB 3; Length 3144;
Pred. No. 0.001;
1; Mismatches 15; Indels 1.
 Sequence 15, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence.
TITLE OF INVENTION: Polypeptides and Methods of Use
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
 6 PAPKPAPQPGPQPPQPPQPPQPQPQPQPEAPAPQPPAG--
 TITLE OF INVENTION: Huntingtin-associated protein FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 3144
 6 РАРКРАРОРБРОРРОРРОРРОРОРОРОРОРЕАРАРОРРАG-
 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
 43.0%;
 43.0%;
 3144 amino acids
 United States
 Query Match
Best Local Similarity 48.3
Matches 28; Conservative
 Best Local Similarity 48.3
Matches 28; Conservative
Lanahan, Anthony
 Snyder, Solomon
 MOLECULE TYPE: protein US-09-041-886-15
 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 TYPE: PRT
ORGANISM: Homo sapiens
 California
 TYPE: amino acid
TOPOLOGY: linear
 San Diego
 CLASSIFICATION:
 ADDRESSEE:
STREET: 43
 COUNTRY: U
 RESULT 14
US-09-041-886-15
 US-08-556-419-21
 STATE:
 APPLICANT:
APPLICANT:
 Query Match
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us-09-855-754b-21.rapb

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein – protein search, using sw model

7, 2003, 16:53:34; Search time 15.5911 Seconds May Run on:

(without alignments)
306.927 Million cell updates/sec

US-09-855-754B-21 298 Perfect score:

Sequence:

1 GAKVPPAPKPAPQPGPQPPQ.........OPQPEAPAPQPPAGRELSAA 52

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

349150 seqs, 92025710 residues Searched:

349150 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep

### SUMMARIES

|                            |                   |                   |                   |                   |                   |                   |                 |                   | -                 |                  |                   |                  |                 |                  |                 |                   |                 |                  |                   |
|----------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|------------------|-------------------|------------------|-----------------|------------------|-----------------|-------------------|-----------------|------------------|-------------------|
| Description                | Sequence 21, Appl | Sequence 22, Appl | Sequence 15, Appl | Sequence 4, Appli | Sequence 18, Appl | Sequence 19, Appl | , A             | Sequence 20, Appl | Sequence 16, Appl | 14, 7            | Sequence 17, Appl | 23,              | 5, 8            | 24,              | 3, A            | 9                 | 7, A            |                  | Sequence 9, Appli |
| ID                         | US-09-855-754-21  | US-09-855-754-22  | US-09-855-754-15  | US-09-855-754-4   | US-09-855-754-18  | US-09-855-754-19  | US-09-855-754-6 | US-09-855-754-20  | US-09-855-754-16  | US-09-855-754-14 | US-09-855-754-17  | US-09-855-754-23 | US-09-855-754-5 | US-09-855-754-24 | US-10-171-384-3 | US-09-765-272-160 | US-09-904-987-7 | US-10-001-873-50 | US-10-077-584-9   |
| DB                         | 6                 | σ                 | 6                 | ڼ                 | 6                 | 6                 | σ               | σ                 | 6                 | σ                | δ                 | σ                | σ               | 6                | 6               | 10                | 10              | σ                | 6                 |
| %<br>Query<br>Match Length | 52                | 54                | 52                | 911               | 26                | 28                | 922             | 48                | 29                | 49               | 25                | 42               | 910             | 39               | 827             | 641               | 1543            | 1134             | 9                 |
| %<br>Query<br>Match        | 100.0             | 96.3              | 86.9              | 86.9              | 86.2              | 85.9              | 85.9            | 83.6              | 81.4              | 80.0             | 79.2              | 72.8             | 72.8            | 62.9             | 47.0            | 43.5              | 43.0            | 42.8             | 41.9              |
| Score                      | 298               | 287               | 259               | 259               | 257               | 256               | 256             | 249               | 242.5             | 238.5            | 236               | 217              | 217             | 196.5            | 140             | 129.5             | 128             | 127.5            | 125               |
| Result<br>No.              | -                 | 7                 | m                 | ₹                 | ហ                 | 9                 | 7               | œ                 | 6                 | 10               | 11                | 12               | 13              | 14               | 15              | 16                | 17              | 18               | 19                |

| Sequence 4, Appl1 Sequence 2, Appl1 Sequence 43, Appl Sequence 43, Appl Sequence 1, Appl1 Sequence 1, Appl1 Sequence 1, Appl1 Sequence 61, Appl1 Sequence 5, Appl1 Sequence 2, Appl1 Sequence 2, Appl1 Sequence 1, Appl1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 9 US-10-077-584-4<br>10 US-09-76-864 967<br>10 US-09-32-240-2<br>9 US-09-976-740-43<br>12 US-110-023-523-43<br>12 US-110-023-523-43<br>12 US-110-023-523-43<br>12 US-10-023-523-47<br>12 US-10-023-523-47<br>12 US-10-023-523-47<br>12 US-10-023-523-1<br>12 US-10-023-523-1<br>12 US-09-298-5238-61<br>9 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-298-5238-62<br>10 US-09-864-761-34988<br>10 US-09-864-761-34988<br>10 US-09-864-761-34988<br>10 US-09-815-242-11345<br>10 US-09-815-242-11345<br>10 US-09-813-242-11345<br>10 US-09-813-242-11345<br>10 US-09-813-240-9<br>10 US-09-813-240-9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 171<br>8015<br>8018<br>8018<br>5338<br>5338<br>8224<br>6910<br>6910<br>6910<br>1011<br>1111<br>1111<br>1111<br>1111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 44-44-44-44-44-44-4-4-4-4-4-4-4-4-4-4-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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### ALIGNMENTS

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APPLICANT: BOUGASON MACLOEF, NICOLES
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORNOHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILLE REPERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/0855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
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 Length 52;
 1 САКУРРАНКРАРОРСРОРРОРРОРРОРРОРРОРОРОРОРЕАРАРОРРАСКЕЦЅАА
 Indels
 Query Match
100.0%; Score 29%; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 52; Conservative 0; Mismatches 0;
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-21
Sequence 21, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
 Sequence 22, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
 US-09-855-754-22
 SEQ ID NO 21
LENGTH: 52
 TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/855,754
 US-09-855-754-19
 US-09-855-754-18
 49;
 LENGTH: 56
 Query Match
Best Local S
Matches 49
 SEQ ID NO 18
 Query Match
 TYPE: PRT
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOSENTIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYERTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERMACUTIN IN BANDAMENT.
 Gaps
 Gaps
 TITLE OF INVENTION: MOSTELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPLICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: US/09.266,969
PRIOR PILING DATE: 2000-05-25
 BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN IMMUNOGENIC COMPOSITIONS
 REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
 5,
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 Score 259; DB 9; Length 52; Pred. No. 7.5e-12; 0; Mismatches 2; Indels
 Length 54;
 Indels
 Score 287; DB 9;
Pred. No. 9.9e-14;
 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-15
 PRIOR APPLICATION NUMBER: 60/206,969
 ORGANISM: Bordetella bronchiseptica
 Sequence 15, Application US/09855754 Publication No. US20020192237a1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Sequence 4, Application US/09855754
Publication No. US20020192237A1
 96.3%;
 Match 86.9%;
Local Similarity 92.5%;
hes 49; Conservative
 PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
 Best Local Similarity 96.3
Matches 52; Conservative
 : PatentIn Ver. 2.1
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
 INVENTION:
INVENTION:
 GENERAL INFORMATION:
 RESULT 3
US-09-855-754-15
 US-09-855-754-22
 US-09-855-754-4
 SEQ ID NO 15
LENGTH: 52
 SEQ ID NO 22
LENGTH: 54
 Query Match
 Query Match
 TYPE: PRT
 SOFTWARE
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REPEATED
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REI
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE R TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
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 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA 52
 Length 911;
 Length 56;
 Indels
 Score 259; DB 9; I
Pred. No. 7.8e-11;
0; Mismatches 2;
 1.1e-11;
 Score 257; DB 9;
 0; Mismatches
 CURRENT APPLICATION NUMBER: US/09/855,754
 CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
 PRIOR APPLICATION NUMBER: 2001-09-10
PRIOR PILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 911
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
 Pred.
 Sequence 19, Application US/09855754
Publication No. US20020192237A1
 Sequence 18, Application US/09855754 Publication No. US20020192237A1
 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
 CAROLINE
 GUISO-MACLOUF, NICOLE
 86.2%;
86.0%;
 86.9%;
ilarity 92.5%;
Conservative
 Conservative
 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE,
 NUMBER OF SEQ ID NOS: 24
 NUMBER OF SEQ ID NOS: 2. SOFTWARE: PatentIn Ver.
 Best Local Similarity
Matches 49; Conserv
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81.4%;
81.4%;
 83.6%;
88.5%;
 2000-05-25
 Query Match
Best Local Similarity 88.5
Matches 46; Conservative
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SOFTWARE: Patentin Ver. 2.1
 Query Match
Best Local Similarity 81.4
Matches 48; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.
US-09-855-754-20
 US-09-855-754-14
 SEQ ID NO 16
LENGTH: 59
 SEQ ID NO 14
 Query Match
 LENGTH:
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 APPLICANT: GUISO-MACLOUR, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PRETACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGFIELLA PARABERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOSTWARE: PATENTIN VET 2.1
 Gaps
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQP--QPQPQPEAPAPQPPAGRELSAA
 9
 Length 922;
 Score 256; DB 9; Length 58; Pred. No. 1.3e-11; 0; Mismatches 3; Indels
 3; Indels
 Score 256; DB 9;
Pred. No. 1.3e-10;
0; Mismatches 3
 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
 TYPE: PRT ORGANISM: Bordetella bronchiseptica
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
 Sequence 20, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 ; ORGANISM: Bordetella parapertussis US-09-855-754-6
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Sequence 6, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 85.9%;
ilarity 84.5%;
Conservative
 ch 85.9%;
l Similarity 84.5%;
49; Conservative
 2000-05-25
SOFTWARE: Patentin Ver. 2.1
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
 Query Match
Best Local Similarity
 Local Similarity
 RESULT 8
US-09-855-754-20
 49;
 SEO ID NO 19
LENGTH: 58
TYPE: PRT
 US-09-855-754-6
 SEQ ID NO 6
 TYPE: PRT
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISPETICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE; 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERPEACTINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARABETUSSIS, AND IN TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE; 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
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 1 GAKVPPAPKPAPKPAPQPGPQP-----PQP-PQPPQPPQ-PQPPQPPAGRELSAA 52
 7;
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 Length 59;
 Length 48;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA
 Indels
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 80.0%; Score 238.5; DB 9;
86.8%; Pred. No. 1.8e-10;
tive 0; Mismatches 2;
Score 249; DB 9;
Pred. No. 3.4e-11;
 Score 242.5; DB 9
Pred. No. 1.1e-10;
 0; Mismatches
 1; Mismatches
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-16
 60/206,969
 . ORGANISM: Bordetella bronchiseptica US-09-855-754-14
 Sequence 14, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 Sequence 16, Application US/0985554
Publication No. US20020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GGISO-MACLOUF, NICOLE
 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUE, NICOLE
 Best Local Similarity 86.8
Matches | 46; Conservative
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNCIENIC COMPOSITIONS
FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
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 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPEAPAPQPPAGRELSAA
 72.8%; Score 217; DB 9; 78.8%; Pred. No. 5.5e-08;
 Mismatches
 PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 24
LENCTH: 39
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
 ; Sequence 24, Application US/09855754
; Publication No. US20020192237A1
 Sequence 3, Application US/10171384 Publication No. US20030031680A1
 Sequence 5, Application US/09855754; Publication No. US20020192237A1; GENERAL INFORMATION:
 CAROLINE
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 ; ORGANISM: Bordetella pertussis
US-09-855-754-5
 Conservative
 APPLICANT: BOURSAUX-EUDE,
 NUMBER OF SEQ ID NOS: 2. SOFTWARE: Patentin Ver.
 Best Local Similarity
Matches 38; Conserv
 Best_Local Similarity
Matches 41; Conserv
 US-09-855-754-24
 LENGTH: 910
 RESULT 15
US-10-171-384-3
 US-09-855-754-5
 TYPE: PRT
 Query Match
 SEQ ID NO 5
 Query Match
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BONDETELLA PARAPERTUSSIS, ANTITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE PEPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR ELLING DATE: 2000-05-25
 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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 TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISBETICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPPQPPQPEAPAPQPPAGRELSAA 52
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPPQPPQPEAPAPQPPAGKELSAA 52
 Length 42;
 Length 52;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 1; Indels
 1; Indels
 Score 217; DB 9;
Pred. No. 4.4e-09;
0; Mismatches 1
 Score 236; DB 9;
Pred. No. 2.7e-10;
1; Mismatches 1
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-23
 ; ORGANISM: Bordetella bronchiseptica US-09-855-754-17
 Sequence 17, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 US-09-855-754-23; Sequence 23, Application US/09855754; Publication No. US20020192237A1
 APPLICANT: BOURSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
 CAROLINE
 ch 72.8%;
1 Similarity 78.8%;
41; Conservative
 Query Match 79.2%;
Best Local Similarity 88.9%;
Matches 48; Conservative
 Patentin Ver. 2.1
 APPLICANT: BOURSAUX-EUDE, APPLICANT: GUISO-MACLOUF
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver.
 NUMBER OF SEQ ID NOS: 24
 Query Match
Best Local Similarity
 GENERAL INFORMATION
 US-09-855-754-17
 SOFTWARE: Pat
SEQ ID NO 23
LENGTH: 42
TYPE: PRT
 SEQ ID NO 17
LENGTH: 52
 TYPE: PRT
 Matches
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Gaps

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Length 910;

52

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APPLICANT: BOURSAUN-EUDE, CAROLINE
APPLICANT: BOURSAUN-EUDE, NICOLE
TITLE OF INVENTION: PEGITORS CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMORGENIC COMPOSITIONS
TITLE OF INVENTION: IMMORGENIC COMPOSITIONS
TITLE OF INVENTION: IMMORGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 Gaps
 13;
 52
 Length 39;
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 Indels
 65.9%; Score 196.5; DB 9; llarity 73.1%; Pred. No. 1e-07; Conservative 0; Mismatches 1;
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; GENERAL INFORMATION:

APPLICANT: The Brigham & Women's Hospital, Inc.

APPLICANT: Beler, David

APPLICANT: Herron, Bruce

APPLICANT: Rao, Cherie

TITLE OF INVENTION: p53 Binding Protein-Related Protein in Cardiomyopathy

FILE REFERENCE: 81994/275368

CURRENT APPLICATION NUMBER: US/10/171,384

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 4

SOFFWARE: Patentin version 3.0

SEQ ID NO 3

LENGTH: 827

TYPE: PRT

COGRANISM: Homo sapiens

US-10-171-384-3
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 0; Gaps
 Query Match
47.0%; Score 140; DB 9; Length 827;
Best Local Similarity 62.5%; Pred. No. 0.0082;
Matches 25; Conservative 1; Mismatches 14; Indels
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Search completed: May 7, 2003, 17:30:54 Job time : 15.5911 secs

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|             |               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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OM protein - protein search, using sw model

7, 2003, 16:41:02 ; Search time 9.7446 Seconds (without alignments) 513.008 Million cell updates/sec Мау Run on:

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52

Scoring table:

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283224 Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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#### SUMMARIES

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|           | Description           | 68K outer membrane | pertactin - Bordet | outer membrane pro | hypothetical 47.8K | protein-tyrosine-p | cysteine-rich exte | pherophorin-S - Vo | sulfated surface q | UL36 protein - hum | hypothetical prol1 |        |        |          | nuclear protein EB | proline-rich prote | proline-rich prote | cysteine-rich exte | chitinase (EC 3.2. | hypothetical prote | hydroxyproline-ric | pistil extensin-li | hypothetical prote | alpha/beta-gliadin | acrosin (EC 3.4.21 | extensin - Volvox | T20H2.9 protein - | glyceraldehyde-3-p | hypothetical prote |        |
| SUMMAKIES | ID                    | A47675             | S15204             | A32560             | JC2301             | T14355             | A48232             | T10798             | A33647             | <b>WMB</b> ЕН6     | A34043             | S16748 | T48814 | AE2295 · | S42442             | T17547             | S21961             | B48232             | S51939             | T24470             | T07907             | JQ1696             | T18281             | E22364             | S47538             | S22697            | A86335            | 149681             | T10340             | в96534 |
|           | DB                    | 7                  | 7                  | 7                  | 7                  | N                  | 7                  | 7                  | ~                  | ч                  | 7                  | ~      | N      | 7        | 7                  | 7                  | ~                  | ~                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | ~                 | 7                 | ~                  | 7                  | 7      |
|           | Query<br>Match Length | 911                | 922                | 910                | 430                | 1494               | 209                | 599                | 485                | 3164               | 141                | 449    | 1952   | 383      | 487                | 544                | 534                | 196                | 439                | 165                | 446                | 426                | 1474               | 320                | 431                | 464               | 1137              | 440                | 875                | 494    |
| æ         | Query                 | 86.9               | 85.9               | 72.8               | 54.5               | 50.0               | 49.7               | 49.7               | 49.3               | 48.8               | 48.7               | 48.5   | 48.5   | 48.0     | 47.3               | 47.0               | 46.1               | 45.5               | 45.3               | 45.1               | 45.1               | 44.8               | 44.8               | 44.6               | 44.5               | •                 | 44.5              | 44.0               | 44.0               | 43.6   |
|           | Score                 | 259                | 256                | 217                | 162.5              | 149                | 148                | 148                | 147                | 145.5              | 145                | 144.5  | 144.5  | 143      | 141                | 140                | 137.5              | 135.5              | 135                | 134.5              | 134.5              | 133.5              | 133.5              | 133                | 132.5              | 132.5             | 132.5             | 131                | 131                | 130    |
|           | Result<br>No.         | 1                  | 7                  | m                  | ₹                  | S                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11     | 12.    | 13       | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                | 56                | 27                 | 28                 | 29     |

| circumsporozoite p | pneumococcal surfa<br>hypothetical prote | Huntington disease hypothetical prote | proline-rich prote | nypotnetical prote<br>alpha/beta-gliadin | AcOrf-66 protein -<br>extensin class I ( | hypothetical prote | unknown protein [1 | hypothetical prote | HD protein - mouse |
|--------------------|------------------------------------------|---------------------------------------|--------------------|------------------------------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|
| OZZOMB<br>OZZOBK   | F95013<br>F75518                         | A46068<br>H83619                      | T17531             | A/1415<br>T06504                         | C72858<br>S14970                         | E87649             | G86441             | 875138             | 149729             |
|                    | 77                                       | 20                                    | ~                  | N (7)                                    | ~ ~                                      | ~                  | 4 73               | 7                  | ~                  |
| 332<br>348         | 744                                      | 3144                                  | 412                | 285<br>282                               | 808<br>132                               | 270                | 1201               | 1749               | 3119               |
| 43.5               |                                          | 4 4<br>2 3<br>8 0                     | 42.8               | 6.6                                      | 42.6                                     | 42.3               | 2.3                | 42.3               | 42.3               |
| 129.5<br>129.5     | 129.5<br>129.5                           | 128                                   | 127.5              | 127                                      | 127                                      | 126                | 126                | 126                | 126                |
| 30                 | 33<br>33                                 | 34<br>35                              | 36                 | 88<br>87                                 | ტ <b>7</b>                               | 41                 | 43                 | 44                 | 45                 |

#### ALIGNMENTS

0

559 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPP-PQRQPEAPAPQPPAGRELSAA 610 g

Pertactin - Bordetella parapertussis
N;Alternate names; outer membrane protein P70
C;Species: Bordetella parapertussis
C;Date: 07-Apr-1994 sequence\_revision 07-Apr-1994 #text\_change 08-Oct-1999
C;Accession: S15204; S14659
R;Li, L.J.; Dougah, G.; Novorny, P.; Charles, I.G.
Mol. Microbiol. 5; 409-417, 1991
A;Title: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo

A; Accession: S15204

A;Molecule type: DNA A;Residues: 1-922 <LIL> A;Cross-references: EMBL:X54547; NID:g39761; PIDN:CAA38419.1; PID:g39762 C;Genetics: A;Gene: prn C;Keywords: membrane protein

Gaps ; 9 Ouery Match
Best Local Similarity 84.5%; Pred. No. 2.4e-10;
Matches 49; Conservative 0; Mismatches 3; Indels

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25 1 GAKVPPAŘKPA----POPGPOPPOPPOPPOP--OPOPOPEAPADOPPAGRELSAA

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A; Status: preliminary
A; Residues: preliminary
A; Residues: preliminary
A; Residues: 1-209 < wub.
A; Cross references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
A; Cross references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
B; G S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
P; A; Tille: Developmental expression of tobacco pistil-specific genes encoding novel ext
A; Reference number: PQ0474; MUID:93005740; PMID:1392607
A; References: DRMA
A; Residues: 39-209 <GGL>
A; Molecule type: mRNA
A; Residues: 39-209 <GGL>
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A; Experimental source: stigma, style; strain Petit Havana SR1
C; Superfamily: glutelin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-209/Product: cystelne-rich extensin-like protein l #status experimental <AAT>
F; 146/Binding site: carbohydrate (Asn) (covalent) #status predicted
 cysteine-rich extensin-like protein 1 precursor - common tobacco C; Species: Nicotiana tabacum (common tobacco) C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000 C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000 C; Accession: A48232; PQ0475; S24617 G. May. H.; Zou. J.; May. B.; Gu., Q.; Cheung, A.Y. Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993 A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A;Reference number: A48232; MUID:93342083; PMID:8341705
 ECM-glycoproteins: The pherophori
 EMBL: AF077000; NID: 93598973; PID: 93598974; PIDN: AAC62959.1
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A;Residues: 1-599 <CGDA
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A;Experimental source: strain HK 10; sub_species Nagariensis
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 Gaps
 Gaps
 A;Description: may be involved in regulating Ha-ras-dependent cell growt C;Keywords: phosphoric monoester hydrolase
 4;
 Length 1494;
 Length 209;
 1 GAKVPP--APKPAPQPGPQPPQPPQP-PQP-PQPQPQPQPEAP--APQP
 45
 C;Accession: T10798
R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM
A;Reference number: Z17154; MUID:97162277; PMID:9009264
A;Accession: T10798
 5 РРАРКРАРОРСРОРОР ---РОРРОРОРОРОРОРОРА
 6
 Score 148; DB 2;
Pred. No. 0.00091;
 Score 149; DB 2;
Pred. No. 0.0036;
3; Mismatches 9
 5; Mismatches
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56.88;
 Query Match 50.0%;
Best Local Similarity 63.3%;
Matches 31; Conservative
 pherophorin-S - Volvox carteri
 Conservative
 A;Cross-references: EMBL:AF07
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C;Genetics:
 A; Residues: 1-1494 <CAO>
 Query Match
Best Local Similarity
 25;
 A; Gene: PTP-TD14
C; Function:
 Matches
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 П
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C; Species: Bordetella pertussis
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C; Accession: A32560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Scl. US.A. 86, 3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.6
A; Reference number: A32560; MUID: 89264462; PMID: 2542937
 A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A;Reference number: JC2299; MUID:96051989; PMID:8535973
 protein-tyrosine-phosphatase (EC 3.1.3.48) TD14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: O'Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14355
R;Cao, L; Zhang, L; Ruiz-Lozano, P; Yang, Q; Chien, K.R.; Graham, R.M.; Zhou, M. A; Bloi. Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase contains a BRO1-like domain and A;Reference number: Z18004; MUID:99361991; PMID:9694860
A;Accession: T14355
A;Status: preliminary; translated from GB/EMBL/DDBJ
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 A; Accession: JC2301
A; Molecule type: DNA
Residues: 1-430 < CMAD>
A; Cross-references: GB: D31909; GB: D17441; NID: q559718; PIDN: BAA06706.1; PID: d1007278;
 ij
 3,
 C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
K;Wada, M; Nakamura, Y.
DNA Res. 1, 163-168, 1994
 42
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A;Residues: 1-910 <CHA>
A;Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
 ---POPOPOPEAPAPO
 AAT
 23;
 10;
 ; DB 2; Length 430;
.00018;
es 4; Indels 23
 52
 A;Note: it is uncertain whether Met-1 or Met-3 is the initiator C;Keywords: membrane protein
C;Keywords: membrane protein
F;1-34/Domain: signal sequence #status predicted <SIG>F;35-910/Product: outer membrane protein P6.9 #status predicted
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 Score 217; DB 2; Length 91
Pred. No. 8.6e-08;
0; Mismatches 1; Indels
 outer membrane protein P.69 precursor - Bordetella pertussis
 hypothetical 47.8K protein - Pneumocystis carinii
 Score 162.5; 1
Pred. No. 0.00
4; Mismatches
 5 PPAPKPAPQPGP-----QPPQPPQPPQPPQ-----
 54.5%;
50.0%;
 72.8%;
78.8%;
 41; Conservative
 31; Conservative
 N; Alternate names: ORF-3
 Query Match
Best Local Similarity
Matches 41; Conserv
 Local Similarity
 A; Accession: A32560
 318
 43 PP 44
 Query Match
 317 PP
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Best Loca Matches

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RESULT 5 T14355 ö

Gaps

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C.Accession: S16748

R.Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J submitted to the EMBL Data Library, August 1991

A.Description: Cloning and characterization of a proline-rich gene expressed specific A.Reference number: S16748
 C; Species: Neurospora crassa
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C; Accession: T48814
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, April 2000
A; Reference number: 224541
 characterized by the repetitio
 C;Species: Brassica napus (rape)
C;Date: 13-Jan 1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
 -----PPQPPQPQPQPEAPAPQPPAG 46
 Length 1952;
 Length 141;
 A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
C;Genetics:
 Indels
 Indels
 hypothetical protein 15E6.220 [imported] - Neurospora crassa
 45
 A;Title: Presence in invertebrate genomes of sequences (
A;Reference number: A90159; MUID:90147742; PMID:2105723
 A; Molecule | type: m|RNA
A; Residues: | 1-449 | <ROB>
A; Cross-references: EMBL:X60376; NID:g22596; PID:g22597
 50 PPPPPASPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPSTPS
 5 PPAPKPA --- PQPGPQPPQPPQPPQPQPQPQPEAPAPQPPA
 19;
 5 PPAPKPAPOPGPQPPQPPQPPQPPQPQPGPEAPAPQPPAGR
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Pred. No. 0.0028;
3; Mismatches 12;
 Score 144.5; DB 2;
Pred. No. 0.0087;
4; Mismatches 13;
 Score 145; DB 2;
Pred. No. 0.0011;
0; Mismatches 1
 66-73, 1990
 proline-rich protein - rape (fragment)
 3 KVPPAPKPAPQPGPQPPQPPQ----
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Best Local Similarity 55.8%;
Matches 24; Conservative
 48.5%;
48.3%;
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Matches 24; Conservative
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Matches 28; Conservative
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A; Cross references: GB:M32217
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 A; Accession: T48814
A; Status: preliminary
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A; Residues: 1-1952, <SCH>
 Biophys. Res.
 A; Gene: NCSP:15E6,220
A; Map position: 2
A; Introns: 281/3
 A; Accession: A34043
 Query Match
 , RESULT 11
S16748
 RESULT 12
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 C; Species: Volvox carteri
C; Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C; Accession: A33647
R; Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A; Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular
A; Reference number: A33647; MUID:90094551; PMID:2689458
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-fre
 C; Accession: I30085
R; McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr A. Gen. Virol. 69, 1531-1574, 1988
A; Title: The complete DNA sequence of the long unique region in the genome of herpes sim A; Reference number: A30083; MUID:88274327; PMID:2839594
A; Accession: I30085
 A;Wolecule type: DNA
A;Residues: 1-3164 <MCG>
A;Cross-references: GB:X14112; NID:91944536; PIDN:CAA32311.1; PID:959536; GB:D00317
 hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment) (Species: Owenia fusiformis C;Species: Ovenia fusiformis C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000 C;Accession: A34043, B34043
R;Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
 ö
 5;
 C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 *sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
 Gaps
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 A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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 Length 3164;
 Score 148; DB 2; Length 599;
Pred. No. 0.0021;
2; Mismatches 15; Indels
 A; Status: nucleic acid sequence not shown; translation not shown
 Score 147; DB 2; Length 485;
Pred. No. 0.002;
1; Mismatches 16; Indels
 Indels
 2939 POPOPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQPQ 2982
 6 PAPKPAPQPGPQP-PQP-PQP-PQP-PQPQPQPEAPAPQPPAG 46
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 A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
 5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРЕАРАРОРР 44
 5 PPAPKPAPQPGPPQPPQPPQPPQPQPQPQPEAPAPQPP 44
 sulfated surface glycoprotein 185 - Volvox carteri
 UL36 protein - human herpesvirus 1 (strain 17)
 Query Match
Best Local Similarity 57.5%;
Matches 23; Conservative
 Match 49.3%;
Local Similarity 57.5%;
Nes 23; Conservative
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <ERT>
 Best Loca
Matches
 C; Genetics
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Gaps

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Gaps

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Length 544;

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1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-544 <GRA>
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A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
 Score 140; DB 2;
Pred. No. 0.0064;
5; Mismatches 8
 Rigraves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: 218806
A;Accession: T17547
 7, 2003, 16:55:39
 47.0%;
illarity 57.8%;
Conservative
 5 PPAPKPAPQPGPQPPQPPQP-
 Query Match
Best Local Similarity
Matches 26; Conserv
 Search completed: May 7
Job time: 10.7445 secs
 Accession: T17547
 A; Gene: A57R
 Q
 δ
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nak Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
 Dambaugh, T.; Hennessy, K.; Chammankit, L.; Kieff, E.
roc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
.iftle: UZ region of Epstein Barr virus DNA may encode Epstein Barr nuclear antigen 2, Reference number: S42447; MUID:85063846; PMID:6209719
 Species: human herpesvirus 4, Epstein-Barr virus
5Dte: 19-Mar-1997 *text_change 20-Jun-2000
5Dte: 19-Mar-1997 *text_change 20-Jun-2000
5Dte: 19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change 20-Jun-2000
5Accession: 842442; 832988; 842440; Birkenbach, M.; Kieff, E.
roc. Natl. Acad. 861, U.S.A. 83, 8056-5100, 1986
Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: 7fitle: Nucleotide sequences of PROFE PROFES PR
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE2295
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 A;Cross-references: GB:BA000019; PIDN:BAB75615.1; PID:917133050; GSPDB:GN00179
A;Experimental source: strain PCC 7120
 A;Molecule type: DNA
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A;Residues: EMBL:R03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
 Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
 Gaps
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 protein all3916 [imported] - Nostoc sp. (strain PCC 7120)
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 ö
 Length 383;
 Score 141; DB 2; Length 487;
Pred. No. 0.005;
1; Mismatches 23; Indels
 16; Indels
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPQPEAPAPGRE 48
 5 РРАРКРАРОРСРОРРОРРОРРОРОРОРОРОРОРОРОРАРОРР 44
 Score 143; DB 2;
Pred. No. 0.0031;
2; Mismatches 16
 T17547
proline-rich protein A57R - Chlorella virus PBCV-1
 Farrell, P.J.

ubmitted to the EMBL Data Library, March 1988; Reference number: S32973
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 - human herpesvirus 4
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Best Local Similarity 55.0%;
Matches 22; Conservative
 47.3%;
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 Molecule type: mRNA
Residues: 1-487 <SAM>
 Similarity
 nuclear protein EBNA2
 Species: Nostoc sp
 Molecule type: DNA
 A; Gene: all3916
 hypothetical
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7, 2003, 16:31:28 ; Search time 27.0187 Seconds (without alignments) 256.453 Million cell updates/sec
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw model
 May
 Run on:
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52 US-09-855-754B-21 298 1 GAKVPPAPKPAPQPGPQPPQ.....QPQPEAPAPQPPAGRELSAA 908470 Total number of hits satisfying chosen parameters: 908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DNT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DNT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DNT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.bAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.bAT /gcgdata/geneseq/genesegp-embl/AA1993.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1997 /SIDS2/gcgdata/geneseg/genesegp-embl/AA1991 A\_Geneseq\_101002:\* : /SIDS2/gcgdata/geneseq/geneseqp-embl/ :: /SIDS2/gcgdata/geneseq/geneseqp-embl/ /SIDS2/gcgdata/geneseq/geneseqp Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|                               | -                                                                                                                                                                                                        |
|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Description                   | B. bronchiseptica B. bronchiseptica B. bronchiseptica Pertactin antigen prn proteins. Bor Bordetella bronchi B. bronchiseptica B. bronchiseptica B. bronchiseptica Bordetella paraper Bordetella paraper |
| SUMMARIES<br>ID               | AAE16200<br>AAE16201<br>AAE16194<br>AAR14320<br>AAR14503<br>AAE16197<br>AAE16198<br>AAR16198<br>AAR16198                                                                                                 |
| ВВ                            | 23 23 23 23 23 23 23 23 23 23 23 23 23 2                                                                                                                                                                 |
| å<br>Query<br>Match Length DB | 525<br>9111<br>9111<br>922<br>922<br>922                                                                                                                                                                 |
| 8<br>Query<br>Match           | 000000000000000000000000000000000000000                                                                                                                                                                  |
| Score                         | 256<br>259<br>259<br>255<br>256<br>256<br>256<br>256                                                                                                                                                     |
| Result<br>No.                 | 100000000000000000000000000000000000000                                                                                                                                                                  |

| B. bronchiseptica B. bronchiseptica B. bronchiseptica Pertactin antigen B. bronchiseptica B. bronchiseptica | ordetella per<br>condetella per<br>condetella per<br>peride BBOS of<br>peride GB3 de<br>geptide | Streptococcus pneu<br>S. pneumoniae 8P09<br>Streptococcus pneu<br>Ser-Pro-Pro ge |
|-------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|
| AAE16195<br>AAE16199<br>AAE16196<br>AAR14321<br>AAE16193<br>AAE16202                                        | AARI 6184 AARI 1146 AARI 1739 AARI 1739 AARI 1737 AARI 2321 AARO 2076 AARO 2076 AARO 2076 AARO 20124 AARO 20136 AARO 20136 AARO 2014 AARO 2016 AARO 2016 AARO 2016 AARO 2017                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | AAV8121/<br>AAY81652<br>ABB78537                                                 |
| 53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>53<br>5                             | 008222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 23 23 23 23 23 23 23 23 23 23 23 23 23 2                                         |
| 9<br>9<br>53<br>4<br>4<br>8<br>8<br>8<br>8<br>8<br>8                                                        | 9910<br>9110<br>9110<br>9110<br>9110<br>9110<br>9110<br>9110                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 745<br>745<br>76                                                                 |
|                                                                                                             | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                  |
| 255<br>249<br>248.5<br>246<br>238.5<br>217                                                                  | 217<br>1961<br>1962<br>1189<br>1189<br>1188<br>1188<br>1181<br>1181<br>1181<br>118                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 129.5                                                                            |
| 11<br>12<br>13<br>15<br>16                                                                                  | 71177                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 4 4 4 4<br>4 4 4 5<br>1 6 4 5                                                    |
| Taki .                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                  |

|              | 25        |           |
|--------------|-----------|-----------|
|              | peptide;  |           |
|              | standard; |           |
| RESULT 1     | AAE16200  | AAE16200; |
| RESU<br>AAE1 | Ω×        | AC        |

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ALIGNMENTS

26-MAR-2002 (first entry)

B. bronchiseptica strain II-8 pertactin outer membrane protein region II. Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.

Bordetella bronchiseptica.

W0200190143-A2. 29-NOV-2001. 

25-MAY-2000; 2000US-206969P. 23-MAY-2001; 2001WO-EP06457

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

```
The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tells, as well as biological animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 52;
 Length
Claim 26; Fig 1c; 47pp; English.
 52 AA;
 Sequence
 Query Match
 S_{X}^{A} \times S_{Y}^{A} \otimes S_{Y
```

```
Gaps
 ó
 1 GAKVPPAPKPAPQPGPQPPQPPQPPQPPQPQPQPGPEAPAPQPPAGRELSAA
 Indels
ch 100.0%; Score 298; DB 23; 1 Similarity 100.0%; Pred. No. 1.6e-16; 52; Conservative 0; Mismatches 0;
 Local Similarity
 Matches
 à
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AAE16201 standard; peptide; 54 AAE16201; **AAE16201** 

AA.

26-MAR-2002 (first entry)

B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

outer membrane protein; vaccine; Bordetella infection; Pertactin; PRN; outer membrane protein; vaccin therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001.

25-MAY-2000; 2000US-206969P

23-MAY-2001; 2001WO-EP06457.

(INSP ) INST PASTEUR.

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

forPolypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods

Claim 26; Fig 1c; 47pp; English.

(outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fillids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of The present invention relates to Bordetella bronchiseptica

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ij
 B. bronchiseptica strain II-2 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
 1; PRN; outer membrane protein; vaccine; Bordetella infection; antibiotic; antibacterial; region II.
 Gaps
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 7
 22
 1 GAKVPPAPKPAPQPGPQPPQPPQPP--PQPQPQPGPEAPAPQPPAGRELSAA
 Length 54;
 0
 Score 287; DB 23;
Pred. No. 1.2e-15;
 0; Mismatches
 Guiso-maclouf N, Boursaux-eude C;
 AAE16194 standard; peptide; 52 AA.
 Claim 26; Fig 1c; 47pp; English.
 Query Match 96.3%;
Best Local Similarity 96.3%;
Matches 52; Conservative
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 Bordetella bronchiseptica,
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 54 AA;
 Pertactin; PRN;
 WO200190143-A2.
 26-MAR-2002
 29-NOV-2001.
 AAE16194;
 Seguence
 AAE16194
 ប្បង្គល
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ä Couter membrane protein) or their fragments. Pertactin (PRN) is used as and used to detect Bordetella antiques in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiques to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a materials. The present sequence is B. bronchiseptica pertactin outer membrane protein region, II. Gaps present invention relates to Bordetella bronchiseptica pertactin 'n 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA 52 Indels 86.9%; Score 259; DB 23; 92.5%; Pred. No. 1.5e-13; 1ve 0; Mismatches 2; 1 Similarity 92.5%; 49; Conservative 52 AA; Query Match Best Local 8 Matches The ŏ

22 셤

membrane protein; piglet; probe; cleavage.

Location/Qualifiers

/label= P.68

RESULT 5

```
DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic. atrophic rhimitis in pigs
 /label= Repeat_region
570.589
/label= Repeat_region
260.262
/label= RGD_tripeptide
701.703
 AAR26503 standard; Protein; 911 AA.
 B. bronchiseptica; P.68; outer
atrophic rhinitis; alternative
 92WO-GB00561
 91GB-0006568
 (WELL) WELLCOME FOUND LTD
 (first entry)
 Bordetalla bronchiseptica
 WPI; 1992-366258/44.
N-PSDB; AAQ34566.
 prn proteins
 27-MAR-1992;
 27-MAR-1991;
 12-MAR-1993
 W09217587-A.
 15-0CT-1992
 Charles IG;
 AAR26503;
 Sequence
 Protein
 Peptide
 Pept1de
 Region
 Region
AAR26503
 à
 pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
 Length 911;
 Pichia microorganisms are transformed for the expression of
 Pichia microorganism transformants – for production of Bordetella pertactin antigens for whooping cough vaccines
 Score 259; DB 12; Length 9:
Pred. No. 1.3e-12;
0; Mismatches 2; Indels
 Pertactin; Pichia; B. pertussis; B. parapertussis.
 Location/Qualifiers
266..270
 AAR14320 standard; Protein; 911 AA.
 Disclosure; Fig 1B; 38pp; English.
 (WELL) WELLCOME FOUNDATION LTD.
 /label= repeat
271..275
 repeat
 repeat
 repeat
 repeat
 repeat
 repeat
 'label- repeat
 599..601
/label- repeat
 Query Match
Best Local Similarity 92.5%;
Matches 49; Conservative
 91WO-GB00487.
 (first entry)
 Bordetella bronchiseptica.
 574..576
/label= re
 578..580
/label- re
 570..572
/label- re
 581..583
 .589
 584..586
 label-
 label=
 label=
 Pertactin antigen P.68.
 Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14319.
 911 AA;
 28-MAR-1991;
 02-APR-1990;
 20-JAN-1992
 W09115571-A
 17-0CT-1991
 Clare JJ,
 AAR14320;
 Sequence
 Peptide
 Peptide
 Pept1de
 Pept1de
 Peptide
 Peptide
 Pept1de
 eptide
 eptide
 1989).
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/label= RGD\_tripeptide

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,
 Gaps
 The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
 .;
;
 Length 911;
 Indels
 Score 259; DB 13;
Pred. No. 1.3e-12;
0; Mismatches 2;
 standard; Protein; 911 AA.
Claim 1; Fig 1; 28pp; English.
 Query Match
Best Local Similarity 92.5%;
Matches 49; Conservative
 entire P.94 sequence.
 911 AA;
 AAE16183
 AAE16183;
 AAE16183
 RESULT
 g
 AXXX
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Gaps

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for

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 Guiso-maclouf N, Boursaux-eude C;
 Claim 26; Fig 1c; 47pp; English.
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 Bordetella bronchiseptica.
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 WO200190143-A2.
 29-NOV-2001
 QO.
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 ä
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
 B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
 for
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Pertactin, PRN, outer membrane protein, vaccine, Bordetella infection, therapy, antibiotic, antibacterial, p.68.
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 Bordetella bronchiseptica pertactin outer membrane protein, p.68.
 ;
;
 Length 911;
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSAA
 Indels
 Score 259; DB 23;
Pred. No. 1.3e-12;
0; Mismatches 2;
 Location/Qualiflers
254..299
/note= "Pertactin region I"
559..60
 Disclosure; Page 28; 47pp; English.
 Guiso-maclouf N, Boursaux-eude C;
 AAE16197 standard; peptide; 56 AA.
 86.9%;
92.5%;
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 26-MAR-2002 (first entry)
26-MAR-2002 (first entry)
 Bordetella bronchiseptica.
 Local Similarity 92.5 tes 49; Conservative
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 911 AA;
 N-PSDB; AAD26440.
 WO200190143-AZ.
 29-NOV-2001.
 Sequence
 AAE16197;
 Query Match
 Region
 Best Loca
Matches
 Region
 RESULT 7
 AAE16197
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Couter membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
 Gaps
The present invention relates to Bordetella bronchiseptica pertactin
 52
 26
 ---POPPOPPOPOPOPOPOPEAPAPOPPAGRELSAA
 Length 56;
 Score 257; DB 23;
Pred. No. 2.3e-13;
0; Mismatches 2;
 ż
 AAE16198 standard; peptide; 58
 86.2%;
86.0%;
 23-MAY-2001; 2001WO-EP06457.
 2000US-206969P.
 (first entry)
 Bordetella bronchiseptica.
 1 GAKVPPAPKPAPQPGPQP---
 49; Conservative
 (INSP) INST PASTEUR
 Best Local Similarity
 56 AA;
 WO200190143-A2
 25-MAY-2000;
 26-MAR-2002
 29-NOV-2001
 AAE16198;
 Sequence
 Query Match
 Matches
 RESULT 8
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us-09-855-754b-21.rag

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Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sa13A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb clai fragment from the pro gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBD811, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein ("P95") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD Antigenic fragments of the protein will be useful in developing an acciliular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
therapy; antibiotic; antibacterial; p.70.
 Acellular vaccine for immunisation against whooping cough -
comprises protein uncontaminated by B. para:pertussis components
and capable of binding antibodies which bind native P70 antigen
 Bordetella parapertussis pertactin outer membrane protein, p.70.
 1 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQP--QPQPQPEAPAPQPPAGRELSAA
 .
9
 Length 922
 Indels
 Score 256; DB 13;
Pred. No. 2.2e-12;
0; Mismatches 3;
 254..304
/note= "Pertactin region I"
554..621
/note= "Pertactin region II"
 Location/Qualifiers
 ¥.
 ວີ
 AAE16185 standard; Protein; 922
 Suiso-maclouf N, Boursaux-eude
 Claim 1; Fig. 1; 20pp; English.
 Query Match
Best Local Similarity 84.5%;
Matches 49; Conservative
 25-MAY-2000; 2000US-206969P
 23-MAY-2001; 2001WO-EP06457
 26-MAR-2002 (first entry)
 Bordetella parapertussis.
 (INSP) INST PASTEUR.
 WPI; 1992-250033/30.
 WPI; 2002-097639/13.
 922 AA;
 N-PSDB; AAQ26509
 N-PSDB; AAD26442
 WO200190143-A2.
 29-NOV-2001
 Sequence
 AAE16185;
 Region
 Reg 1on
 RESULT 10
AAE16185
 g
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 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 for
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 22
 /note= "contains 9 direct repeats of Pro-Gln-Pro" 712..714
/note= "motif associated with cell-cell adhesion"
 ..612
te- "contains 9 direct repeats of Pro-Gln-Pro"
 "motif associated with cell-cell adhesion"
 Whooping cough; P70 antigen; P95 precursor protein; vaccination.
 Gakvppapkpa----popgpoppoppoppopp--opoppeapadoppagrelsaa
 ;
0
 Length 58;
 "contains 5 direct, tandem repeats"
 Indels
 Score 256; DB 23;
Pred. No. 2.8e-13;
0; Mismatches 3;
 Bordetella parapertussis P95 antigen precursor
 Location/Qualifiers
 ¥
 Boursaux-eude C;
 Claim 26; Fig 1c; 47pp; English.
 AAR25578 standard; Protein; 922
 85.9%;
illarity 84.5%;
Conservative 0
 35..643
/label= P70
 91WO-GB02302
 WELL) WELLCOME FOUND LID.
 (first entry)
 260..262
/note= "m
 Bordetella parapertussis.
 . 285
 /note-
 WPI; 2002-097639/13
 Similarity
Guiso-maclouf N,
 58 AA;
 Binding-site
 08-JAN-1993
 sinding-site
 23-DEC-1991;
 21-DEC-1990;
 409211292-A
 09-JUL-1992
 49;
 Charles IG;
 Sequence
 AAR25578;
 Query Match
 Local
 Protein
 Region
 Region
 Best Loc
Matches
 RESULT
 AAR2557
q
 å
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Gaps

9

Disclosure; Page 34; 47pp; English. 

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in manial such as human or other animal tissue and human or other animal cells, as well as blological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis

922 AA; Sequence

Gaps. ; 9 Length 922; Indels Score 256; DB 23; 1 Pred. No. 2.2e-12; 0; Mismatches 3; / Match 85.9%; Local Similarity 84.5%; nes 49; Conservative Query Match Best Loca Matches

ð qq RESULT 11 AAE16195

AAE16195 standard; peptide; 60 AAE16195;

26-MAR-2002 (first entry)

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B. bronchiseptica strain II-3 pertactin outer membrane protein region

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II. SECOND SE

Bordetella bronchiseptica

WO200190143-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-EP06457

25-MAY-2000; 2000US-206969P

(INSP ) INST PASTEUR.

ΰ Guiso-maclouf N, Boursaux-eude

WPI; 2002-097639/13.

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 4jycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the

ñ antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II. 1 GAKVPPAPKPAPQPGPQP-----PQPPQPPQPPQPQPQPQPEAPAPQPPAGRELSA 10; Length 60; Score 255; DB 23; Pred. No. 3.5e-13; 0; Mismatches 2; 85.68; 80,38; Query Match 85.6 Best Local Similarity 80.3 Matches 49; Conservative 60 AA; 52 A 52 60 A 60 Sequence g 2225×8 οŽ 셤 ð

RESULT 12 AAE16199

AAE16199 standard; peptide; 48 AA.

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AAE16199;

(first entry) 26-MAR-2002 B. bronchiseptica strain II-7 pertactin outer membrane protein region II.

Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2

29-NOV-2001

23-MAY-2001; 2001WO-EP06457.

25-MAY-2000; 2000US-206969P

INSE ( INST

Guiso-maclouf N, Boursaux-eude C;

WPI; 2002-097639/13.

for Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods 

Claim 26; Fig 1c; 47pp; English.

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin protein) or their fragments. Pertactin (PRN) is used as und used to detect Bordetella antigens in biological preparations or in burifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloogical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

48 AA; Sequence

Gaps 4; Score 249; DB 23; Length 48; Pred. No. 8.5e-13; 0; Mismatches 2; Indels 83.6%; 88.5%; Best Local Similarity 88.5 Matches 46; Conservative Query Match

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Pertactin; Pichia; B. pertussis; B.bronchiseptica; ss.
 Location/Qualifiers
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610..612
/label- repeat
 (WELL) WELLCOME FOUNDATION LTD.
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 91WO-GB00487
 Bordetella parapertussis.
 575..577
/label= r
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/label- r
 266..270
/label= r
 .275
 .597
 . 600
 583..585
 586..588
 /label=
 /label=
 'label-
 label-
 label-
 Pertactin antigen P.70.
 Clare JJ, Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14320.
 932 AA;
 28-MAR-1991;
 02-APR-1990;
 WO9115571-A.
 17-0CT-1991.
 Sequence
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 Couter membrane protein) or their fragments. Pertactin (PRN) is used as waccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antipens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures, when used in affinity chromatographic columns. Pertactin is useful as antipens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological and to determine the concentration of Ab in those materials. Thus the antipens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica bertactin outer membrane protein region II.
 B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Gaps
 present invention relates to Bordetella bronchiseptica pertactin
 ÷
 1 GAKVPPAPKPAPQPGPQP-PQP-PQPPQPPQPQPQPEAPAPQPPAGRELSAA 52
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPPQP-PQRQPEAPAPQPPAGRELSAA 53
 Length 53;
 83.4%; Score 248.5; DB 23; Length 90.7%; Pred. No. 9.9e-13; 1ve 0; Mismatches 2; Indels
 AAR14321 standard; Protein; 922 AA.
 Guiso-maclouf N, Boursaux-eude C;
 AAE16196 standard; peptide; 53 AA.
 Claim 26; Fig 1c; 47pp; English.
 23-MAY-2001; 2001WO-EP06457.
 25-MAY-2000; 2000US-206969P.
 26-MAR-2002 (first entry)
 Bordetella bronchiseptica
 49; Conservative
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 Best Local Similarity
Matches 49; Conserv
 53 AA;
 WO200190143-A2.
 29-NOV-2001
 AAE16196;
 Sequence
 Query Match
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pertactin antigens. DNA sequence used are represented in AAO14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
 1 GAKVPPAPKPAPQPGPQP-PQPPQPPQP---PQP--QPQPEAPAPQPPAGRELSAA
 ..
6
 The 46 Xs represent amino acids missing in the specification
 Pichla microorganisms are transformed for the expression of
Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
 Indels
 Query March 82.6%; Score 246; DB 12;
Best Local Similarity 84.5%; Pred. No. 1.3e-11;
Matches 49; Conservative 0; Mismatches 3;
 Disclosure; Fig 1C; 38pp; English
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20-JAN-1992 (first entry)

AAR14321;

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RESULT 14

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AAR1432

RESULT 15

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
 Guiso-maclouf N, Boursaux-eude C;
 AAE16193 standard; peptide; 49 AA.
 Claim 26; Fig 1c; 47pp; English.
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P.
 26-MAR-2002 (first entry)
 Bordetella bronchiseptica
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 49 AA;
 WO200190143-A2
 29-NOV-2001.
 AAE16193;
 Sequence
AAE16193
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Gaps , , Score 238.5; DB 23; Length 49; Pred. No. 5.4e-12; 0; Mismatches 2; Indels 5 Query Match
Best Local Similarity 86.8°
Matches 46; Conservative ò

80.0%; 86.8%;

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Search completed: May 7, 2003, 16:47:10 Job time : 28.0187 secs

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Q9alp3 bordetella Q9alp3 bordetella Q9k5g1 bordetella Q9k5g1 bordetella Q9k5g1 bordetella Q9k1g4 bordetella Q9alg6 bordetella Q9alm8 bordetella Q9as6m9 bordetella Q9as6m1 bordetella Q9as6m1 bordetella Q9as6m1 bordetella Q9as6m1 bordetella Q9as6m1 bordetella Q9as6m1 bordetella Q91198 bordetella Q91198 bordetella Q91198 bordetella Q9119 bordetella Q9121 pneumocysti Q9121 pneumocysti Q9121 bomo sapien Q9674 pneumocysti Q9674 pneumocysti Q9674 pneumocysti Q9674 pneumocysti Q9674 pneumocysti Q91115 homo sapien Q8177 oryza sativ Q9674 pneumocysti Q8116 dictyostell Q6128 brassica ol Q9x16 arabidopsis
 MEDLINE-20355389; PubMed=10899896; MEDLINE-20355389; PubMed=10899896; MEDLINE-20355389; PubMed=10899896; Boursaux-Eude C., Gulso N.; Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000). EMBL; AJ250091; CAB76445.1; InterPro; IPR004899; Pertact.sup. InterPro; IPR002965; P_rich_extensn. Pfm. PF03212; Pertactin; 1.
 Gaps
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 Length 105;
 Bordecella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Protecobacteria: beta subdivision; Alcaligenaceae;
 23 GAKAPPAPKPAPQPGGPQPPQPPQPPQPPQPEAPAPQPPAGRELSAA 70
 1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 105 105
105 AA; 10884 MW; 813F1422271962B2 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Matches 48; Conservative 0; Mismatches 0;
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09S6M0
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093198
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 PRELIMINARY;
 SEQUENCE FROM N.A.
 Bordetella.
NCBI_TaxID-518;
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403.166 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 bordetell
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 US-09-855-754B-20
272
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 09kjyl 09
 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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 671580 seqs, 206047115 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

 0985H9
0985H7
0985H7
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0981H0
0981H9
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RESULT 2

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"Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
 "Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families camino acid repeats.";
 DB 2; Length 115;
 DB 2; Length 115;
 Bordetella bronchiséptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Pertactin (Fragment).
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 1 GAKAPPAPKPAPQPGPQP-PQPPQPPQRPQRPQPPAGRELSAA 48
 42 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPQPGARAPQPPAGRELSAA 90
 1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 96.1%; Score 261.5; DB 2; Length 98.0%; Pred. No. 4.5e-16; Live 0; Mismatches 0; Indels
 Indels
 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF156772; AAF82396.1; -
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF156771; AAF82395.1; -...
InterPro; IPR004999; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfan: PF03212; Pertactin; 1...
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 ö
 96.1%; Score 261.5; DB 2
98.0%; Pred. No. 4.5e-16;
Live 0; Mismatches 0
 115 AA
 115 AA
 (TrEMBLrel. 15, Created)
 PRT;
 PRT;
 Query Match
Best Local Similarity 98.0
Matches 48; Conservative
 Local Similarity 98.0
nes 48; Conservative
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 PRELIMINARY;
 115
 Keil D.J., Fenwick B.;
 Keil D.J., Fenwick B.;
 Pertactin (Fragment
 SEQUENCE FROM N.A.
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 NCBI_TaxID=518;
 Bordetella.
NCBI_TaxID=518;
 -OCT-2000
 Bordetella.
 NON_TER
NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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 STRAIN-B;
 Query Match
 Q9KJYO
Q9KJYO;
 Q9KJY1
 Best Loca
Matches
 RESULT 5
RESULT 4
 O9KJY0
 Q9KJY.
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 Boursaux Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250077; CAB76431.1; ...
InterPro; IPR004899; Pertact_sup.
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MEDILINE=20359389; PubMed=10899896;
MEDILINE=20359389; PubMed=10899896;
BOUTSBAIN-EDGC C., Guiso N.;
BOUTSBAIN-EDGC C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL, AJS50079; CABS76433.1; -.
InterPro; IPR004899; Pertact_sup.
PF03212; Pertact_in; 1.
 Gaps
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 Score 261.5; DB 2; Length 104;
Pred. No. 4.2e-16;
0; Mismatches 0; Indels 1
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 22 GAKAPPAPKPAPQPGPQPGPQPPQPPQRQPEAPAPQPPAGRELSAA 70
 105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
 104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
 104 AA.
 PRT;
 PRT;
 STRAIN-9.73H+;
MEDLINE-20359389; PubMed-10899896;
 Pfam; PF03212; Pertactin; 1.
 96.1%;
ilarity 98.0%;
Conservative
 Pertactin (P.68) (Fragment).
 PRELIMINARY;
 105
 Local Similarity
les 48; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 Bordetella.
NCBI_TaxID=518;
 NON_TER
SEQUENCE
 SEQUENCE
 Query Match
 NON_TER
 NON_TER
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 Q9K5H7
Q9K5H7;
 09К5Н9;
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Matches
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RESULT 3

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Created)
 PRT;
 STRAIN-KM22;
MEDLINE-21117018; PubMed-11179374;
Register K.B.;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
95.6%;
92.3%;
 01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
Pertactin (Fragment).
 Best_Local Similarity 92.3
Matches 48; Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 STRAIN-B14;
 Pertactin.
 NON_TER
NON_TER
SEQUENCE
 Query Match
 Q9L4E2;
 Q9ALP9
 RESULT 8
Q9ALP9
 RESULT 9
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 Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
Porymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL: AJ250081; CAB76435.1; -.
InterPro: IPR004899; Pertact.sup.
InterPro: IPR002965; P.ich_extensn.
Pfan: PF03212; Pertactin; II
 Gaps
 DB 2; Length 198;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella
 96.1%; Score 261.5; DB 2; Length 98.0%; Pred. No. 7.1e-16; Live 0; Mismatches 0; Indels
 198
20575 MW; AC940EC331A725AF CRC64;
 107 AA; 11036 MW; 1AC13209D0238107 CRC64;
 09K5H5 PRELIMINARY; PRT; 107 AA. 09K5H5; 10.0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 bronchiseptica Pertactin.";
Infect. Immun. 65:1917-1921(2001).
EMBL; AF298590; AR16691.1;
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact. Sup.
InterPro; IPR002965; P_rich_extensn.
 PRT;
 MEDLINE=21117018; PubMed=11179374;
Register K.B.;
 MEDLINE-20359389; PubMed-10899896;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
 Pertactin (P.68) (Fragment).
 Local Similarity 98.0
nes 48; Conservative
 PRELIMINARY;
 Pertactin (Fragment).
 198 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID-518;
 NCBI_TaxID=518;
 STRAIN-MBORD831
 Bordetella.
 Bordetella.
 NON_TER
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 Query Match
 09AHP0
Q9AHP0;
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 RESULT 6
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 09K5H5
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Mind A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K., Mooi F.R.;
"Role of the polymorphic region of the B.pertussis protein pertactin in immunity: implications for the design of pertussis vaccines.";
Submitted (AuG.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ245927; CAB82515.1; -.
InterPro; IPR003992; pertactin.
 Gaps
 Gaps
 4
 127 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRPQPPQRPPQPPAPQPPAGKELSAA 178
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Borteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
NCBI_TaxID=518;
 PRN. de production (Alcaligenes bronchisepticus). Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetelia.
Length 107;
 Length 200;
 Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin."; Infect. Immun. 69:1917-1921(2001).
EMBL; AKO70727; AAG38447.1; -.
InterPro; IPRO19992; pertactin.
InterPro; IPRO1999; Pertact.sup.
InterPro; IPRO3995; P. Inch.—extensn.
PF03212; Pertactin; 1.
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
 01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Last sequence update)
Last annotation update)
 Query Match 95.6%; Score 260; DB 2; L
Best Local Similarity 92.3%; Pred. No. 9.7e-16;
Matches 48; Conservative 0; Mismatches 0;
Score 260; DB 2;
Pred. No. 5.7e-16;
 911 AA
 0; Mismatches
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Gaps

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**Q9K5H1 09K5H1** 

RESULT 10 Q9K5H1

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1 GAKAPPAPKPA------PQPGPQPPQPPQPPQRPQRPPAPAPQPPAGRELSAA 48
 1 GAKAPPAPKPAPQPGPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 76
 140 GAKAPPAPKPAPQFGPQFGPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 192
 Score 259.5; DB 2; Length 215;
Pred. No. 1.1e-15;
0; Mismatches 0; Indels 5
 Pertactin (Fragment).

Bordetella bronchiseptica (Alcaligenes bronchisepticus).

Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

Bordetella.
 Bordetella bronchiseptica (Alcaligenes bronchisepticus). astetaria; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella. NCBL_TaxID=518;
 1 GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 94.9%; Score 258; DB 2; Length 11
85.7%; Pred. No. 8.8e-16;
ive 0; Mismatches 0; Indels
 22327 MW; 5C21D45CF784B4AE CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
 122 AA
 111 AA
 Interpro; IPR003992; pertactin.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
 PRT;
 PRT;
 MEDLINE-20359389; PubMed-10899896;
Infect. Immun. 69:1917-1921(2001).
EMBL; AY007263; AAG38439.1; -.
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 95.4%;
90.6%;
 Query Match 95.4
Best Local Similarity 90.6
Matches 48; Conservative
 Best Local Similarity 85.7
Matches 48; Conservative
 PRELIMINARY;
 PRELIMINARY;
 215
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215 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 STRAIN-BBCH;
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 MEDILINE—20359389; PubMed=10899896;
BOUTSBUX Ende C., Guiso N.;
POlymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250085; CAB76439.1; -
InterPro: IPR0044895; Pertact.gup.
Pfam; PF03212; Pertactin; 1.
NON_TER 109 109
 Gaps
 Gaps
 5;
 4;
 1 GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 22 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQRPPQRPEAPAPQPPAGRELSAA 74
 DB 2; Length 109;
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Ouery Match 95.6%; Score 260; DB 2; Length 911; Best Local Similarity 92.3%; Pred. No. 3.4e-15; Matches 48; Conservative 0; Mismatches 0; Indels
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 MEDLINE-21117018; PubMed-11179374;
Register K.B.;
"Novel Genetic and Phenotypic Heterogeneity in Bordetella
bronchiseptica Pertactin.";
 Indels
 109 AA; 11192 MW; 85EBEF748366DD3 CRC64;
 PRINTS; PRO1482; PERTACTIN.
PRINTS; PRO1484; PRTACTURAMLY.
SEQUENCE 911 Aa; 94093 MW; DF531A9EB4383A32 CRC64;
 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
 Score 259.5; DB 2;
Pred. No. 6.4e-16;
0; Mismatches 0;
 215 AA
 109
 InterPro; IPR003991; pertactin_vir.
InterPro; IPR004899; Pertact_sup.
Pfam; PF03212; Pertactin; 1.
 PRT;
 PRT;
 95.4%;
 Local Similarity 90.6 ses 48; Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=518;
 NCBI_TaxID=518;
 STRAIN-S010328;
 Bordetella
 SEQUENCE
 SEQUENCE
 Query Match
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Gaps

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RESULT 11 Q9ALQ4

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Length 111;

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Pertactin (P.68) (Fragment)
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 STRAIN-16039;
"Variability in the pertactin genes of Bordetella bronchiseptica solates includes regions coding for the GGXXP and PQP families of amino acid repeats.";
 1 GAKAPPAPKPA-----PQPGPQPPQPPQPPQPPQRPAPAPQPPAGRELSAA 48
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
 Length 122;
 Length 252;
 Register K.B.;

Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";

Infect. Immun. 69:1917-1921(2001).

EMBL; AY007265; AAG38441.1;

InterPro; IPR003992; pertactin.

InterPro; IPR004899; Pertact.

InterPro; IPR002965; Perich_extensn.
 94.9%; Score 258; DB 2; Length 25:
85.7%; Pred. No. 1.7e-15;
ive 0; Mismatches 0; Indels
 94.9%; Score 258; DB 2; Length 12
85.7%; Pred. No. 9.5e-16;
11ve 0; Mismatches 0; Indels
 NON_TER 1 1
NON_TER 252 252
SEQUENCE 252 AA; 26107 MW; 368C142508D77057 CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TEMBLrel. 21, Last annotation update)
Pertactin (Fragment).
 Created)
Last sequence update)
Last annotation update)
 252 AA
 PRT;
 SEQUENCE FROM N.A.
STRAIN-ATCC19395;
MEDLINE-21117018; Pubmed-11179374;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 Q9K5G7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
 Pfam; PF03212; Pertactin; 1
 Best_Local Similarity 85.79
Matches 48; Conservative
 Best Local Similarity 85.7
Matches 48; Conservative
 PRELIMINARY;
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 FROM N.A.
 Bordetella.
NCBI_TaxID=518;
 Query Match
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 09K5G7
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|----------------|------------|--------|-------|---------|-----------------|---------|------------|------------|--------------|-------------------------------|-------------|----------|---------------------------------------|-------|-------------|----------------|-------------|--------------|
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| 6              |            |        |       |         |                 |         |            |            |              |                               |             |          |                                       |       |             |                |             |              |
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|                |            | 8.     |       | ٠       |                 |         |            | •          |              |                               |             |          |                                       |       |             |                |             |              |
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| ď              | 17-<br>17- |        |       |         |                 |         | •          |            |              |                               |             |          |                                       |       |             |                |             | Ž            |
|                | • *        |        |       |         |                 |         |            | Adra d     | u.3          |                               |             |          |                                       |       |             | * 36           | 4           |              |

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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: May 7, 2003, 16:31:49; Search time 4.66099 Seconds

(without alignments)

427.133 Million cell updates/sec
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(without alignments)
427.133 Million cell updates/s
Title:
US-09-855-754B-20
Perfect score: 272
Sequence: 1 GAKAPPAPKPAPQPGPPPQ......QRQPEAPAPQPPAGRELSAA 48

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| g         |        | Description |            | P24328 bordetella |            |            | _        | _          | homo s     |           |           |        | _          |            |            | Q83949 orgyia pseu | nicotia    |            | Q9fpq6 chlamydomon | _          | P42858 homo sapien | _          |           | Q9umn6 homo sapien | _        | P78621 emericella | P10220 herpes simp | P06914 plasmodium | P08001 sus scrofa | P14918 zea mays (m |            | P58840 homo sapien | homod      | 70000      |
|-----------|--------|-------------|------------|-------------------|------------|------------|----------|------------|------------|-----------|-----------|--------|------------|------------|------------|--------------------|------------|------------|--------------------|------------|--------------------|------------|-----------|--------------------|----------|-------------------|--------------------|-------------------|-------------------|--------------------|------------|--------------------|------------|------------|
| SUMMAKIES |        | a.          | PERT_BORBR | PERT_BORPA        | PERT_BORPE | SSGP_VOLCA | EBN2_EBV | YPRO_OWEFU | BRD4_HUMAN | APG_BRANA | MOZ_HUMAN | HD_RAT | G3PT_MOUSE | Y066_NPVAC | KPC1_TRIRE | Y066_NPVOP         | EXLP_TOBAC | HXA3_MOUSE | GP1_CHLRE          | MEFD_MOUSE | HD_HUMAN           | ACRO_RABIT | APG_ARATH | TRX2_HUMAN         | HD_MOUSE | SEPA_EMENI        | TEGU_HSV11         | CSP_PLAYO         | ACRO_PIG          | EXTN_MAIZE         | RFX1_HUMAN | ACRL_HUMAN         | HXB4_HUMAN | VDRS CAPPT |
|           |        | B           | ч          | П                 | Н          | -          | Н        | ~          | -          | -         | -         | -      | -          | -          | -          | -                  | -          | -          |                    | -          | -                  | -          |           | ٦                  | Н        | -                 | Н                  |                   | -                 | -                  | -          | -                  | -          | ,          |
|           |        | Length      | 911        | 922               | 910        | 485        | 487      | 141        | 1362       | 449       | 2004      | 3110   | 440        | 808        | 1139       | 875                | 426        | 443        | 552                | 514        | 3144               | 431        | 534       | 2715               | 3119     | 1790              | 3164               | 367               | 415               | 267                | 979        | 232                | 251        | 270        |
| æ         |        | Match       | 95.6       | 94.5              | 82.0       | 46.7       | 46.7     | 45.6       | 45.2       | 45.0      |           |        |            | •          | 43.6       | •                  | ٠          | 43.2       | •                  |            | 42.6               | ٠          | 42.3      |                    | 41.5     | 41.4              | •                  | •                 | 40.1              | Ġ.                 | 6          | ς.                 | 39.5       | ٥          |
| •         |        | Score       | 260        | 257               | 223        | 127        | 127      | 124        | 123        | 122.5     | 120.5     | 119.5  | 119        | 118.5      | 118.5      | 118                | 117.5      | 117.5      | 117.5              | 117        | 116                | 115        | 115       | 114                | 113      | 112.5             | 112.5              | 109.5             | 109               | 108                | 108        | 107.5              | 107.5      | 107        |
|           | Result | No.         | 7          | 7                 | m          | 4          | 5        | φ          | 7          | 8         | 6         | 10     | 11         | 12         | 13         | 14                 | 15         | 16         | 17                 | 18         | 19                 | 20         | 21        | 22                 | 23       | 24                | 22                 | 56                | 27                | 28                 | 29         | 30                 | 31         | 33         |

|             | 043365 homo sapien<br>Q62203 mus musculu |                                                                                 |                   |                      |                   |  |
|-------------|------------------------------------------|---------------------------------------------------------------------------------|-------------------|----------------------|-------------------|--|
| ME<br>AN    | AN<br>SE                                 | AN<br>SE                                                                        | SE                | AN                   | ens<br>Ensura     |  |
| CAPU_DRO    | HXA3_HUMAN<br>S3A2_MOUSE                 | CIKF_HUM<br>PRP2_MOU                                                            | TONB_NEI          | S3A2_HUM<br>FM14_MOU | FMN1_MOU          |  |
|             |                                          |                                                                                 |                   |                      |                   |  |
| 1059<br>421 | 443                                      | 757                                                                             | 283<br>296        | 464<br>1206          | 1468<br>339       |  |
| 39.3        | 39.2                                     | 9. 8.<br>0. 8.                                                                  | 38.8<br>8.8       | 38.6                 | 38.6<br>38.4      |  |
| 107         | 106.5                                    | 105.5                                                                           | 105.5             | 102                  | 105<br>104.5      |  |
| 34<br>35    | 36                                       | 30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>3 | <b>4</b> 4<br>1 7 | 4 4<br>3 6           | <b>4</b> 4<br>5 5 |  |

## ALIGNMENTS

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 Gaps
 DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH. MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
 CELL ATTACHMENT SITE (POTENTIAL).

3 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 4
 CELL ATTACHMENT SITE (INVOLVED IN
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRPAPAPAPAPAFLSAA 48
 Length 911;
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.70) (P.95).
 0; Indels
 (APPROXIMATE).
X 3 AA REPEATS OF P-Q-P.
3078DF6EC2D987A1 CRC64;
 Pred. No. 3.1e-10;
 Score 260; DB 1;
 P.95.
PERTACTIN (P.70).
POTENTIAL.
 922 AA
 (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 41, Last annotation update
 0; Mismatches
 Signal; Virulence; Repeat.
 SUBCELLULAR LOCATION: Outer membrane.
 POTENTIAL.
 PRT;
 PIR; SI4659; SI4659.
Interpro; IPR004899; Pertact_sup.
Interpro; IPR003992; pertactin.
Interpro; IPR003991; pertactin_vir.
 MEDLINE=91251771; PubMed=2041476;
 93995 MW;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNEAMLY
 EMBL; X54547; CAA38419.1; -. EMBL; A26124; CAA01786.1; -. EMBL; A19182; CAA01454.1; -.
 95.6%;
92.3%;
 Pfam; PF03212; Pertactin; 1.
 Bordetella parapertussis.
 Conservative
 STANDARD;
 PIR; S15204; S15204.
PIR; S14659; S14659.
 911 AA;
 CONCENTRATIONS
 Similarity
 SEQUENCE FROM N.A.
 701
266
266
271
276
570
 Outer membrane;
 NCBI_TaxID=519;
 01-MAR-1992
15-JUN-2002
 01-MAR-1992
 48;
 PERT_BORPA
P24328;
 SEQUENCE
 Query Match
 Local
 REPEAT
REPEAT
REPEAT
 DOMAIN
 DOMAIN
 PERT_BORPA
 Matches
 CHAIN
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 Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.; "Structure of Bordetella pertussis virulence factor P.69 pertactin."; Nature 381:90-92(1996).
 Gaps
 STRAIN=CN2992;
MEDLINE-89254462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chaffield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular clouding and characterization of protective outer membrane protein P.69 from Bordetella pertussis.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
 1- FUNCTION: AGGLUTINGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS
 SUBCELLULAR LOCATION: Outer membrane.
DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
 (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC58D4712478 CRC64;
 48
 LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 MEDIATED BY THE R-G-D SEQUENCE: PERTACTIN MAY HAVE A PROF BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE. SUBUNIT: MONOMER.
 Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
 ADHESION TO VARIOUS EUKARYOTIC CELL
 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 10;
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella,
 Length 922;
 01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRN OR OMP69A.
 Indels
 Score 257; DB 1; L. Pred. No. 4.8e-10; 0; Mismatches 0;
 910 AA
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 Gen. Microbiol. 138:1697-1705(1992).
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-96196517; Pubmed-8609998;
 PRT;
 REVISIONS TO 264 AND 332.
MEDLINE=92407514; PubMed=1527510;
 01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last seq
 ¥.
 94.5%;
 95178
 Local Similarity 82.8
les 48; Conservative
 STANDARD;
 290
270
275
280
285
603
 Bordetella pertussis,
 922 AA;
 CONCENTRATION
 bronchiseptica.
 NCBI_TaxID=520;
 PERT_BORPE
 SEQUENCE
 Query Match
 REPEAT
REPEAT
 DOMAIN
 REPEAT
 REPEAT
 DOMAIN
 P14283
 PERT_BORPE
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Matches
 RESULT
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EMBL; J04560; AAA22980.1; ALT\_SEQ.

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21;
 SEQUENCE
 SEQUENCE
 Query Match
 EBN2 EBV
 DOMAINS
 DOMAIN
 DOMAIN
 Matches
 RESULT 5
 EBN2_EBV
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 ETTI H., Mengele R., Wenzi S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of the cellular compartment.";
J. Cell Biol. 109:349-350/1(1989).
-1- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSCUBBLE FIRROWS LAYERS THAT SURROWND INDIVIDIDAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE). THE COVALENT CROSS-LINKS ARE FORNED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
-1- FTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
 Gaps
 LINES).
5 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3067;
 CELL ATTACHMENT SITE (INVOLVED IN
ADHESION TO VARIOUS EUKARYOTIC CELL
 ;
9
 (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
 Length 910;
 Score 223; DB 1; Length 91
Pred. No. 6.3e-08;
0; Mismatches 0; Indels
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 PERTACTIN (P.69).
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-0cr-1996 (Rel. 34, Last annotation update)
101-6cr-1996 (Rel. 34, Last annotation update)
Volvox carteri.
 (APPROXIMATE).
 PRINTS; PRO1482; PERTACTIN, 1.
PRINTS; PRO1484; PRTACTINALY.
Outer membrane; Signal; Virulence; Repeat.
SIGNAL
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-f. Nagariensis / HK10;
MEDLINE-90094551; PubMed-2689458;
 3lycoprotein; Sulfation; Hydroxylation
 InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
 93452 MW;
 EMBL; X51616; CAA35953.1; -, PIR; A33647; A33647.
 82.08;
 llarity 87.5%;
Conservative
 STANDARD;
 266
266
271
276
281
286
579
910 AA;
 Local Similarity
 42;
 SSGP_VOLCA
P21997;
 DOMAIN
SEQUENCE
 Query Match
 CHAIN
 DOMAIN
 REPEAT
 REPEAT
 REPEAT
 CHAIN
 SSGP_VOLCA
 SITE
 Matches
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 MEDLINE-84270667; PubMed-6087149;
Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.G., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
 Cohen J.I., Wang F., Kieff E.;
"Epstein-Barr virus nuclear protein 2 mutations define essential domains for transformation and transactivation.";
J. Virol. 65:2545-2554(1991).
-I- FUNCTION: INVOLVED IN LATENT CYCLE. TRANSACTIVATES THE EXPRESSION
 -!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
 Gaps
 Gaps
 SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
MEDLINE-90265473; PubMed-2161150;
PELLILL, Sample C., Kieff E.;
"Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
 ranscription regulation; Activator; Nuclear protein; DNA-binding;
 ö
 ö
 6 X 2 AA TANDEM REPEATS OF R-G. DEF40D7F8ED61D1A CRC64;
 Score 127; DB 1; Length 487;
Pred. No. 0.038;
1; Mismatches 18; Indels
 DB 1; Length 485;
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=10377;
 195 POLY-PRO.
50436 MW; A52216400A031421 CRC64;
 15;
 46.7%; Score 127; DB 1; 54.1%; Pred. No. 0.038; Live 2; Mismatches
 40
 01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
 487 AA.
 4 АРРАРКРАРОРСРОРРОРРОРРОРОРОРОРОР
 POLY-PRO.
 EMBL; (V01555; CAA24877.1; ALT_INIT.
 MEDLINE=91202599; PubMed=1850028;
 52544 MW;
 46.78;
 Plarity 54.18;
Conservative
 Conservative
 Phosphorylation; Repeat.
 STANDARD;
 !- PIM: PHOSPHORYLATED.
 3BNA-2 nuclear protein.
 100
228
260
285 AA;
 487 AA;
 TRANSFAC; TO1618; -
 Best Local Similarity
Matches 20; Conserv
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 OF LMP-1
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
 Brassica napus (Rape).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
 "Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
Plant J. BILL-120(1993).
PLOYELOPHENPENTAL FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
-1- DEVELOPMENTAL STRAGE: EXPRESSED IN AMALE GAMETOGRAFISIS. DURING MICROSPORE DEVELOPMENT. HIGHER EXPRESSION IS FOUND DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
 -1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
 Roberts M.R., Foster G.D., Blundell R.P., Robinson S.W., Kumar A.,
 01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
 18; Indels
 -> GP (IN REF, 2).
D52EFE1CF9960907 CRC64;
 749 APAPVPOOPPPPPOOPPPPPPOOQOOPPPPPPPPPSMPQQAA 790
 7 APKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 DB 1;
 Score 123; DB 1
Pred. No. 0.14;
2; Mismatches
 Ş
 BROMODOMAIN 1.
 449
 EM -> GP
 PRO
 PRO.
 POLY-ARG
 LYS-RICH
 POLY-SER
 protein
 PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS50014; BROMODOMAIN_2; 2.
 POLY-
 POLY-
 POLY-POLY-
 InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 2.
PRINTS; PR00503; BROMODOMAIN.
 POLY
 SEQUENCE FROM N.A.
MEDLINE=94004980; PubMed=8401599;
 01-FEB-1995 (Rel. 31, Created)
 Repeat; Nuclear
 45.2%;
 1larity 52.4%;
Conservative
 EMBL; AF386649; AAL26987.1;
 152219
 EMBL; Y12059; CAA72780.1;
HSSP; Q92831; 1B91.
 STANDARD;
 ; BROMO; 2
 Genew; HGNC:13575; BRD4
 1033
1300
1308
1338
721
 Draper J., Scott R.;
 ¥
 Local Similarity
nes 22; Conserv
 NCBI_TaxID=3708;
 MATURATION
 SMART; SM00297
 Bromodomain;
 APG OR CEX.
 APG_BRANA
P40603;
 CONFLICT
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Matches
 DOMAIN
 APG_BRANA
 RESULT 8
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 ö
 Gaps
 MEDILINE-90147742; PubMed=2105723;
MEDILINE-90147742; PubMed=2105723;
Bakalara N., Collet J., Planells N., Thouveny Y., Fontes M.;
"Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";
Blochen. Blochen. Blochys. Res. Commun. 166:66-73(1990).
PIR; A34043; B34043.
 Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_FaxID=9606;
 Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
 ö
 Score 124; DB 1; Length 141;
Pred. No. 0.023;
0; Mismatches 18; Indels
 Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
 15745 MW; B294E884D152BDB9 CRC64;
 H-T-H MOTIF (POTENTIAL).
 BRD4_HUMAN STANDARD; PRT; 1362 AA. 060885; Q96PD3; 116-OCT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Bromodomain-containing protein 4 (HUNK1 protein).
 PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRE 44
 5 PPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGR 43
 !- SUBCELLULAR LOCATION: Nuclear (Potential).
!- SIMILARITY: CONTAINS 2 BROMODOMAINS.
 Last sequence update)
Last annotation update)
 Hypothetical proline-rich protein (Fragment).
 141 AA
 POLY - PRO
 Hypothetical protein; DNA-binding. NON_TER 1 1 DOMAIN 9 58 POLY-
 P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
01-NOV-1995 (Rel. 32, Last ann
 ch 45.6%;
l Similarity 53.8%;
21; Conservative
 SEQUENCE FROM N:A.
French C.A., Fletcher J.A.;
"Human BRD4 protein.";
 SEQUENCE OF 1-722 FROM N.A.
 STANDARD;
 141 AA;
 Query Match
Best Local Similarity
 Owenia fusiformis
 IISSUE-Placenta;
 NCBI_TaxID=6347;
 BRD4 OR HUNK1
 YPRO_OWEFU
 DNA_BIND
NON_TER
SEQUENCE
 RESULT 7
BRD4_HUMAN
 21
 Matches
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Gaps

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Length 1362;

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 and the EMBL outstation
the Swiss Institute of Bioinformatics and the EMBL outstational Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
 Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Civin C.I., Disteche C., Dube I., Frischauf A.M., Horsman D., Mitelman F., Volinia S., Watmore A.E., Housman D.E.; "The translocation r(8:16)(pll;pl3) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein."; Nat. Genet. 14:33-41(1996).
 Gaps
 SUBCELLULAR LOCATION: Nuclear.
DISEASE: PARTICIPATES IN A T(8:16)(P11;P13) CHROMOSOMAL
TRANSILOCATION THAT PRODUCES A MOZ-CBP (SHMAERA OBSERVED IN THE
M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
STMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
 42
 67
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MONOCYTIC leukemia zinc finger protein (Zinc finger protein 220).
ZNF220 OR MOZ.
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
 Pred. No. 0.068;
3; Mismatches 12; Indels 17;
 3 KAPPAPKPAPQPGPQPPQPPQ------PPQPPQRQPE---APAPQPPAG
 Score 122.5; DB 1; Length 449;
 9EFB6A3AB28EEA15 CRC64;
 2004 AA
 SIMILARITY.
 Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
 PRT;
 InterPro; IPR001386; Histone_HI/H5.
InterPro; IPR002717; MOZ_SAS.
InterPro; IPR001965; Znf_PHD.
Pfam; PF00628; PHD; 2.
Pfam; PF01853; MOZ_SAS; 1.
SMART; SM00526; H15; 1.
 IPR001087; Lipase_GDSL.
 SEQUENCE FROM N.A. MEDLINE=96376968; PubMed=8782817;
 ΒX
 48779 MW;
 EMBL; X60376; CAA42924.1; -.
 ch 45.0%;
L Similarity 43.9%;
25; Conservative
 EMBL; U47742; AAC50662.1; -. Genew; HGNC:13013; ZNF220.
 STANDARD;
 (Human).
 428 4
449 AA;
 PIR; S16748; S16748
InterPro; IPR001087
 NCBI_TaxID=9606;
 MIM; 601408;
 Homo sapiens
 MOZ_HUMAN
Q92794;
 ACT_SITE
SEQUENCE
 SITE
 Query Match
 Local
 Matches
 RESULT
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-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- TISSUE SPECIFICITY: EXPRESSED TO A HIGH DEGREE IN ALL THE REGIONS
OF THE BRAIN OF ADULTS AND IN MEIOTIC CELLES OF THE TESTIS. IN
ADDITION, VERY LOW LEVELS ARE DEFFECTED IN VARIOUS NON-NEURONAL
TISSUES (HEART, MUSCLE, LIVER, LUNG AND KIDNEY).
-i- DEVELOPMENTAL STAGE: IDENTIFIED AT HIGH LEVELS IN NEURONAL TISSUES
 Schmitt I., Baechner D., Megow D., Henklein P., Boulter J., Hamelster H., Epplen J.T., Rabes O., Hamelster H., Epplen J.T., Rabes O., "Expression of the Huntington disease gene in rodents: cloning the rat homologue and evidence for downregulation in non-neuronal tissues
 Gaps
 Rattus norvejicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 BREAKPOINT FOR TRANSLOCATION TO FORM
SMART; SM00249; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS5016; ZF_PHD_2; 2.
Protofoncogene; Chromosomal translocation; Zinc-finger; Repeat;
 ï
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Huntingtin (Huntington's disease protein homolog) (HD protein).
 Length 2004;
 Indels
 9FFBBAC3792854BA CRC64;
 13;
 DB 1;
 PPAPKPAPQPGPQPPQP-PQPPQPPQRQPEAPAPQPP 40
 Pred. No. 0.28;
1; Mismatches
 POLY-GLU.
POLY-SER.
GLN/PRO-RICH.
 Score 120.5;
 PHD-TYPE 1.
PHD-TYPE 2.
POLY-SER.
C2HC-TYPE.
POLY-GLU.
 POLY-GLU.
POLY-ARG.
POLY-GLU.
POLY-LYS.
GLU-RICH.
GLU-RICH.
 MET-RICH
 MOZ-CBP
 Hum. Mol. Genet. 4:1173-1182(1995).
 MEDLINE-96133292; PubMed-8528205;
 MEDLINE-94100980; PubMed-8275091;
 SEQUENCE OF 1773-1926 FROM N.A.
 44.3%;
 225054
 Conservative
 2004 AA;
 Similarity
 development.
 SEQUENCE FROM N.A.
 NCBI_TaxID-10116;
 Nuclear protein
 Query Match
Best Local Simi
Matches 22;
 SEQUENCE
 ZN_FING
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CONFLICT
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 3
OF EMBRYOS AS EARLY AS DAY 14.5. THIS EXPRESSION REMAINS CONSTANT IN ALL FURTHER DEVELOPMENT STAGES (UP TO THE ADULT). ON THE OTHER HAND THE EXPRESSION IN NON-NEURONAL TISSUES IS DOWN-REGULATED FROM STAGE 17.5 DAY OLD EMBRYOS.
 -1- POLYMORPHISM: THE POLY-GIN REGION DOES NOT APPEAR TO BE POLYMORPHIC, EXPLAINING THE ABSENCE OF A RODENT HD-LIKE DISORDER.
-1- SIMILARITY: CONTAINS 10 HEAT REPEATS.
-1- SIMILARITY: BELONGS TO THE HUNGTINTIN FAMILY.
 Gaps
 STRAIN-ICR SW185; TISSUE-Testis;
MEDLINE-92254745; PubMed-773666;
Welch J.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate
dehydrogenase gene (Gapd-s) expressed in post-meiotic spermatogenic
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 6
 Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.; "Expression of a glyceraldehyde 3-phosphate dehydrogenase gene specific to mouse specmatogenic cells."; Blol. Reprod. 46:869-878(1992).
 Score 119.5; DB 1; Length 3110;
 G3PT_MOUSE STANDARD: PRT; 440 AA.
064467; Q60650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
G1yceraldehyde 3-phosphate dehydrogenase, testis-specific
 10; Indels
 18 QPPPQPPPPPPPPQPPQPPQQPPPPPPUPGPAEEPLHRPKKELSA 65
 9 KPAPQPGPQPPQPPQ-PPQRQPEAPAPQP-PA-----GRELSA 47
 33C357E8FC141550 CRC64;
 DOMAIN 1.
DOMAIN 2.
DOMAIN 3.
 0.44;
 REPEATS D
REPEATS D
REPEATS D
 2; Mismatches
 POLY-GLN.
POLY-PRO.
POLY-PRO.
POLY-THR.
 Pred. No.
 POLY-GLU
 EMBL; U18650; AAA90987.1; ALT_SEQ.
 HEAT
HEAT
 HEAT
 SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-Testis;
MEDLINE-92273722; Pubmed-1375514;
 InterPro; TPR000091; Huntingtin.
Pfam; PF03541; Huntingtin; 1.
PRINTS; PR00375; HUNTINGTIN.
 3110 AA; 343757 MW;
 Genet. 16:179-189(1995).
 43.98;
 56.2%;
 Conservative
 2611
 (GAPDH)
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 GAPDS OR GAPD-S
 001022;
 Best Local Sim
Matches 27;
 SEQUENCE
 Query Match
 Repeat
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 G3PT_MOUSE
 RESULT 11
 à
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 NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: HOWOTETRAMER (BY SIMILARIYY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-WEIOTIC GERM CELLS. LEVELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
 Gaps
 GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING THE SWITCH
 + phosphate
 Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.; "The complete DNA sequence of Autographa californica nuclear
 16;
 40
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
4 (Rel. 36, Day protein in Pol-LER3 intergent region autographa californica nuclear polyhedrosis virus (AcMNPV)
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
 Length 440;
 5 PPAPK-----EAPAPQPGPQPPQPPQPPQPPQRQP----EAPAPQPP
 SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 11; Indels
 (BY SIMILARITY).
MISSING (IN REF. 2).
L -> V (IN REF. 2).
; 05FF0A093DlABD9C CRC64;
 SPERMIOGENESIS AND IN THE SPERMATOZOON.
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate
 Score 119; DB 1;
 Pred. No. 0.11;
 808 AA
 1; Mismatches
 CYS/PRO-RICH.
 HSSP; P56649; 1DSS.
MGD; MG1:95653; Gapda.
InterPro; IPR000173; GaP_dhdrogenase.
Pfam; PF02004; gpdh; 1.
Pfam; PF02800; gpdh; 2.
PRIMYS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
 POLY - PRO.
 PRT;
 MEDLINE=94303173; PubMed=8030224;
 Glycolysis; Oxidoreductase; NAD.
DOMAIN 21 41 CYS
 47657 MW;
 EMBL; M60978; AAA53033.1; -.
 46.28;
 43.8%;
 polyhedrosis virus.";
Virology 202:586-605(1994).
 U09964; AAAB0276.1;
 24; Conservative
 DEHYDROGENASE FAMILY.
 STANDARD;
 256
 283
 Nucleopolyhedrovirus.
 DURING MATURITY
 440 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=46015;
 283
 066_NPVAC
 CONFLICT
 ACT_SITE
 Query Match
```

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PF00433; pkinase_C; 1.
 KOGE_NPVOP
 Query Match
Best Local S
Matches 27
 ACT_SITE
SEQUENCE
 NP_BIND
BINDING
 DOMAIN
 DOMAIN
 DOMAIN
 RESULT 14
Y066_NPVOP
 739
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 ð
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 ï
 Gaps
 Kubicek C.P.;
*Cloning and characterisation of genes (pkc1 and pkcA) encoding
protein kinase C homologues from Trichoderma reesei and Aspergillus
 [. Gen. Genet. 250:17-28(1996).
ENZYME REGULATION: STIMULATED ABOUT TWOFOLD BY PHOSPHOLIPIDS OR
 SEQUENCE FROM N.A.
STRAIN=QM9414 / Rut C-30;
MEDLINE=96158841; Pubmed-8569684;
MOTAWELZ R., Lendenfeld T., Mischak H., Muehlbauer M., Gruber F.,
Goodnight J., de Graaff L.H., Visser J., Mushinski J.F.,
Kubicek C.P.;
 BINDING DOMAINS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 ŝ
 Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
NCBI_TaxID-51453;
 DB 1; Length 808;
 -1- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV AND LDMNPV.
 13; Indels
 POLY-PRO. 76A871D2B6633F8A CRC64;
 5 РРАРКРАРОРСРОРРОРРОРРОРО 40
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein kinase C-like (EC 2.7.1.-).
 Score 118.5; Di
Pred. No. 0.19;
 PRT; 1139 AA
 0; Mismatches
 richoderma reesel (Hypocrea jecorina).
 InterPro; IPR000861; REM_repeat.
InterPro; IPR002290; Ser_thr_pkinase.
 InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind
InterPro; IPR000719; Euk_pkinase.
 Euk_pkinase.
Pkinase_C.
 SEQUENCE 808 AA; 93973 MW;
 Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 2.
 EMBL; L22858; AAA66696.1; -.
Hypothetical protein.
 43.68;
56.18;
 EMBL; U10016; AAA97432.1; -.
 23; Conservative
 STANDARD;
 InterPro; IPR000961;
 Similarity
 PHORBOL ESTERS
 PKC SUBFAMILY.
 KPC1_TRIRE
Q99014;
 Query Match
 Local
 DOMAIN
 KPC1_TRIRE
 Matches
SSSSSSSSS
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 Gaps
 11)
MEDLINE-97271300; PubMed-9126251;
MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
"The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
 Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
 MEDLINE-95343549; PubMed-7618274;
Marons C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3,
gene essential for Orgyia pseudotsugata baculovirus DNA
 PROSITE; PSG0479; DAG_PE_BIND_DOM_1; 2.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_ADW; 1.
PROSITE; PSG0108; PROTEIN_KINASE_DOW; 1.
Transferase; Serine/threenine-protein kinase; ATP-binding; Zinc;
 3
 DB 1; Length 1139;
 083949; 065364; 000323; 01-007-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 98.6 kDa protein (ORF71). 0rgyja pseudoissugata multicapsid polyhedrosis virus (OPMNPV). Viruses; daDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
 DAG BINDING
DAG BINDING
 Virology 210;372-382(1995).
-1- SIMILARIȚY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
 3 KAPPAPKPAPQPGPQPPQPPQPPQP-PQRQPEA--PAPQPPAGRELSAA 48
 Indels
 937BB0DAB727B65C CRC64;
 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
 15;
 PHORBOL-ESTER AND PHORBOL-ESTER AND
 Score 118.5; DB pred. No. 0.24;
 Pred. No. 0.24;
4; Mismatches
 875 AA
 POLY-ALA.
POLY-GLN.
POLY-GLN.
 SEQUENCE OF 1-807 FROM N.A. MEDLINE-96201426; PubMed-8609478;
Euk_pkinase; 1.
 126055 MW;
 Gen. Virol. 77:825-837(1996).
 binding; Repeat
 SMART, SM00109; C1; 2.
SMART, SM00239; C2; 1.
SMART, SM0074; HR1; 2.
SMART, SM00133; S_TK, 1.
SMART, SM00133; S_TK, 1.
 43.6%;
 SEQUENCE OF 806-875 FROM N.A
 1 Similarity 55.1 27; Conservative
 STANDARD;
 1139 AA;
 NCBI_TaxID-164623;
ProDom; PD000001;
 Phorbol-ester
 replication."
 pseudosugata
```

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 <u>ب</u>
EMBL outstation
 Gaps
 STRAIN-cv. Petit Havana; TISSUE-Pistil;
MEDLINE-93005740; PubMed-1392607;
Goldman M.H., Pezzotti M., Seurinck J., Mariani C.;
Developmental expression of tobacco pistil-specific genes encoding novel extensin-like proteins.";
 PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN. 4 X 5 AA REPEATS OF S-P(4).
 Nicotiana tabacum (Common tobacco)
Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 Plant Cell 4:104176 [1922].
-1- TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
-1- DEVELOPMENTAL STACE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 18;
 5 PPAPKP-----APQPGPQPPQPPQPP----QPPQRQPEAPAP--QPP 40
 Score 118; . DB 1; . Length 875; Pred. No. 0.21;
 Indels
the Swiss Institute of Bioinformatics and the
 01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
 86 91 POLY-PRO.
875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
 InterPro; IPR000419; Pollen_Ole_e_I.
Pfam; PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
 426 AA
 3; Mismatches
 EMBL; U75930; AAC59070.1; -.
EMBL; U39145; AAB04047.1; -.
EMBL; D45397; BAA08236.1; -.
HSCP; P01100; IFOS.
HYPOThetical protein.
BOMAIN 86 91 PR
 Created)
 ch 43.4%;
il Similarity 46.3%;
25; Conservative
 EMBL; 214019; CAA78397.1;
PIR; JQ1696; JQ1696.
 STANDARD;
 (Rel. 29,
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=4097;
 POLLINATION
 EXLP_TOBAC Q03211;
 01-JUN-1994
 REPEAT
REPEAT
CARBOHYD
 SEQUENCE
 Query Match
 between
 SIGNAL
 DOMAIN
REPEAT
 DOMAIN
 EPEAT
 RESULT 15
EXLP_TOBAC
 CHAIN
 Matches
 a
ä
```

426 AA; 44278 MW; 51A495CC94017812 CRC64;

SEQUENCE

;

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

7, 2003, 16:41:02 ; Search time 8.99489 Seconds (without alignments) 513.008 Million cell updates/sec

Perfect score:

US-09-855-754B-20 272 1 GARAPPAPKPAPQPCPQPPQ......QRQPEAPAPQPPAGRELSAA 48 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         | 68K outer membrane |        | bra    | hypothetical 47.8K | pherophorin-S - Vo | sulfated surface q | nuclear protein EB | hypothetical prote |        |        | proline-rich prote | hydroxyproline-ric | hypothetical prote |        | proline-rich prote | proline-rich prote | lehyd  | Acorf-66 protein - | protein kinase C ( | protein-tyrosine-p | hypothetical prote |        | g      | chitinase (EC 3.2. |        |        | hypothetical prote | •⊢     | hypothetical prote |
|---------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------|--------------------|
| Ö                   | A47675             | S15204 | A32560 | JC2301             | T10798             | A33647             | S42442             | C96623             | T02632 | A34043 | S16748             | T07907             | T48814             | A48232 | S21961             | T17547             | 149681 | C72858             | S61918             | T14355             | AE2295             | T10340 | JQ1696 | S51939             | B56201 | A56201 | T00063             | A46068 | T18281             |
| DB                  | 2                  | ~      | 7      | 7                  | 7                  | 7                  | 7                  | 7                  | ~      | 7      | 7                  | 7                  | ~                  | ~      | 7                  | 7                  | 7      | ~                  | Н                  | ~                  | N                  | ~      | N      | ~                  | ~      | ~      | ~                  | ~      | 7                  |
| Length              | 911                | 922    | 910    | 430                | 599                | 485                | 487                | 929                | 1684   | 141    | 449                | 446                | 1952               | 209    | 534                | 544                | 440    | 808                | 1139               | 1494               | 383                | 875    | 426    | 439                | 206    | 514    | 1388               | 3144   | 1474               |
| %<br>Query<br>Match | 95.6               | 4      | •      | 50.9               | 47.1               | 46.7               | 46.7               | 46.7               | 46.3   | 45.6   | 45.0               | 44.7               | 44.5               | 44.1   | 44.1               | 43.9               | 43.8   | 43.6               | 43.6               | 43.6               | 43.4               |        | 43.2   | 43.2               | ٠      | 43.0   | 42.8               | 42.6   | 42.5               |
| Score               | 260                | 257    | 223    | 138.5              | 128                | 127                | 127                | 127                | 126    | 124    | 122.5              | 121.5              | 121                | 120    | 120                | 119.5              | 119    | 118.5              | 118.5              | 118.5              | 118                | 118    | 117.5  | 117.5              | 117    | 117    | 116.5              | 116    | 115.5              |
| Result<br>No.       | -                  | 7      | ю      | 4                  | D.                 | 9                  | 7                  | 80                 | o      | 10     | 11                 | 12                 | 13                 | 14     | 15                 | 16                 | 17     | 18                 | 19                 | 50                 | 21                 | 22     | 23     | 24                 | 25     | 56     | 27                 | 28     | 53                 |

|   | acrosin (EC 3.4.21 | OmpA family protei | extensin homolog T | T20H2.9 protein - | hypothetical prote | protein F2401,6 [1 | extensin-like prot | HD protein - mouse | cysteine-rich exte | extensin-like prot | extensin - Volvox | hypothetical prote | UL36 protein - hum | pistil extensin-li | hypothetical prote | . —    |  |
|---|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--|
| , | S47538             | D87682             | T06291             | A86335            | T31611             | A96650             | JQ1686             | 149729             | B48232             | T10741             | S22697            | A71416             | <b>ММВЕН6</b>      | PQ0476             | н83619             | B96534 |  |
|   | N                  | N                  | N                  | ~                 | ~                  | ~                  | ~                  | N                  | ~                  | ~                  | ~                 | ~                  | -                  | ~                  | ~                  | ~      |  |
|   | 431                | 449                | 160                | 1137              | 1585               | 70                 | 151                | 3119               | 196                | 461                | 464               | 645                | 3164               | 154                | 270                | 464    |  |
|   | 42.3               | 42.3               | 42.3               | 42.3              | 42.1               | 41.7               | 41.5               | 41.5               | 41.4               | 41.4               | 41.4              | 41.4               | 41.4               | 41.2               | 41.2               | 9.04   |  |
| _ | 115                | 115                | 115                | - 115             | 114.5              | 113.5              | 113                | 113                | 112.5              | 112.5              | 112.5             | 112.5              | 112.5              | 112                | 112                | 110.5  |  |
|   | 30                 | 31                 | 32                 | 33                | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                 | 42                 | 43                 | 44                 | 45     |  |

### ALIGNMENTS

| RESULT 1                                                                                 |                |
|------------------------------------------------------------------------------------------|----------------|
| . A47675                                                                                 |                |
| 68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica                    |                |
| C; Species: Bordetella bronchiseptica                                                    |                |
| C;Date: 19@Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999              | 1999           |
| C; Accession: A47675                                                                     |                |
| R; Li, J.; Fairweather, N.F.; Novotny, P.; Dougan, G.; Charles, I.G.                     |                |
| J. Gen. Microbiol. 138, 1697-1705, 1992                                                  |                |
| A; Title: Cloning,   nucleotide sequence and heterologous expression of the protective o | e protective o |
| A; Reference number: A47675; MUID: 92407514; PMID: 1527510                               | 4              |
| A; Contents: CN7531                                                                      |                |
| A; Accession: A47675                                                                     |                |
| A;Status: preliminary                                                                    |                |
| A;Molecule∥type: hucleic acid                                                            |                |
| A; Residues: 1-911 <li1></li1>                                                           |                |
| A; Cross-references: GB:X54815; GB:S46416; NID:q39396; PIDN:CAA38584.1; PID:q39397       | PID: 939397    |
| A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)              | 19)            |
| Query Match 95.6%; Score 260; DB 2; Length 911;                                          |                |
| Best Local Similarity 92.3%; Pred. No. 7.2e-11;                                          |                |
|                                                                                          | ps 1;          |
| Qy 1 GAKAPPAPAPKDAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48                                  |                |
|                                                                                          |                |
| Db 559 GAKAPPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP                                           |                |
|                                                                                          |                |

pertactin - Bordetella parapertussis
N.Alternate names: outer membrane protein P70
C.Species: Bordetella parapertussis
C.Species: Bordetella parapertussis
C.Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 08-Oct-1999
C.Accession: 515204; S14659
R.Lii, L.J.; Dougan, G.; Novotny, P.; Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
A.File: P.70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A.Reference number: 515204; MUID:91251771; PMID:2041476
A.Accession: S15204
A.Molecule type: DNA
A.Residues: 1-922 (LLIL)
A.Cross-references: EMBL:X54547; NID:939761; PIDN:CAA38419.1; PID:939762
C.Genetics:
A.Genetics:
A.Gene

Gaps Query Match 94.5%; Score 257; DB 2; Length 922; Best Local Similarity 82.8%; Pred. No. 1.2e-10; Matches | 48; Conservative 0; Mismatches 0; Indels 10;

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---PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48 1 GAKAPPAPKPAPQPG---á

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Gaps

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Length 599; 15; Indels

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A;Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-C;Keywords: extracellular matrix; glycoprotein; pheromone
 Wilton H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A.Title: The extracellular matrix of Volvox carteri: molecular structure of A; Reference number: A33647; MUID: 90094551; PMID: 2689458
A.Accession: A3364
A.Status: preliminary
A.Molecule type: mannA
A.Residues: 1-485 < CRIX
A.Residues: 1-485 < CRIX
A.Residues: GB.X51616; NID: 921999; PIDN: CAA35953.1; PID: 91405821
C; Keywords: glycoprotein
 C;Species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
 DB 2;
 Score 127; DB 2, Pred. No. 0.032; 2; Mismatches
 4 APPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPP 40
 Score 128; DB 2
Pred. No. 0.032;
1; Mismatches
 sulfated surface glycoprotein 185 – Volvox carteri
 РРАРКРАРОРСРОРРОРРОРРОРОЯВАРАРОРР 40
 nuclear protein EBNA2 - human herpesvirus 4
 Query Match
Best Local Similarity 54.1%;
Matches 20; Conservative
 Query Match 47.1%;
Best Local Similarity 55.6%;
Matches 20; Conservative
A; Residues: 1-599 <GOD>
 A; Accession: S42442
 RESULT 6
 ò
 셤
 g
 ö
 딥
 C; Species: Pneumocystis carinii
C; Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C; Acaesion: JC2301
R; Wada, M.; Nakamura, Y.
BDNA Res. 1, 163-168, 1994
A; Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis A; Reference number: JC2299; MUID:96051989; PMID:8535973
A; Accession: JC2201
 P.; Morrisa
 C;Species: Bordetella pertussis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: A32560
R;Charles, 1G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss
Proc. Natl. Acad. Sci. U.S.A. 86, 3554-3558, 1989
A;Title: Molecular cloning and characterization of protective outer membrane protein P.6
A;Reference number: A32560; MUID:89264462; PMID:2542937
 C;Accession: T10798
R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin A;Reference number: 217154; MUID:97162277; PMID:9009264
A;Accession: T10798
 A; Molecule type: DNA
A; Residues: 1-430
A; Residues: 1-430
A; Cross-references: GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06706.1; PID:d1007278;
 3;
 ij
 C;Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 Gaps
 Gaps
 ---PAPQP 39
 A Molecule type: DNA
A Residues: 1-910 < CHA>
A Residues: 1 is uncertain whether Met-1 or Met-3 is the initiator
A ROCE: 1 is uncertain whether Met-1 or Met-3 is the initiator
A ROCE = 1 is uncertain whether met-1 or met-3 is the initiator
C Reywords: membrane protein
E 3-1-34/Domain: signal sequence #status predicted <81G>
E 3-10/Product: outer membrane protein P6.9 #status predicted <MAT>
 564 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 621
 25;
 9
 Length 430;
 Length 910;
 Indels
 Indels
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 outer membrane protein P.69 precursor - Bordetella pertussis
 Score 138.5; DB 2;
Pred. No. 0.005;
1; Mismatches 6;
 9;
 Score 223; DB 2; L
Pred: No. 2.1e-08;
0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
 5 PPAPKPAPQPGP-----QPPQPPQPPQPPQ--RQPEA---
 hypothetical 47.8K protein - Pneumocystis carinii N; Alternate names: ORF-3
 50.9%;
ilarity 47.5%;
Conservative
 82.0%;
ilarity 87.5%;
Conservative
 - Volvox carteri
 Query Match
Best Local Similarity
Matches 42; Conserv
 Query Match
Best Local Similarity
Matches 29; Conserv
 318 P 318
 40 P 40
 pherophorin-S
 RESULT 5
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Length 485;

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A.Molecule type: mRNA
A.Residues: 1487 <SAM>
B.Farrell, P.J.

R.Farrell, P.J.

R.Farrell, P.J.

R.Farrell, P.J.

R.Accession: 53298
A.Reference number: S32973
A.Reference number: S3298
A.References: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
A.Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
A.Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
A.Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
A.T.: Hennessy, K.; Chammankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S. 81, 7632-7636, 1984
A.Title: UZ region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen
A.Reference number: S42447; MUID:85063846; PMID:6209719
C; Species: human herpesvirus 4, Epstein-Barr virus
C; Date: 19-Mar.1997 #sequence_revision 19-Mar.1997 #text_change 20-Jun-2000
C; Accession: $42442; $32988; $42447
R; Sample, J.; Human-I, M.; Braun, D.; Birkenbach, M.; Kieff, E.
Proc. 17, Human-I, M.; Braun, D.; Birkenbach, M.; Kieff, E.
A; Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: A; Reference number: $42440; MUID:86259739; PMID:3460083
 A;Molecule type: DNA
A;Realdues: 1-88', PPP', 99-487 <DAM>
A;Cross-references: EMBL:RO3333; NID:9330443; PIDN:AAA45903.1; PID:9330444
C;Superfamily: hydroxyproline-rich glycoprotein
 Score 127; DB 2
Pred. No. 0.032;
 46.7%;
52.5%;
 Query Match
Best Local Similarity
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Gaps

S Matches

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C; Species: Brassica napus (rape)
C; Species: Brassica napus (rape)
C; Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C; Accession: S16748
R; Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J. R; Description: Cloning and characterization of a proline-rich gene expressed specific A; Reference number: S16748
A; Molecule type: mRNA
A; Residues: 1.449 CROB>
A; Cross-references: EMBL; X60376; NID:922596; PID:922597
 characterized by the repetitio
 C. Species: Chlamydomonas reinhardtii
C. Date: 14-May-1999 $sequence_revision 14-May-1999 $text_change 08-Oct-1999
C. Accession: T0990 $sequence_revision 14-May-1999 $text_change 08-Oct-1999
C. Accession: T0999 $sequence_revision 14-May-1999 $text_change 08-Oct-1999
R. Rodriguez-Martinez, H.; Haring, M.A.; Von Gromof, E.; Beck, C.F.
Submitted to the EMBL Data Library, July 1997
A. Rodriguez-Martinez, E. 16207
A. Accession: T07907
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Gross-references: EMBL.AF015883; NID:92384728
A. Status: preliminary squence $status predicted <SIG>
F. 31-29/Domain: signal sequence $status predicted <MIP>
F. 30-446/Product: hydroxyproline-rich glycoprotein GAS28
 C; Species: Owenla flusiformis C; Species: Owenla flusiformis C; Species: Owenla flusiformis C; Species: Owenla flusiformis C; Date: 07-Jun-1990 #text_change 01-Dec-2000 C; Accession: A34043 B34043 R; Bakalara, N.; Ccllet, J.; Planells, R.; Thouveny, Y.; Fontes, M. Biochem. Blophys. Res. Commun. 166, 66-73, 1990
A; Title: Presence in invertebrate genomes of sequences characterized by the repe A; Reference number: A90159; MuID:90147742; PMID:2105723
A; Recession: A34043
A; Residues: 1-141 | CBAK>
A; Cross references GB: M32217
A; Accession: B34043
A; Accession: B34043
A; Accession: B34043
A; Residues: 59-136 CBAZ>
A; Cross references: GB: M32217
A; Residues: 59-136 CBAZ>
A; Cross references: GB: M32217
 proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
 hydroxyproline-rich glycoprotein GAS28 precursor - Chlamydomonas reinhardtii
 17; Gaps
 ö
 3 КАРРАРКРАРОРОРОРРОРРО------РРОРРОРОРОВЕ---АРАРОРРАС
 11 KPQPKPPPAPTPSPCPPQPPKPQPKPPAPTPSPCPPQPPKPPPAPGPSPKPG
 Length 446;
 Length 141;
 Indels
 Indels
 18;
 12;
 DB 2;
 DB 2;
 Score 124; DB 2;
Pred. No. 0.019;
0; Mismatches 18
 5 PPAPKPAROPGPOPPOPPOPPOPPOROPEAPAPOPPAGR 43
 Score 121.5; DE Pred. No. 0.07; 4; Mismatches
 Score 122.5; Di
Pred. No. 0.06;
3; Mismatches
 proline-rich protein - rape (fragment)
 Query Match
Best Local Similarity 53.8%;
Matches 21; Conservative
 45.0%;
 Query Match 44.7%;
Best Local Similarity 51.1%;
Matches 23; Conservative
 Query Match
Best Local Similarity 43.9
Matches 25; Conservative
 hypothetical
 RESULT 11
S16748
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 hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: C96623
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Luros, J.S.; Maiti, R.; Maiziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakon, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUID:21016719; PMID:11130712
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-929 <STO>
A; Conney 1.
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 A;Cross-references: EMBL:AC004991; NID:g3342751; PIDN:AAC27675.1; PID:g3342752
C;Genetics:
 Species: Homo sapiens (man)

Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
 Gaps
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 Score 126; DB 2; Length 1684;
Pred. No. 0.098;
0; Mismatches 15; Indels
 Score 127; DB 2; Length 929;
Pred. No. 0.053;
4; Mismatches 14; Indels
 C; Accession: T02632
R; Bemis, G.; Rohlfing, T.; Morris, M.
submitted to the EMBL Data Library, July 1998
A; Reference number: 214682
A; Reference number: 214682
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1684 < BEM>
 2 AKAPPAPK-PAPQPGPQPPQ-----PPQPPQRQPEAPAPQPPAGRE 44
Indels
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A;Map position: 7
A;Note: intron positions not resolved (incomplete sequence)
A;Note: WUGSC:H_DJ1186C01.1
 PPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPGRE 44
 hypothetical protein DJ1186C01.1 - human (fragment)
 4 АРРАРКРАРОРСРОРОРОРОРОРОВОРОВАРАРОРР 40
Mismatches
 4;
1;
 46.7%;
illarity 51.0%;
Conservative
 Query Match
Best Local Similarity 59.5%;
Matches 22; Conservative
 Query Match
Best Local Similarity
 A; Map position: 1
 25;
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Matches

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42 67 <MAT>

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Gaps

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Indels

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proline-rich protein APG - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997 (SAccession: S21961 (S. A. R.) Foster, G. D.; Blundell, R. P.; Robinson, S. W.; Draper, J.; Scott, R. J submitted to the EMBL Data Library, August 1991 A; Description: Cloning and characterization of a proline-rich gene expressed specific A; Reference number: S16748
 5 PPAPKPAPQPGPQP----PQPPQPPQ-----PPQRQPEAPAPQP-PA 41
 A;Accession: S21961
A;Molecule type: DNA
A;Residues: 1-534 <ROB>
A;Cross_references: EMBL:X60377; NID:g22598; PID:g22599
C;Genetics:
A;Gene: APG
 Search completed: May 7, 2003, 16:55:38
Job time : 17.9949 secs
 A; Introns: 256/1; 299/3; 387/3; 470/1
 Query Match
Best Local Similarity 53.2%;
Matches 25; Conservative
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 A;Title: Developmental expression of tobacco pistil-specific genes encoding novel extens
A;Reference number: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0475
 C; Accession: T48814
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
 CiSpecies: Nicotiana tabacum (common tobacco)
CiSpecies: Schway-1994 #sequence_trevision 26-May-1994 #text_change 01-Dec-2000
CiAccession: A4823; P00475; S24617
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain A;Reference number: A48232; MUDD:93342083; PMID:8341705
 C; Superfamily: glutelin
C; Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted
 5
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 C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 Gaps
 Gaps
 A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
 9
 Score 121; DB 2; Length 1952;
Pred. No. 0.24;
3; Mismatches 10; Indels
 cysteine-rich extensin-like protein 1 precursor - common tobacco
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 A;Molecule type: DNA
A;Residues: 1-1952 <SCH>
A;Crossreferences: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Experimental source: cosmid contig 15E6; strain 74
C;Genetics:
 A; Molecule type: mRNA
A; Residues: 39-209 <GOL>
A; Coss-references: EMBL:214020; NID:g19918; PID:g19919
A; Experimental source: stigma, style; strain Petit Havana SR1
C; Superfamily: glutelin
C; Keywords: cell
 hypothetical protein 15E6.220 [imported] - Neurospora crassa
33 SPPSPSPPPPSPPPPPPPPPPPPPPPPPPPQPDAPARKRPPPPA 276
 5 PPA-PKPAPQPGPQPPQPPQPPQRQPEAPAPQPP 40
 44.5%;
 Query Match
Best Local Similarity 59.5
Matches 22; Conservative
 A; Reference number: 224541
 Status: preliminary
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Residues: 1-209 <WUA>
 A; Gene: NCSP:15E6.220
A; Map position: 2
A; Introns: 281/3
 Status: preliminary
 A; Accession: T48814
 54
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5 PPAPKPAPQPGPQP-----PQPPQPPQP-PQRQPEAPAPQPPA 41

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Gaps

10;

Score 120; DB 2; Length 534; Pred. No. 0.1; 2; Mismatches 10; Indels

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2003, 16:53:34 ; Search time 14.3918 Seconds (without alignments) 306.927 Million cell updates/sec Мау Run on:

US-09-855-754B-20 272 Perfect score:

Sequence:

1 GAKAPPAPKPAPQPGPQPPQ......QRQPEAPAPQPPAGRELSAA 48

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

349150 seqs, 92025710 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA: Database

/cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_PUB.ppp:\*
/cgn2\_6/ptodata/2/pubpaa/PUSO6\_NEW\_PUB.ppp:\*
/cgn2\_6/ptodata/2/pubpaa/ROSO6\_NEW\_PUB.ppp:\*
/cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.ppp:\*
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep. /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

# SUMMARIES

| c                        | ! .              | 14, Appl         | 15, Appl         | 4. Appli        | 18, Appl         | 19, Appl         | 6, Appli        | 21, Appl         | 22, Appl         | 17, Appl          | 16, Appl         | 23, Appl         | 5, Appli        |                  |                  | m           | 43. Appl         | . ~              |                  |
|--------------------------|------------------|------------------|------------------|-----------------|------------------|------------------|-----------------|------------------|------------------|-------------------|------------------|------------------|-----------------|------------------|------------------|-------------|------------------|------------------|------------------|
| Description              | Sequence 20      | Sequence         | Sequence         | Sequence        | Sequence         | Sequence         | Sequence        | Sequence         | Sequence         | Sequence          | Sequence         | Sequence         | Sequence        | Sequence 24,     | Sequence 43      | Sequence 43 | Sequence 43      | Sequence 47,     | Seguence 47      |
| ID                       | US-09-855-754-20 | US-09-855-754-14 | US-09-855-754-15 | US-09-855-754-4 | US-09-855-754-18 | US-09-855-754-19 | US-09-855-754-6 | US-09-855-754-21 | US-09-855-754-22 | ·US-09-855-754-17 | US-09-855-754-16 | US-09-855-754-23 | US-09-855-754-5 | US-09-855-754-24 | US-09-976-740-43 |             | US-10-023-523-43 | US-09-976-740-47 | US-10-023-529-47 |
| DB                       | 6                | σ                | σ                | 6               | σ                | σ                | 6               | 6                | σ                | 6                 | 6                | 6                | o,              | σ                | 6                | 12          | 12               | σ                | 12               |
| Query<br>Match Length DB | 49               | 49               | 52               | 911             | 26               | 58               | 922             | 52               | 54               | 52                | 59               | 42               | 910             | 39               | 538              | 538         | 538              | 550              | 550              |
| Query<br>Match           | 100.0            | 96.1             | 92.6             | 92.6            | 94.9             | 94.5             | 94.5            | 91.5             | 91.2             | 89.7              | 88.4             | 82.0             | 82.0            | 74.4             | 43.2             | 43.2        | 43.2             | 42.6             | 42.6             |
| Score                    | 272              | 261.5            | 260              | 260             | 258              | 257              | 257             | 249              | 248              | 244               | 240.5            | 223              | 223             | 202.5            | 117.5            | 117.5       | 117.5            | 116              | 116              |
| Result<br>No.            | Н                | 7                | e                | 4               | S                | 9                | 7               | 8                | 6                | 10                | 11               | 12               | 13              | 14               | 15               | 16          | 17               | 18               | 19               |

| Sequence 47, Appl Sequence 7, Appl Sequence 2, Appl Sequence 4, Appl Sequence 4, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 22, Appl Sequence 23, Appl Sequence 2, Appl Sequence 2, Appl Sequence 34, Appl Sequence 36, Appl Sequ | Sequence 63, Appl   |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------|
| 12 US-10-023-523-47 10 US-09-904-987-7 9 US-10-077-584-9 10 US-09-823-240-2 9 US-10-077-584-4 9 US-10-171-384-3 10 US-09-925-300-1444 9 US-10-171-384-3 10 US-09-925-300-1444 9 US-10-067-45-5 10 US-09-925-300-1444 9 US-10-067-45-5 9 US-10-067-45-5 9 US-09-298-5238-61 9 US-09-298-5238-61 9 US-09-298-5238-61 9 US-09-298-5238-61 9 US-09-298-5238-61 10 US-09-298-5238-62                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 9 US-09-298-523B-63 |
| 550<br>68<br>80<br>171<br>171<br>138<br>638<br>638<br>639<br>690<br>691<br>1134<br>701<br>707<br>707<br>316                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 670                 |
| 44444466666666666666666666666666666666                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 37.7                |
| 1116<br>1116<br>1117<br>1118<br>1118<br>1119<br>1119<br>1119<br>1119<br>1119                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 102.5               |
| 01102222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 45                  |
| Acres 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                     |

### ALIGNMENTS

```
APPLICANT: BOURSAUX EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERFACTIN IN BORDETELLA PERFUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTISSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTISSIS, AND BORDETELLA
TITLE OF INVENTION: BORDETELLA PARAPERTISSIS, AND IN
FILLE REPERBOUED: 10495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
SUFTWARE: PATEUTING DATE: 2000-05-25
SUFTWARE: PATEUTIN VET: 2.1
 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF, INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
 Gaps
 ö
 Length 48;
 1 GAKAPPARKPAPQPGPQPPQPPQPPQPQRQPEAPAPQPPAGRELSAA 48
 Query Match 100.0%; Score 272; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 48; Conservative 0; Mismatches 0;
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-20
Sequence 20, Application US/09855754 Publication No. | US20020192237A1 GENERAL INFORMATION:
 Sequence 14, Aprlication US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 RESULT 2
US-09-855-754-14
 SEQ ID NO 20
LENGTH: 48
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CURRENT APPLICATION NUMBER: US/09/855,754
 US-09-855-754-19
 SEQ ID NO 18
LENGTH: 56
 Query Match
Best Local S
Matches 48
 TYPE: PRT
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PARABERTISSIS, AND BONDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 2001-09-10
 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPLICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
 Gaps
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 TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEY: 2.1
 REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
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 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 Length 49;
 Query Match 95.6%; Score 260; DB 9; Length 52; Best Local Similarity 92.3%; Pred. No. 2.2e-12; Matches 48; Conservative 0; Mismatches 0; Indels
 1 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 Score 261.5; DB 9;
Pred. No. 1.6e-12;
 0; Mismatches
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-14
 Sequence 15, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 Sequence 4, Application US/09855754; Publication No. US20020192237A1; GENERAL INFORMATION:
 FILE REFERENCE: 03495-0206-00000
 ch 96.1%;
1 Similarity 98.0%;
48; Conservative
 2000-05-25
 PRIOR FILING DATE: 2000-05-7
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
 PRIOR APPLICATION NUMBER:
 Query Match
Best Local Similarity
 RESULT 3
US-09-855-754-15
 RESULT 4
US-09-855-754-4
 SEQ ID NO 15
LENGTH: 52
 SEQ ID NO 14
 LENGIH:
 Matches
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REPEATED
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 GENERAL INFORMATION:
APPLICANT: BOURSAND: CAROLINE
APPLICANT: BURSAND: EUDE, CAROLINE
APPLICANT: BURSAND: EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REF
TITLE OF INVENTION: REGIONS OF PERTACTION IN BORDETELLA PERTUGSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND ITLE OF INVENTION: IMMUNOSENIC COMPOSITIONS
FILE REPERRENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT ELLING DATE: 2001-09-10
PRIOR APPLICANION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RE
TITLE OF INVENTION: PREJECT OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOSERIC COMPOSITIONS
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
 1 GAKAPPAPKPA------PQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 4
 Length 911;
 Length 56;
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 0; Indels
 Score 260; DB 9;
Pred. No. 2.3e-11;
0; Mismatches 0;
 94.9%; Score 258; DB 9;
85.7%; Pred. No. 3.2e-12;
iive 0; Mismatches 0
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
 ; TYPE: PRT; ORGANISM: Bordetella bronchiseptica
US-09-855-754-18
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-4
 Sequence 19, Application US/09855754
Publication No. US/0020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX_EUDE, CAROLINE
 US-09-855-754-18
; Sequence 18, Application US/09855754
; Publication No. US20020192237A1
 ch 95.6%;
1 Similarity 92.3%;
48; Conservative
 Query Match 94.99
Best Local Similarity 85.79
Matches 48; Conservative
 PatentIn Ver. 2.1
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
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Gaps

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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTINI IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONDETELLA PARABERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGCENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: USO/9/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: PREGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQP-----PQRQPEAPAPQPPAGRELSAA
 Length 52;
 Length 54;
 Length 52;
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQP----PQRQPEAPAPQPPAGRELSAA
 Indels
 89.7%; Score 244; DB 9; I
88.7%; Pred. No. 2.8e-11;
Live 0; Mismatches 0;
 Score 249; DB 9;
Pred. No. 1.3e-11;
 Score 248; DB 9;
Pred. No. 1.5e-11;
 0; Mismatches
 0; Mismatches
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-17
 ; ORGANIȘM: Bordetella bronchiseptica
US-09-855-754-22
 60/206,969
 Sequence 17, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 US-09-855-754-22

Sequence 22, Application US/09855754

Publication No US20020192237A1

GENERAL INFORMATION:
 APPLICANT: BOUKSAUX-EUDE, CAROLINE APPLICANT: GUISO-MACLOUF, NICOLE
 91.5%;
88.5%;
 Query Match
Best Local Similarity 85.2%;
Matches 46; Conservative
 2000-05-25
 Query Match
Best Local Similarity 88.5
Matches | 46; Conservative
 Best_Local Similarity 88.7
Matches 47; Conservative
 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.
 US-09-855-754-17
US-09-855-754-21
 SEQ ID NO 22
LENGTH: 54
 SEQ ID NO 17
LENGTH: 52
 Query Match
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 APPLICANT: GUISO-MACLOUF, NICOLEMENT GUISO-MACLOUF, NICOLEMENT GUISO-MACLOUF, NICOLEMENT GUISO-MACLOUF, NICOLEMENT GUISO-MACLOUF, NICOLEMENT GUISO-MACLOUF, NICOLEMENT GUINDENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT PELLING DATE: 2010-09-10

PRIOR FILLING DATE: 2000-05-25
 Gaps
 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILLE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT FILING DATE: 2001-09-10
 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 10;
 10
 Length 922;
 Score 257; DB 9; Length 922
Pred. No. 3.8e-11;
0; Mismatches 0; Indels
 Length 58;
 Score 257; DB 9; Pred. No. 3.8e-12; 0; Mismatches 0;
 TYPE: PRT ORGANISM: Bordetella bronchiseptica
 ; ORGANISM: Bordetella bronchiseptica
US-09-855-754-19
 PRIOR APPLICATION NUMBER: 60/206,969
 ; ORGANISM: Bordetella parapertussis
US-09-855-754-6
 Sequence 21, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
 APPLICANT: BOURSAUX-EUDE, CAROLINE
 CAROLINE
 US-09-855-754-6
; Sequence 6, Application US/0985754
; Publication No. US20020192237A1
; GENERAL INFORMATION:
 / Match 94.5%;
Local Similarity 82.8%;
nes 48; Conservative
 ch 94.5%;
1 Similarity 82.8%;
48; Conservative
 3000-05-25
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.
 APPLICANT: BOURSAUX-EUDE,
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
 Query Match
Best Local Similarity
 RESULT 8
US-09-855-754-21
 SEQ ID NO 19
LENGTH: 58
TYPE: PRT
 SEQ ID NO 21
LENGTH: 52
 SEQ ID NO 6
 PE: PRT
 Query Match
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Matches
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US/09855754

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GUISO-MACLOUF, NICOLE
 Sequence 5, Application US/0985; Publication No. US20020192237A1
 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE,
 RESULT 15
US-09-976-740-43
 Query Match
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 APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDEFELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNICABLICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNICABLICAL COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PAPELCATION NUMBER: 60/206,969
 THE REPEATED
 Gaps
 Gaps
 1 GAKAPPAPKPA------PQPGPQPPQPPQPPQPPQRQPEAPAPPQPPAGRELSAA 48
 APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLONE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING FOLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BONDETELLA PRARPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND INTILE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
THIS REPERBUSE: 03409-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
 13;
 ;
48
 DB 9; Length 59;
 GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 / Match 82.0%; Score 223; DB 9; Length 42; Local Similarity 87.5%; Pred. No. 6.8e-10; es 42; Conservative 0; Mismatches 0; Indels
 Indels
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 ö
 Score 240.5; DB 9
Pred. No. 5.5e-11;
 0; Mismatches
 , ORGANISM: Bordetella bronchiseptica US-09-855-754-23
 PRIOR APPLICATION NUMBER: 60/206,969 PRIOR FILING DATE: 2000-05-25
 ORGANISM: Bordetella bronchiseptica US-09-855-754-16
 Sequence 23, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
 US-09-855-754-16
; Sequence 16, Application US/09855754
; Publication No. US20020192237Al
; GENERAL INFORMATION:
 ch 88.4%;
1 Similarity 78.3%;
47; Conservative (
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver.
 Query Match
Best Local Similarity
 US-09-855-754-23
 SEQ ID NO 23
 SEQ ID NO 16
 Query Match
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Gaps
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PRAAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
 ΝÏ
 TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE RETITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISSEPTICA, THEIR USE IN DIAGNOSTICS, AND FITLE OF INVENTION: BRONCHISSEPTICA, THEIR USE IN DIAGNOSTICS, AND FILLE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
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9
 DB 9; Length 39;
 Length 910;
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 1 GAKAPPAPKPAPQPEQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 score 223; DB 9;
Pred. No. 8.8e-09;
0; Mismatches 0;
 74.4%; Score 202.5; DB 981.2%; Pred. No. 1.7e-08;
 0; Mismatches
 Score 223;
 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
 Sequence 43, Application US/09976740 Publication No. US20020194633A1
 Sequence 24, Application US/09855754 Publication No. US20020192237A1
 GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
 GUISO-MACLOUF, NICOLE
 ;
 : TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-855-754-5
 82.0%;
11 Similarity 87.5%;
42; Conservative
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 910
 Best Local Similarity 81.2
Matches 39; Conservative
 Query Match
Best Local Similarity
Matches 42; Conserv
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us-09-855-754b-20.rapb
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APPLICANT: Law, Simon W.

APPLICANT: Law, Simon W.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THERSOLEROSIS

FILE REFERENCE: 1079-004001

CURRENT FILING DATE: 2001-10-12

PRIOR PAPLICATION NUMBER: 09/616,289

PRIOR PAPLICATION NUMBER: 09/616,289

PRIOR PAPLICATION NUMBER: 08/979,608

NUMBER OF SEX ID NOS: 53

ORGANISM: Homo sapiens

ORGANISM: Homo sapiens

ORGANISM: Homo sapiens

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| e de la companya de l |                                                                     |                                       |                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
pertusis, Bordetella parapertusis, and Bordetella bronchiseptica.";
Infect, Immun. 68:4815-4817(2000).
EMBL; AJ2500099; CAB76443.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; Prich_extensn.
 GAKAPPAFKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
 Bordetella bronchiseptica (Alcaligenes bronchisepticus). astoteia; Proteobacteria; beta subdivision; Alcaligenaceae; Bordetella. RCBL_TaxID-518;
 11.1 AA; 11453 MW; 9B67012D3B9AEECA CRC64;
 Q9K5G7 PRELIMINARY; PRT; 111 AA. Q9K5G7; C1-C2T-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 15, Last annotation update) Pertactin (Pl.68) (Fragment).
 100.0%; Score 335; DB 2;
100.0%; Pred. No. 3.3e-21;
iive 0; Mismatches 0;
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 Q96VI4
P93797
Q8T1Y6
Q9SBM1
Q948Y6
 Q9UVD1
Q9RCX9
Q9P944
Q9UVD0
 Q8YQB7
Q69023
 0986M9
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Q8RSU0
Q01823
 09ALP3
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 MEDLINE-20359389; PubMed-10899896;
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 Pfam; PF03212; Pertactin; 1. PRINTS; PRO1217; PRICHEXTENSN.
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Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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Length 111;

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 Keil D.J., Fenvick B.;
Variability in the pertactin genes of Bordetella bronchiseptica isolates includes regions coding for the GGXXP and PQP families of amino acid repeats.

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF156773: AAF82397.1; .

InterPro: IPR004899; Pertact_sup.

PinterPro: IPR004899; Pertact_sup.

Pfan: PF03121; PRICHEXTENSN.
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Pertactin (Fragment).
Bordeteila bronchissptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Length 122;
 Register K.B.;

Novel Genetic and Phenotypic Heterogeneity in Bordetella bronchiseptica Pertactin.";

Infect. Immun. 69:1917-1921(2001).

EMBL; AY007265; AAG38441.1;

InterPro; IPR003995; Pertactin.

InterPro; IPR004899; Pertactin.

InterPro; IPR004899; Pertactin.

PRINTS; PR01482; PERTACTIN.

PRINTS; PR01482; PERTACTIN.
 1; Indels
 122 122
122 AA; 12395 MW; 8ED00966A40FF994 CRC64;
 1-UUN-2001 (TIENBLIE). 17, Last sequence update)
1-JUN-2002 (TIENBLIE). 21, Last annotation update)
 (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 21, Last annotation update)
 90.4%; Score 303; DB 2;
94.8%; Pred. No. 1.5e-18;
Live 0; Mismatches 1.
 252 AA
 Q9ALQ2;
01-JUN-2001 (TrEMBLrel. 17, Created)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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 MEDLINE-21117018; PubMed-11179374;
 Query Match
Best Local Similarity 94.8
Matches 55; Conservative
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 Pertactin (Fragment).
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 STRAIN-ATCC19395;
 NCBI_TaxID=518;
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 STRAIN=16039
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MEDIATRE-20159189; PubMed-10899896;
BOUTSBAUX-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella perapertussis, pertussis, bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250087; CAB76441.1;
 MEDITRE-20359389; PubMed-10899896;
Boursaux-Eude C., Guiso N.;
Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJJ50083; GAB7643-11. -
InterPro; IPR002965; P. Into.—Ext.—Sup.
InterPro; IPR002965; P. Into.—Extensn.
Pefan; PF0212; Pertactin; PRICHEXTENSN.
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 1 GAKAPPAPKPAPQPGPQPGPQP-PQP-PQPPQPPQPPQPPQRPQREPAPPQPPAGRELSAA 58
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 90.4%; Score 303; DB 2; Length 111; 94.8%; Pred. No. 1.4e-18; tive 0; Mismatches 1; Indels
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Score 314; DB 2; Length 115;
Pred. No. 1.8e-19;
0; Mismatches 0; Indels
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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 111 AA; 11416 MW; 5140669692808F8E CRC64;
 115 115
115 AA; 11795 MW; 3ECCBE62E901DB11 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
 01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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Interpro; IPR002965; P_info_extensn.
Pfam; PF0312; Pertactin; 1.
PRIMTS; PR01217; PRICHEXTENSN.
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96.78;
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Best Local Similarity 94.8
Matches 55; Conservative
 58; Conservative
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 NCBI_TaxID=518;
 NCBI_TaxID=518;
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 Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL; AJ250081; CAB76435.1;
InterPro; IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
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 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQRPAPAPAPAGRELSAA
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
 Length 252;
 Length 107;
 Score 284; DB 2; Length lu. Pred. No. 5.1e-17;
 Novel Genetic and Phenotypic Heterogeneity in Bordetella
 Indels
368C142508D77057 CRC64;
 11036 MW; 1AC13209D0238107 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Pertactin (P.68) (Fragment).
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 Score 303; DB 2;
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0; Mismatches 1;
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01-JUN-2002 (TrEMBLrel. 21, Last ann
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 STRAIN=KM22;
MEDLINE=21117018; PubMed=11179374;
 bronchiseptica Pertactin. ;;
nifect. Immun. 69:1917-1931(2001).
EMBL: AYOU721; AAG38447 1;
InterPro; IPR003992; pertactin.
 MEDLINE-20359389; PubMed-10899896;
26107 MW;
 Pfam; PF03212; Pertactin; 1.
PRINTS; PR01217; PRICHEXTENSN
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 Query Match 90.4%;
Best Local Similarity 94.8%;
Matches 55; Conservative
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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"Role of the polymorphic region of the B.pertussis protein pertactin in immunity; implications for the design of pertussis vaccines."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ245927; CAB82515.1; -.
InterPro; PR003992; pertactin.
InterPro; IPR003991; pertactin.
InterPro; IPR003991; pertactin.vir.
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 King A., Berbers G., Hoogerhout P., Oirschot van H.F., Knipping K.,
Mooi F.R.;
 610
 1 GAKAPPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria: Proteobacteria: beta subdivision; Alcaligenaceae;
Bordetella.
 Length 200;
 Indels
 200 AA; 20826 MW; 9F3AC6E4128942E6 CRC64;
 911 AA; 94093 MW; DF531A9EB4383A32 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P:68) (Fragment).
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 84.8%; Score 284; DB 2; I
89.7%; Pred. No. 8.3e-17;
tive 0; Mismatches 0;
 Score 284; DB 2; L
Pred. No. 2.8e-16;
0; Mismatches 0;
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InterPro, IPR004899; Pertact_sup.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF03212; Pertactin; 1.
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PRINTS; PRO1217; PRICHEXTENSN.
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MEDINE-20359389; PubMed-10899896;

Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Boursaux-Eude C., Guiso N.;

Polymorphism of Repeated Regions of Pertactin in Bordetella

Protymorphism of Repeated Regions of Pertactin in Bordetella

Infect. Immun. 68.4815.4817(2000).

EMBL; AJ250095; CAB76449.1;

EMBL; AJ250095; Pertact_sup.

InterPro; IPR0024899; Pertact_sup.

InterPro; IPR0024899; Prich extensn.
 19 GAKVPPAPKPA----PQPGPQPPQPPQPPQPPQPQPQPQPQPQPQPAPAPQPPAGRELSAA 72
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRDPAPQPPAGRELSAA
 79.1%; Score 265; DB 2; Length 10
84.5%; Pred. No. 1.9e-15;
iive 0; Mismatches 5; Indels
 107 107
107 AA; 11073 MW; AOA339BFF0EABBC6 CRC64;
 PRINTS; PRO1217; PRICHEXTENSN.
 Best Local Similarity 84.5
Matches 49; Conservative
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 SEQUENCE FROM N.A.
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 Bordetella.
NCBI_TaxID=518;
 NCBI_TaxID=518;
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 Boursaux-Eude C., Guiso N.;
"Polymorphism of Repeated Regions of Pertactin in Bordetella
"Polymorphism of Repeated Regions of Pertactin in Bordetella
pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68:4815-4817(2000).
EMBL. AJZS0085; CAB76439.11;
-InterPro; IPR004899; Pertact_Sup.
Pfam; PF03212; Pertactin; 1.
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 140 GAKAPPAPKPAPQPGPQPGPQPG----GPQPPQPPQPPQPQPGPAPAPQPPAGKELSAA 192
 1 GAKAPPAPKPAPQPGPQPQPPQPPQPPQPPQPPQPPQPPQRQPAPAPQPPAGRELSAA 58
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
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 Query Match 84.3%; Score 282.5; DB 2; Length 215; Best Local Similarity 89.7%; Pred. No. 1.2e-16; Matches 52; Conservative 0; Mismatches 1; Indels 5
 DB 2; Length 109;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 "Novel Genetic and Phenotypic Heterogeneity in Bordetella Bornofhiseptica Pertractin."; Infect. Immun. 69:1917-1921(2001).

EMBL, AY007263; AAG38439.1; ...
InterPro; IPR003992; pertactin.
InterPro; IPR004899; Pertact Sup.
 ch 84.3%; Score 282.5; DB 2; Length 1 Similarity 89.7%; Pred. No. 6.8e-17; 52; Conservative 0; Mismatches 1; Indels
 22327 MW; 5C21D45CF784B4AE CRC64;
 109 AA; 11192 MW; 85EBEF7483666DD3 CRC64;
 01-ocr-2000 (TrEMBLrel. 15, Created)
01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pertactin (P.68) (Fragment).
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 107 AA.
 01-JUN-2001 (TrEMBLrel. 17, Created)
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MEDLINE-21117018; PubMed-11179374;
MEDLINE-20359389; PubMed-10899896;
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01217; PRICHEXTENSN.
 Pfam; PF03212; Pertactin; 1.
 PRELIMINARY;
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 Pertactin (Fragment).
 215 AA;
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 Bordetella.
NCBI_TaxID=518;
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Boursaux-Eude C., Guiso N.;
Polymorphism of Repeated Regions of Pertactin in Bordetella
Ppertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
Infect. Immun. 68.4815-4817(2000).
EMBL; AJ250077; CAB76431.1;
InterPro; IPR004899; Pertact_sup.
 Gaps
 69
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 21 GAKAPPAPKPAPQPGPQPG-------PQPPQPPQPPQPPQPGAPAPQPPAGRELSAA
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 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 Indels
 104 AA; 10714 MW; 4C7248E86CFF1189 CRC64;
 01-OCT-2000 (TIEMBLREL. 15, Created)
01-OCT-2000 (TIEMBLREL. 15, Last sequence update)
01-UTN-2002 (TIEMBLREL. 21, Last annotation update)
Pertactin (P.68) (Fragment).
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 Ouery Match 78.7%; Score 263.5; DB 2; Best Local Similarity 84.5%; Pred. No. 2.4e-15; Matches 49; Conservative 0; Mismatches 0;
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 Pfam; PF03212; Pertactin; 1.
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"Polymorphism of Repeated Regions of Pertactin in Bordetella pertuussis, Bordetella parapertussis, and Bordetella bronchiseptica."; Infect. Immun. 68.4815.4815.4817(2000).
EMBL: AJ250079; CAB76433.1;
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 Reil D.J., Fenwick B.;
"Variability in the pertactin genes of Bordetella bronchiseptica
isolates includes regions coding for the GGXXP and PQP families of
 42 GAKAPPAPKPAPQPGPQPG------PQPPQPPQPPQPPQROPEAPAPQPPAGRELSAA 90
 1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPAPAPAPAGRELSAA 58
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 DB 2; Length 105;
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beta subdivision; Alcaligenaceae;
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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105 AA; 10861 MW; 1F97255EB792F4B7 CRC64;
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Human ORFX ORF2085
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Novel human diagno
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Synthetic Bordetel
Human polypeptide
 Pertactin antigen
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 B. bronchiseptica strain II-7 pertactin outer membrane protein region II.
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 Bordetella parapen
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 ALIGNMENTS
 AAW99022
AAY33500
 AAW36888
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 AA002036
 ABB70063
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 AAR28150
 AAB82806
 ABB93838
 ABG09876
 AA004573
 AAB82807
 AAE1620]
 AAE16184
 AAB4232
 AAE16199 standard; peptide; 48 AA.
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 Guiso-maclouf N, Boursaux-eude
 25-MAY-2000; 2000US-206969P
 23-MAY-2001; 2001WO-EP06457
 26-MAR-2002 (first entry
 Bordetella bronchiseptica
 325
325
406
439
538
125
 444
244
89
89
89
89
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 WO200190143-A2.
 29-NOV-2001.
257
256
249
249
247
223
202.5
202.5
165
165
135.5
135.5
 124
124
124
124
123
123
123
120.5
 117
116.5
116.5
116.5
 AAE16199;
 RESULT 1
 B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
Pertactin antigen
prin proteins. Bor
Bordetella bronchi
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
B. bronchiseptica
 ; Search time 24.9404 Seconds
(without alignments)
256.453 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1: SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*
4: SIDSZ/gcgdata/geneseqy-geneseqp-embl/AA1982.DAT:*
5: SIDSZ/gcgdata/geneseqy-geneseqp-embl/AA1983.DAT:*
5: SIDSZ/gcgdata/geneseqy-embl/AA1984.DAT:*
6: SIDSZ/gcgdata/geneseqy-embl/AA1986.DAT:*
7: SIDSZ/gcgdata/geneseqy-embl/AA1986.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1991.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA1992.DAT:*
8: SIDSZ/gcgdata/geneseqy-embl/AA19992.DAT:*
 Description
 272
1 GAKAPPAPKPAPQPGPPQPPQ......QRQPEAPAPQPPAGRELSAA
 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT.
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT.
 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 hits satisfying chosen parameters:
 908470 seqs, 133250620 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 AAE16199
AAE16193
AAE16194
AAR14320
AAR26503
AAE16196
AAE16196
AAE16198
AAE16198
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 7, 2003, 16:31:28
 a
 A_Geneseq_101002:*
 length: 0
length: 2000000000
 US-09-855-754B-20
 DB
 Length
 48
49
52
911
911
911
53
58
58
 Query
 996.1
995.6
995.6
94.9
94.5
94.5
```

of

Total number

Searched:

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

Minimum DB seq Maximum DB seq

Database

115: 116: 117: 118: 120: 131: 131:

Score

8

Result

272 261.5 260 260 260 260 250 259.5 258 257

```
The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying carresponding proteins, glycoproteins or their mixtures when used in affinity arcomatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal by fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
 B. bronchiseptica strain II-1 pertactin outer membrane protein region II.
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 Length 48;
 Indels
 1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 1 GAKAPPAPKPAPQPGPPQPPQPPQPPQRPPRAPAPAPPPAGRELSAA 48
 ch 100.0%; Score 272; DB 23; Similarity 100.0%; Pred. No. 5.1e-15; 48; Conservative 0; Mismatches 0;
 pertactin outer membrane protein region II.
 ວັ
 AAE16193 standard; peptide; 49 AA.
 Suiso-maclouf N, Boursaux-eude
 claim 26; Fig 1c; 47pp; English.
Claim 26; Fig 1c; 47pp; English.
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 Bordetella bronchiseptica
 PASTEUR
 Query Match
Best Local Similarity
 WPI; 2002-097639/13.
 48 AA;
 WO200190143-A2.
 INSP) INST
 26-MAR-2002
 29-NOV-2001.
 Sequence
 AAE16193;
 Matches
 g
G
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(outer membrane protein) or their fragments. Pertactin (FRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antiquen in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquent to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antiquen can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.

 B. bronchiseptica strain II-2 pertactin outer membrane protein region II.

 for
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Gaps
 The present invention relates to Bordetella bronchiseptica pertactin
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region {\rm II}\,.
 ï
 48
 Length 52;
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 Length
 GAKAPPAPKPAPQPGPQP-PQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 Score 261.5; DB 23; Length
Pred. No. 3.4e-14;
0; Mismatches 0; Indels
 95.6%; Score 260; DB 23;
ilarity 92.3%; Pred. No. 4.7e-14;
Conservative 0; Mismatches 0;
 Boursaux-eude C;
 Ź
 Claim 26; Fig 1c; 47pp; English.
 AAE16194 standard; peptide; 52
 96.1%;
98.0%;
 23-MAY-2001; 2001WO-EP06457
 (first entry)
 Bordetella bronchiseptica.
 48; Conservative
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 Best Local Similarity
Matches 48; Conserv
 Similarity
 52 AA;
 Guiso-maclouf N,
 49 AA;
 25-MAY-2000;
 26-MAR-2002
 29-NOV-2001.
 Sequence
 AAE16194;
 Query Match
 Sequence
 Query Match
Best Local
 Н
 Matches
 RESULT 3
 AAE16194
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Gaps

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for

20-JAN-1992

Peptide Peptide Peptide Peptide Peptide

Peptide Peptide Peptide Peptide

AAR14320;

RESULT 4 **AAR14**320

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The sequence given is the P.94 antigen from B. bronchiseptica. The P.68 antigen is formed by alternative cleavage of this protein. P.68 is an outer membrane protein with a molecular weight of 68 kD which is associated with protection of piglets against atrophic rhinitis. The DNA sequence encoding these proteins was derived by standard recombinant DNA techniques using P.68 probes to isolate the
 DNA encoding a Bordetella bronchiseptica protein - used for obtaining vaccines for preventing respiratory diseases, partic.
 B. bronchiseptica; P.68; outer membrane protein; piglet; probe;
 1 GAKAPPAFKPA----PQPGPQPPQPPQPPQRPQPEAPAPQPPAGRELSAA
 DB 13;
 Score 260; DB 13
Pred. No. 4e-13;
0; Mismatches
 cleavage
 /label= RGD_tripeptide 701..703
 701..703
/label= RGD_tripeptide
 266. 279
/label Repeat_region
 Repeat_region
 Location/Qualifiers
35..632
 AAR26503 standard; Protein; 911 AA.
 AAE16183 standard; Protein; 911 AA.
 atrophic rhinitis; alternative
 Claim 1; Fig 1; 28pp; English
 35..632
/label= P.68
 Query Match
Best Local Similarity 92.3%;
Matches 48; Conservative (
 92WO-GB00561.
 91GB-0006568
 (WELL) WELLCOME FOUND LTD
 /label= Ro
 Bordetalla bronchiseptica
 atrophic rhinitis in pigs
 570..589
 entire P.94 sequence.
 WPI; 1992-366258/44.
N-PSDB; AAQ34566.
 911 AA;
 prn proteins
 27-MAR-1992;
 27-MAR-1991;
 W09217587-A.
 12-MAR-1993
 15-0CT-1992
 Charles IG;
 Sequence
 AAR26503;
 AAE16183;
 Protein
 Peptide
 Peptide
 Region
 Region
RESULT 5
AAR26503
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 pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 ancoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
 Gaps
 48
 95.6%; Score 260; DB 12; Length 911;
1larity 92.3%; Pred. No. 4e-13;
Conservative 0; Mismatches 0; Indels
 Pichia microorganisms are transformed for the expression of
 1 GAKAPPAPKPA----PQPGPQPPQPPQPPQPPQREAPAPQPPAGRELSAA
 Pichia microorganism transformants – for production of
Bordetella pertactin antigens for whooping cough vaccines
 Pertactin; Pichia; B. pertussis; B. parapertussis.
 Location/Qualiflers
266.270
/label= repeat
271.275
/label= repeat
 AAR14320 standard; Protein; 911 AA.
 Disclosure; Fig 1B; 38pp; English
 (WELL) WELLCOME FOUNDATION LTD.
 repeat
 repeat
 78..580
label- repeat
 repeat
 repeat
 'label - repeat
 599..601
/label- repeat
 91WO-GB00487.
 (first entry)
 574..576
/label= re
 Bordetella bronchiseptica.
 581..583
/label= re
 84..586
 ..589
 Pertactin antigen P.68.
 label
 Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14319.
 Local Similarity
nes 48; Conser
 911 AA;
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28-MAR-1991; 02-APR-1990;

Clare JJ,

Sequence Query Match

Best Loca Matches

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17-0CT-1991 W09115571-A

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Gaps

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Indels

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Length 911;

48

WO200190143-A2 29-NOV-2001

Region Region

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(outer membrane protein) or their fragments. Pertactin (FRN) is used as and used to detect Bordetella antiquens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antiquens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 B. bronchiseptica strain II-5 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
 1 GAKAPPAPKPAPQPGPQP-----PQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 The present invention relates to Bordetella bronchiseptica
 Score 259.5; DB 2
Pred. No. 5.2e-14;
0; Mismatches 0
 Boursaux-eude C;
 AAE16197 standard; peptide; 56 AA
 Claim 26; Fig 1c; 47pp; English.
 95.4%;
 23-MAY-2001; 2001WO-EP06457.
 23-MAY-2001; 2001WO-EP06457.
 25-MAY-2000; 2000US-206969P.
 (first entry)
 Bordetella bronchiseptica.
 Bordetella bronchiseptica.
 48; Conservative
 (INSP) INST PASTEUR.
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 Query Match
Best Local Similarity
Matches 48; Conserv
 53 AA;
 Guiso-maclouf N,
 WO200190143-A2.
 WO200190143-A2.
 26-MAR-2002
 25-MAY-2000;
 29-NOV-2001.
 29-NOV-2001
 Sequence
 AAE16197;
 RESULT 8
 XSXXX
 g
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 ij
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as bloodgical fluids, such as human or other animal cells, as well as bloodgical fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein, p.68.
 B. bronchiseptica strain II-4 pertactin outer membrane protein region II.
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods -
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
 Gaps
 Bordetella bronchiseptica pertactin outer membrane protein, p.68.
 4;
 Score 260; DB 23; Length 911;
Pred. No. 4e-13;
0; Mismatches 0; Indels
 Location/Qualifiers
254..299
/note= "Pertactin region I"
559..610
/note= "Pertactin region II"
 therapy; antibiotic; antibacterial; p.68.
 Disclosure; Page 28; 47pp; English.
 Guiso-maclouf N, Boursaux-eude C;
 Ą.
 AAE16196 standard; peptide; 53
 Query Match
Best Local Similarity 92.3%;
Matches 48; Conservative
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 26-MAR-2002 (first entry)
26-MAR-2002 (first entry)
 Bordetella bronchiseptica
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 911 AA;
 N-PSDB; AAD26440
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AAE16196;

**AAE16196** RESULT

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Sequence

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Gaps

5. 48

DB 23; Length 0; Indels

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Sequence
 AAR25578;
 Query Match
 Protein
 Region
 Region
 RESULT 10
 888888888888%
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 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, qlycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica
 B. bronchiseptica strain II-6 pertactin outer membrane protein region II.
 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections
 for
 for
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antiblotic; antibacterial; region II.
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 1 GAKAPPAPKPA-----PQPGPQPPQPPQPPQPPQRPQRPAPAPAPGRELSAA 48
 94.9%; Score 258; DB 23; Length 56; 85.7%; Pred. No. 7.1e-14; 1ve 0; Mismatches 0; Indels
 Boursaux-eude C;
 Boursaux-eude C;
 Ź
 Claim 26; Fig 1c; 47pp; English.
 AAE16198 standard; peptide; 58
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 Bordetella bronchiseptica
 Conservative
 INSP) INST PASTEUR
 WPI; 2002-097639/13.
 Similarity
Guiso-maclouf N,
 ¥
 Guiso-maclouf N,
 Pertactin; PRN;
 WO200190143-A2.
 26-MAR-2002
 29-NOV-2001
 AAE16198;
 Sequence
 Query Match
 Local
 Best Loca
Matches
 AAE16198
 RESULT
```

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and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify intibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 Gaps
 A cosmid library was constructed by transforming E.coli HB101 with recombinant cosmids prepared by partial digestion of B.parapertussis chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb
 48
 /note="contains 9 direct repeats of Pro-Gln-Pro" 712..714
/note="motif associated with cell-cell adhesion"
 35..643
/label= P70
260..262
/note= "motif associated with cell-cell adhesion"
266..285
 Whooping cough; P70 antigen; P95 precursor protein; vaccination.
 components
 Acellular vaccine for immunisation against whooping cough - comprises protein uncontaminated by B. para:pertussis components and capable of binding antibodies which bind native P70 antigen
 --POPPOPPOPPOROPEAPAPOPPAGRELSAA
 Length 58;
 "contains 5 direct, tandem repeats"
 Score 257; DB 23;
Pred. No. 8.7e-14;
0; Mismatches 0;
 Bordetella parapertussis P95 antigen precursor.
 Location/Qualifiers
35..643
 Ź
 AAR25578 standard; Protein; 922
 Claim 1; Fig 1; 20pp; English.
 94.5%;
82.8%;
 (WELL) WELLCOME FOUND LTD
 (first entry)
 Conservative
 Bordetella parapertussis.
 575..612
 1 GAKAPPASKPAPQPG----
 /note=
 WPI; 1992-250033/30.
 Best Local Similarity
Matches 48; Conserv
 53 AA;
 N-PSDB; AAQ26509
 Binding-site
 Binding-site
 23-DEC-1991;
 21-DEC-1990;
 08-JAN-1993
 09-JUL-1992
 Charles IG;
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antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. parapertussis pertactin outer membrane protein, p.70.

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Gaps

10;

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Score 257; DB 23; Pred. No. 6.9e-13; 0; Mismatches 0;

Ouery Match 94.5%; Best Local Similarity 82.8%; Matches 48; Conservative

922 AA;

Sequence

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Length 922;

621 48

1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRPPARAPAPQPPAGRELSAA

AAE16195 standard; peptide; 60 AA.

RESULT 12 AAE16195

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Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; p.70.
clai fragment from the prn gene of B.pertussis. The insert from one positive colony, harbouring cosmid pBDB11, was sequenced and found to contain an open reading frame encoding a 922 amino acid protein with calculated mol.wt. 95.177. This precursor protein (P995") is processed in vivo to the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE, but with actual mol.wt. 61kD. Antigenic fragments of the protein will be useful in developing an acellular vaccine against B.parapertussis. Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to Pro612.
 Gaps
 48
 Bordetella parapertussis pertactin outer membrane protein, p.70.
 1 GAKAPPAPKPAPQPG------PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
 Indels 10;
 Length 922;
 Score 257; DB 13;
Pred. No. 6.9e-13;
0; Mismatches 0;
 /note= "Pertactin region II"
 254..304
/note= "Pertactin region I"
564..621
 Location/Qualifiers
 AAE16185 standard; Protein; 922 AA.
 Guiso-maclouf N, Boursaux-eude C;
 94.5%;
82.8%;
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 Bordetella parapertussis.
 48; Conservative
 (INSP) INST PASTEUR.
 WPI; 2002-097639/13.
 Best Local Similarity
 922 AA;
 N-PSDB; AAD26442
 WO200190143-A2.
 26-MAR-2002
 29-NOV-2001
 AAE16185;
 Sequence
 Query Match
 Region
 Reg ton
 Matches
 RESULT 11
 Key
 AAE16185
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B. bronchiseptica strain II-3 pertactin outer membrane protein region II.

(first entry)

26-MAR-2002

AAE16195;

Pertactin, PRN, outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.

Bordetella bronchiseptica.

WO200190143-A2.

29-NOV-2001

23-MAY-2001; 2001WO-EP06457. 25-MAY-2000; 2000US-206969P.

(INSP ) INST PASTEUR.

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 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 for
 1 GAKAPPAPKPA------PQPGPQPPQPPQPPQPPQRQPEAPAPPGPAGRELSAA 48
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 Length 60;
 Indels
 ö
 Score 256; DB 23;
Pred. No. 1.1e-13;
0; Mismatches 0;
 Boursaux-eude C;
 Claim 26; Fig 1c; 47pp; English.
 Query Match 94.1%;
Best Local Similarity 80.0%;
Matches 48; Conservative
 WPI; 2002-097639/13.
 Guiso-maclouf N,
 60 AA;
 Sequence
 g
ò
```

The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the

Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions for treating infections caused by Bordetella and in diagnostic methods

Disclosure; Page 34; 47pp; English.

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Peptide
 Peptide
 Peptide
 Peptide
 eptide
 RESULT 15
 AAR14321
à
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 The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Pertactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, 91ycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the antigens can be used for qualitative or quantitative determination of Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region II.
 B. bronchiseptica strain II-8 pertactin outer membrane protein region II.

 B. bronchiseptica strain II-9 pertactin outer membrane protein region II.

 for
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection; therapy; antibiotic; antibacterial; region II.
 Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 91.5%; Score 249; DB 23; Length 52;
llarity 88.5%; Pred. No. 3.4e-13;
Conservative 0; Mismatches 2; Indels
 Suiso-maclouf N, Boursaux-eude C;
 AAE16200 standard; peptide; 52 AA.
 AAE16201 standard; peptide; 54 AA
 Claim 26; Fig 1c; 47pp; English.
 23-MAY-2001; 2001WO-EP06457
 25-MAY-2000; 2000US-206969P
 (first entry)
 (first entry)
 Bordetella bronchiseptica
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 Similarity
 52 AA;
 40200190143-A2
 Local S...
 26-MAR-2002
 26-MAR-2002
 29-NOV-2001
 Sequence
 AAE16200;
 AAE16201;
 Query Match
 Matches
 RESULT 14
AAE16201
 RESULT 13
 AAE16200
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a

XXEX DXXXX

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The present invention relates to Bordetella bronchiseptica pertactin (outer membrane protein) or their fragments. Pertactin (PRN) is used as vaccine. Perfactin antibody is useful for treating Bordetella infections and used to detect Bordetella antigens in biological preparations or in purifying corresponding proteins, glycoproteins or their mixtures when used in affinity chromatographic columns. Pertactin is useful as antigens to identify antibodies to Bordetella in materials such as human or other animal tissue and human or other animal cells, as well as biological fluids, such as human or other animal body fluids, including human sera, and to determine the concentration of Ab in those materials. Thus the Bordetella in a material. The present sequence is B. bronchiseptica pertactin outer membrane protein region ii.
 Gaps
 Polypeptides containing polymorphisms of the repeated regions of pertactin in Bordetella species, useful in immunogenic compositions treating infections caused by Bordetella and in diagnostic methods
 ..
 91.2%; Score 248; DB 23; Length 54; 85.2%; Pred. No. 4.2e-13; Live 0; Mismatches 2; Indels
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therapy; antiblotic; antibacterial; region II.
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 Claim 26; Fig 1c; 47pp; English.
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 25-MAY-2000; 2000US-206969P.
 20-JAN-1992 (first entry)
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 271..275
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Best Local Similarity 85.2 Matches 46; Conservative
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 Pertactin antigen P.70.
 (INSP) INST PASTEUR
 WPI; 2002-097639/13.
 W0200190143-A2.
 29-NOV-2001
 AAR14321;
 Sequence
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for

ij

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Pichia microorganisms are transformed for the expression of pertactin antigens. DNA sequence used are represented in AAQ14319-20 encoding the B. bronchiseptice P.68 and B. parapertussis P.70 antigen respectively or the B. pertussis P.69 encoding sequence described by I.G. Charles et al. Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448
 90.8%; Score 247; DB 12; Length 922;
82.8%; Pred. No. 4.2e-12;
tive 0; Mismatches 0; Indels 10
 the 46 Xs represent amino acids missing in the specification
 Pichia microorganism transformants - for production of
Bordetella pertactin antigens for whooping cough vaccines
 Disclosure; Fig 1C; 38pp; English.
 592..594
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595..597
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598..600
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610..612
 (WELL) WELLCOME FOUNDATION LTD.
 583..585
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586..588
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589..591
 79..581
label- repeat
label= repeat
 91WO-GB00487.
 90GB-0007416.
 Clare JJ, Romanos MA;
 WPI; 1991-325214/44.
N-PSDB; AAQ14320.
 922 AA;
 28-MAR-1991;
 02-APR-1990;
 W09115571-A.
 17-0CT-1991.
 Sequence
 Query Match
 Peptide
 Pept1de
 Peptide
 Peptide
 eptide
 Peptide
 Peptide
 Peptide
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g ð

0; Indels 10;

Best Local Similarity 82.8 Matches 48; Conservative

Search completed: May 7, 2003, 16:47:09 Job time: 25.9404 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2003, 16:41:51; Search time 7.93186 Seconds

(without alignments)

178.054 Million cell updates/sec
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Title: US-09-855-754B-20
Perfect score: 272
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Sequence: 1 GAKAPPAPKPAPQPGPQPPQ.
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued\_Patents\_AA:\*

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5: /cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/laa/PcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|   | Description           | Sequence 4, Appli | ė,               | 7                | Sequence 11, Appl | 11,              | 8,               | 16,               | 16,              | 28,              | 29,              | Sequence 30, Appl | 31,              | 6, 4             | ý               | 42,               | 21,              | 15,              | . 520     | Patent No. 5202236 | Sequence 8, Appli | 7               | 99               | 149,              | 134,              | 4, Ar           | 4               | Sequence 21, Appl |
|---|-----------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-----------------|-------------------|------------------|------------------|-----------|--------------------|-------------------|-----------------|------------------|-------------------|-------------------|-----------------|-----------------|-------------------|
|   | ID                    | US-08-460-269C-4  | US-08-460-269C-6 | US-08-460-269C-2 | US-08-237-716-11  | US-08-750-624-11 | US-08-460-269C-8 | US-08-246-982A-16 | US-08-453-265-16 | US-09-041-886-28 | US-09-041-886-29 | US-09-041-886-30  | US-09-041-886-31 | US-08-246-982A-6 | US-08-453-265-6 | US-08-457-273B-42 | US-08-556-419-21 | US-09-041-886-15 | 5202236-3 | 5202236-37         | US-08-457-273B-8  | US-08-155-888-2 | US-09-179-558-66 | US-09-314-268-149 | US-09-314-268-134 | US-09-026-587-4 | US-09-227-420-4 | US-08-860-635A-21 |
|   | DB                    | 4                 | 4                | 4                | н                 | 4                | 4                | -                 | Н                | 4                | 4                | 4                 | 4                | -                | -1              | ~                 | ٣                | 4                | 9         | 9                  | 7                 | m               | 4                | 4                 | 4                 | 7               | ~               | 4                 |
|   | Query<br>Match Length | 911               | 922              | 910              | 33                | 24               | 23               | 3119              | 3119             | 513              | 530              | 552               | 589              | 3144             | 3144            | 3144              | 3144             | 3144             | 334       | 331                | 3118              | 478             | 311              | 75                | 106               | 380             | 380             | 209               |
| æ | Query<br>Match        | 95.6              | 94.5             | 82.0             | 48.9              | 46.7             | 45.6             | 42.8              | 42.8             | 42.6             | 42.6             | 42.6              | 42.6             | 42.6             | 42.6            | 42.6              | 42.6             | 42.6             | 42.3      | 41.9               | 41.5              | 40.3            | 39.2             | 38.8              | 38.4              | 38.4            | 38.4            | 38.5              |
|   | Score                 | 260               | 257              | 223              | 133               | 127              | 124              | 116.5             | 116.5            | 116              | 116              | 116               | 116              | 116              | 116             | 116               | 116              | 116              | 115       | 114                | 113               | 109.5           | 106.5            | 105.5             | 104.5             | 104.5           | 104.5           | 104               |
| • | Result<br>No.         | -                 | 8                | m                | 4                 | 'n               | 9                | 7                 | 80               | 6                | 10               | 11                | 12               | 13               | 14              | 15                | 16               | 17               | 18        | 19                 | 20                | 21              | 22               | 23                | 24                | 25              | 56              | 27                |

| Sequence 21, Appl | Sequence 143, App | Sequence 138, App |                   |                   | Sequence 160, App |                 | 7               | 7               | 7                | 7               | Sequence 2, Appli | 7               | 7               | Sequence 32, Appl | 4 , A            | 6                | Sequence 65, Appl |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-----------------|------------------|-----------------|-------------------|-----------------|-----------------|-------------------|------------------|------------------|-------------------|
| US-09-281-476-21  | US-08-818-112-143 | US-08-818-111-138 | US-09-056-556-143 | US-09-072-596-138 | US-08-961-083-160 | US-07-945-283-2 | US-07-882-292-2 | US-08-331-644-2 | PCT-US93-04102-2 | US-09-095-443-2 | US-08-929-417-2   | US-08-749-391-2 | US-09-390-200-2 | US-08-642-255-32  | US-09-142-551A-4 | US-09-142-551A-3 | US-07-609-716-65  |
| 509 4             | 174 4             | 174 4             | 174 4             | 174 4             | 641 4             | 958 1           | 480 1           | 480 2           | 480 5            | 274 4           | 351 2             | 485 2           | 485 4           | 330 1             | 370 4            | 396 4            | 408 1             |
| 38.2              | 38.1              | 38.1              | 103.5 38.1        | 38.1              | 38.1              | 37.7            | 37.5            | 37.5            | 37.5             | 37.1            | 36.9              | 36.9            | 36.9            | 36.6              | 36.6             | 36.6             | 36.6              |
| 28                | 29 10             | 30 10             | 31 10             | 32 10             | 33 10             | 34 10           | 35              | 36              | 37               | 38              | 39 10             | 40 10           | 41 10           | 42                | 43               | 44               | 45 9              |

#### ALIGNMENTS

RESULT 1

APPLICANT: CLARE, JEFFREX J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN CORRESPONDENCE ADDRESS:
ADDRESSEE: Milen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SEARING SYSTEM: PC-DOS/MS-DOS
SOFTWHARE: Patentin Release #1.0, Version #1.30 NT APPLICATION DATA: APPLICATION NUMBER: US/08/460,269C FILING DATE: 02-Jun-1995 ATTORNEY, AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION: MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-08-460-269C-4 TELEPHONE: (703) 243-6333 Sequence 4, Application US/08460269C Patent No. 6197548 SEQUENCE CHARACTERISTICS: LENGTH: 911 amino acids COMPUTER READABLE FORM: INFORMATION FOR SEQ ID NO: TYPE: amino acid NUMBER OF SEQUENCES: (703) FILING DATE: INFORMATION: CURRENT GENERAL

Query Match 95.6%; Score 260; DB 4; Length 911; Best Local Similarity 92.3%; Pred. No. 6.9e-16; Matches 48; Conservative 0; Mismatches 0; Indels 4; Gaps

ä

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APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
 GENERAL INFORMATION:
APPLICANT: LIPSCOMBE, MATTIN J
APPLICANT: CIRALES, Ian G
APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Neil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 11, Application US/08237716 Patent No. 5589384
 ATTORNEY/AGENT INFORMATION
 32,955
 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION:
 82.0%;
87.5%;
 33 amino acids
 Query Match 82.0 Best Local Similarity 87.5 Matches 42; Conservative
 TELEPHONE: 705 cr
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
 NAME: Wilson, Mary J
REGISTRATION NUMBER:
 MOLECULE TYPE: peptide
 amino acid
 linear
 Virginia
: USA
 STRANDEDNESS:
 22201
 US-08-237-716-11
 COUNTRY:
 LENGTH:
 ò
 g
 1 GAKAPPAPKPAPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 48
 10;
 Sequence 2, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
TILLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
 Length 922;
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
 ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400 CITY: ARLINGTON STATE: VA
 Indels
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 SOFTWARE: Patentin Release #1.0, Version #1.30
 Score 257; DB 4;
Pred. No. 1.3e-15;
0; Mismatches 0
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TOPOLOGY: Linear ;
MOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-460-269C-6
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
 ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 Sequence 6, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
 LENGTH: 922 amino acids TYPE: amino acid
 TELEFAX: (703) 243-6410 INFORMATION FOR SEQ ID NO: 6:
 ATTORNEY/AGENT INFORMATION
 CURRENT APPLICATION DATA:
 94.5%;
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 NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
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 Best Local Similarity 82.8 Matches 48; Conservative
 USA
 COUNTRY: USA
 COUNTRY: U
 STATE: VA
 JS-08-460-269C-2
 JS-08-460-269C-6
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 RESULT 2
 q
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Length 910;
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 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATE: US/08/237,716
APPLICATION NUMBER: US/08/237,716
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-JUN-1992
APPLICATION NUMBER: GB 9112553.4
FILING DATE: 11-JUN-1991
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Nixon & Vanderhye, P.C. STREET: 1100 No. 5589384th Glebe Road, 8th Floor CITY: Arlington STATE: Virginia
Score 223; DB 4;
Pred. No. 1.2e-12;
0; Mismatches 0
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Gaps

Region

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 US-08-246-982A-16
 RESULT 6
US-08-460-269C-8
 COUNTRY:
 δ
 셤
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TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
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pertussis sequence
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Pred. No. 1.2e-05;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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 3: Sim & McBurney
6th Floor, 330 University Avenue
LOCATION: 1... OTHER INFORMATION: /label- LTB sequence
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 UMBER: US/08/750,624
26-FEB-1997
 Sequence 11, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Randil, All
 FILLIN CALL.

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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ilarity 79.3%;
Conservative (
 Query Match
Best Local Similarity 70.6%;
Matches 24; Conservative
 APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
 LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
 CORRESPONDENCE ADDRESS:
ADDRESSEE: S1m & MCE
 NAME/KEY: Region
CCATION: 10.31
CTHER INFORMATION:
US-08-237-716-11
 LOCATION: 4.7
OTHER INFORMATION:
 NAME/KEY: Region
 STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
 Query Match
Best Local Similarity
Matches 23; Conserv
 Toronto
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US-08-750-624-11
 RESULT 5
US-08-750-624-11
 COUNTRY:
 ä
 g
 g
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```
Gaps
 ..
 APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Duyao, Mabel P.
APPLICANT: Hunding F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
 APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROFEIN IN
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
 Length 23;
 COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 Score 124; DB 4;
Pred. No. 2.1e-05;
0; Mismatches 0
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
 NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
 TOPOLOGY: linear MALECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 8: 05-08-460-269C-8
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 Sequence 16, Application US/08246982A Patent No. 5686288 GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
Sequence 8, Aprilication US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
 LENGTH: 23 amino acids
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS
 45.68;
79.38;
 READABLE FORM:
 TYPE: amino acid
 Ouery Match
Best Local Similarity 79.3
Matches 23; Conservative
 NUMBER OF SEQUENCES:
 CITY: ARLINGTON
```

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Gaps

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Best Local Similarity 49.0%; Pred. No. 0.0076;
Matches 25; Conservative 2; Mismatches 13; Indels
 Sequence 29, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell 6 Flores LLP
 | Sequence 28, Application US/09041886
| Patent No. 6235872
| GENERAL INFORMATION:
| APPLICANT: Bardesen, Dale E.
| APPLICANT: Rabizadeh, Sharroz
| TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
| TITLE OF INVENTION: Polypeptides and Methods of Use
| NUMBER OF SEQUENCES: 72
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Campbell & Flores LLP
| STREET: 4370 La Jolla Village Drive, Suite 700
| STREET: San Diego
| STATE: California
| COUNTRY: United States
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 5: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
 DB 4;
 Score 116; DB 4;
Pred. No. 0.0017;
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 1; Mismatches
 6 РАРКРАРОРСРОРРОРРОРРОРОВРАРАРОРА-
 NAME: Campbell, Cathryn A. REGSTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION: TELECOMMUNICATION: (619) 535-9001
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 Query Match 42.6%;
Best Local Similarity 46.4%;
Matches 26; Conservative
 ATTORNEY/AGENT INFORMATION:
 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
 LENGTH: 513 amino acids TYPE: amino acid
 SEQUENCE CHARACTERISTICS:
 , MOLECULE TYPE: peptide US-09-041-886-28
 CITY: San Diego
STATE: California
 FILING DATE:
CLASSIFICATION:
 92122
 US-09-041-886-29
 US-09-041-886-28
 STREET:
 RESULT 9
 δ
 g
 Gaps
 .5; DB 1; Length 3119; 0.0076;
 Sequence 16, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Amboose, Christine M.
APPLICANT: Cusella, James F.
APPLICANT: Cusella, James F.
APPLICANT: Loyao, Mabel P.
APPLICANT: Amboose, Christine M.
APPLICANT: Applicant: 20mella, James F.
APPLICANT: 20mella, James F.
ANDER OF SEQUENCES: 25
 6 PAPKPAPQPGPQPPQPPQPPQRQPEAPAPQPPA------GRELSA 47
 SUFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTONNEY/AGENT ...
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
 E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
 FILING DATE: MAY 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKEY NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2600
 2; Mismatches
 42.8%; Score 116.5; 49.0%; Pred. No. 0.0
 NAME: Ludwig, Steven R.
REGISTRATION UNBER: 36,203
REFERENCE/DOCKET UNBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
 TELEPAN: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3119 amino acids
 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
 ATTORNEY/AGENT INFORMATION:
 3119 amino acids
 SEQUENCE CHARACTERISTICS:
 25; Conservative
 , MOLECULE TYPE: protein US-08-453-265-16
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-246-982A-16
 CORRESPONDENCE ADDRESS:
 amino acid
 Best Local Similarity
 amino acid
 Washington
 U.S.A.
 ZIP: 20005
 ADDRESSEE:
 TOPOLOGY:
 -08-453-265-16
 COUNTRY:
 STREET:
 STATE:
 Matches
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Indels 14;

Length 3119;

42.8%; Score 116.5; DB 1;

Query Match

5

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Gaps
 Gaps
 6 PAPKPAROPGPOPPOPPOP--PORQPEAPAPOPPAG------RELSA 47
 Indels 14;
 15; Indels 14;
 Sequence 6, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Mabrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
 Score 116; DB 4; Length 552;
Pred. No. 0.0018;
1; Mismatches 15; Indels
 Score 116; DB 4; Length 589;
Pred. No. 0.0019;
1; Mismatches 15; Indels
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG--
 P-LJ 2626
 Sequence 31, Application US/09041886
Patent. No. 6235872
 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
 Query Match
Best Local Similarity 46.4%;
Matches 26; Conservative 1
 TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 31
 Query Match
Best Local Similarity 46.4%;
Matches 26; Conservative
 ADDARD STREET: 4370 LL. STREET: 4370 LL. STATE: Callifornia STATE: Callifornia United States
 SEQUENCE CHARACTERISTICS:
 ; MOLECULE TYPE: peptide US-09-041-886-31

// MOLECULE TYPE: peptide
US-09-041-886-30
 amino acid
 GENERAL INFORMATION:
 CLASSIFICATION:
 FILING DATE:
 RESULT 13 US-08-246-982A-6
 US-09-041-886-31
 TOPOLOGY:
 LENGTH:
 RESULT 12
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 ð
 Gaps
 14;
 Score 116; DB 4; Length 530;
Pred. No. 0.0017;
1; Mismatches 15; Indels
 APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharioz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: PolyPeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE, Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
 6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG----
 ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISSTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
 S-09-041-886-30
Sequence 30, Application US/09041886
Patent No. 6235972
GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
 42.68;
 Best Local Similarity 46.4%;
Matches 26; Conservative
 : 530 amino acids
amino acid
 CITY: San Diego
STATE: California
COUNTRY: United States
21P: 92122
United States
 ; MOLECULE TYPE: peptide US-09-041-886-29
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 linear
 amino acid
 TOPOLOGY: linear
 CLASSIFICATION:
 FILING DATE:
 FILING DATE:
 TOPOLOGY:
 LENGTH:
 Query Match
 RESULT 11
```

g ò

```
Gaps
 15; Indels 14;
 GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Lin, Blaoyang
APPLICANT: Lin, Blaoyang
APPLICANT: Nasir, Jamal
TITLE OF INVENTION: Mouse Model for Huntington's Disease and
TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
 Length 3144;
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,273B
 Score 116; DB 2;
Pred. No. 0.0085;
 Score 116; DB 1;
Pred. No. 0.0085;
1; Mismatches 15
 6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG-
 6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG-
 Pred. No. 0.00
1; Mismatches
 Sequence 42, Application US/08457273B Patent No. 5849995
 CITY: Raleigh
CITY: Raleigh
STATE: No. 5849995th Carolina
 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virgina C.
REGISTRATION NUMBER: 37,092
 E: Virginia Bennett
PO Box 37428
 REFERENCE/DOCKET NUMBER: 34
FELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
 42.6%;
illarity 46.4%;
Conservative
 Query Match 42.6%;
Best Local Similarity 46.4%;
Matches 26; Conservative
 SEQUENCE CHARACTERISTICS:
LENGTH: 3144 amino acids
 TELEFAX: 919-854-1401
:NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 INFORMATION FOR SEQ ID NO:
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-265-6
 MOLECULE TYPE: peptide
 amino acid
 Query Match
Best Local Similarity
Matches 26; Conserva
 linear
 TYPE: amino acid
 STRANDEDNESS:
 FILING DATE:
 ADDRESSEE:
 RESULT 15
US-08-457-273B-42
TELEFAX:
 STREET:
 δ
 a
 Gaps
 APPLICANT: MacDoald, Marcy E.
APPLICANT: MacDoald, Marcy E.
APPLICANT: Duyao, Mabel P.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
 -----RELSA 47
 14;
 DB 1; Length 3144;
 Indels
 COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC Comparible
COMPUTER: IBN PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
CLASSIFCATION: 435
 6 PAPKPAPQPGPQPPQPPQP--PQRQPEAPAPQPPAG---
 Sterne, Kessler, Goldstein & Fox
 Pred. No. 0.00
1; Mismatches
 NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
FELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
 Score 116;
 Sequence 6, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
 ATTONNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
 1100 New York Avenue
 46.48;
 Query Match
Best Local Similarity 46.4[†]
Matches 26; Conservative
 ; MOLECULE TYPE: protein US-08-246-982A-6
 CORRESPONDENCE ADDRESS:
 STATE: D.C.
 amino acid
 linear
 U.S.A.
 RY: U.S.A.
20005
 COUNTRY: U.
 COUNTRY:
```

q ò

Search completed: May 7, 2003, 16:57:24 Job time: 10.0228 secs

# GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 7, 2003, 16:31:49 ; Search time 5.63203 Seconds (without alignments) 427.133 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-855-754B-19 335 1 GARAPPAPKPAPQPGPGPGP......QRQPEAPAPQPPAGRELSAA 58

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|           | Description   |     | ~          | Q03035 bordetella | _          | P21997 volvox cart | P40603 brassica na | P21260 owenia fusi | P12978 epstein-bar |            |           |            |            | arabido   | -          | Snm        | Q05860 mus musculu |           | -          | P22670 homo sapien | Q03211 nicotiana t | 024120 drosophila | P08001 sus scrofa | P22576 herpesvirus |            | _          | P25050 herpesvirus | PO5142 mus musculu | P05143 mus musculu | Q99014 trichoderma | P51111 rattus norv | 008816 rattus norv | Q95107 bos taurus | 21         | Q09442 caenorhabdi |
|-----------|---------------|-----|------------|-------------------|------------|--------------------|--------------------|--------------------|--------------------|------------|-----------|------------|------------|-----------|------------|------------|--------------------|-----------|------------|--------------------|--------------------|-------------------|-------------------|--------------------|------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|------------|--------------------|
| SUMMAKIES | ID            | - 1 | PERT_BORPA | PERT_BORBR        | PERT_BORPE | SSGP_VOLCA         | APG_BRANA          | YPRO_OWEFU         | EBN2_EBV           | ACRO_RABIT | GP1_CHLRE | Y066_NPVOP | TEGU_HSV11 | APG_ARATH | G3PT_MOUSE | FM14_MOUSE | FMN1_MOUSE         | MOZ_HUMAN | SEPA_EMENI | RFX1_HUMAN         | EXLP_TOBAC         | CAPU_DROME        | ACRO_PIG          | COLL_HSVSC         | S3A2_HUMAN | S3A2_MOUSE | COLL_HSVS7         | PRP2_MOUSE         | PRP3_MOUSE         | KPC1_TRIRE         | HD_RAT             | WASL_RAT           | WASL_BOVIN        | WASL_HUMAN | YP85_CAEEL         |
|           | th DB         |     | 922 1      |                   |            |                    |                    |                    |                    |            |           |            |            |           |            |            |                    |           |            | 79 1               |                    |                   |                   |                    |            |            |                    |                    |                    |                    |                    |                    | 505 1             | 505 1      | 79 1               |
|           | Length        |     |            |                   |            |                    |                    |                    |                    | 4          | ī.        | œ          |            |           |            |            |                    |           |            | 979                |                    |                   |                   |                    |            |            |                    |                    |                    | -                  | m                  | œ<br>Ñ             |                   |            | m                  |
| dР        | Query         |     | 100.0      | 84.8              | 62.4       | 49.6               | 49.4               | 48.1               | 45.5               | 44.9       | 44.2      | 44.2       | 43.7       | 42.2      | 42.1       | 41.9       | 41.9               | 41.5      | 41.2       | ö                  | 。                  | ö                 | 40.1              |                    |            |            |                    |                    |                    | 39.0               |                    |                    | ω.                | 38.8       | 38.7               |
|           | Score         |     | 335        | 284               | 209        | 166                | 165.5              | 161                | 152.5              | 150.5      | 148       | 148        | 146.5      | 141.5     | 141        | 140.5      | 140.5              | 139       | 138        | 136.5              | 135.5              | 135.5             | 134.5             | 134                | 133        |            | 131.5              | 131.5              | 131.5              | G                  | 130.5              | 130                | 130               |            | 129.5              |
|           | Result<br>No. | !   | 1          | 8                 | e          | 4                  | S                  | ø                  | 7                  | œ          | 6         | 10         | 11         | 12        | 13         | 14         | 15                 | 16        | 17         | 18                 | 19                 | 20                | 21                | 22                 | 23         | 24         | 25                 | 26                 | 27                 | 28                 | 29                 | 30                 | 31                | 35         | 33                 |

| mus musculu<br>homo sapien | mus musculu<br>mus musculu<br>trypanosoma | rattus norv<br>pseudomonas<br>mus musculu | mus musculu<br>triticum ae<br>homo sapien |
|----------------------------|-------------------------------------------|-------------------------------------------|-------------------------------------------|
| P70315<br>060885           | P02831<br>070324<br>P09791                | P10164<br>005613<br>063943                | P42859<br>P04723<br>P42858                |
| WASP_MOUSE<br>BRD4_HUMAN   | HXA3_MOUSE MOT8_MOUSE PARB_TRYBB          | PRP2_RAT<br>TONB_PSEPU<br>MEFD_MOUSE      | HD_MOUSE<br>GDA3_WHEAT<br>HD_HUMAN        |
|                            |                                           |                                           |                                           |
| 520<br>1362                | 443<br>565<br>129                         | 172<br>243<br>514                         | 3119<br>282<br>3144                       |
| 8 8 8<br>8 4 6             | 38.1<br>1.08<br>1.08<br>1.08<br>1.08      | .7.8<br>.7.8<br>.7.8                      | 27.8<br>37.6<br>37.6                      |
| 129<br>128.5<br>128        | 127.5<br>127.5<br>126.5                   | 126.5<br>126.5<br>126.5                   | 126.5<br>126<br>126                       |
| 35                         | 33<br>38<br>39                            | 4 4 4<br>2 1 2                            | 444<br>6443                               |

## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ö
 0; Gaps
 -!- SUBGILT: MONOMER.
-!- SUBGILTALAR LOCATION: Outer membrane.
-!- DISEASE: MAY COUTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-!- MISCELLANDOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
CONCENTRATIONS.
 621
 (APPROXIMATE).
X 3 AA APPROXIMATE REPEATS OF P-Q-P.
3DF7BC56D4712478 CRC64;
 1 GAKAPPAPKPAPQPGPQPPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 58
 LINES).
4 X 5 AA TANDEM REPEATS OF G-G-A-V-P.
 Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G.; "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella bronchiseptica.";
 J. Gen. Microbiol. 138:1697-1705(1992).
-!- FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROC
MEDIATED BY THE R-G-D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN
BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRGLENCE.
ADHESION TO VARIOUS EUKARYOTIC CELL
 CELL ATTACHMENT SITE (INVOLVED IN
 Length 922;
 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.68) (P.94).
 Indels
 100.0%; Score 335; DB 1;
100.0%; Pred. No. 9.6e-14;
1ve 0; Mismatches 0;
 PERTACTIN (P.68).
 911 AA
 SEQUENCE FROM N.A., AND SEQUENCE OF 35-44.
 Outer membrane; Signal; Virulence; Repeat
 POTENTIAL.
 PIR; A47675; A47675.
InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin.
Pfam; PF03212; Pertactin, 1.
 PRT;
 MEDLINE-92407514; PubMed-1527510;
 Σ
 PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY
 EMBL; X54815; CAA38584.1; -. EMBL; A19180; CAA01453.1; -.
 92178
 Local Similarity 100.
nes 58; Conservative
 STANDARD;
 922 AA;
 NCBI_TaxID=518;
 Bordetella.
 PERT_BORBR
Q03035;
 SEQUENCE
 Query Match
 CHAIN
PROPEP
SITE
 REPEAT
REPEAT
REPEAT
 SIGNAL
 DOMAIN
 DOMAIN
 REPEAT
 Best Loca
Matches
 PERT_BORBR
 RESULT 2
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96196517; Pubmed-8600998;
Emsley P., Charles I.G., Fairweather N.F., Isaacs N.W.;

Nature 381:90-92(1996).

-1 FUNCTION: AGGLUTINOGEN THAT BINDS TO EUKARYOTIC CELLS; A PROCESS MEDIATED BY THE R.G. D SEQUENCE. PERTACTIN MAY HAVE A ROLE IN BACTERIAL ADHESION, AND THUS PLAY A ROLE IN VIRULENCE.

-1 SUBUNIT: MONOMER.
-1 DISEASE: MAY CONTRIBUTE TO THE DISEASE STATE OF WHOOPING COUGH.
-1 MISCELLANEOUS: SYNTHESIZED ONLY IN THE PRESENCE OF LOW MG(2+)
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89264462; PubMed-2542937;
Charles I.G., Dougan G., Pickard D., Chatfield S., Smith M.,
Novotny P., Morrissey P., Fairweather N.F.;
"Molecular cloning and characterization of protective outer membrane
protein P.69 from Bordetella pertusais.";
Proc. Natl. Acad. Sci. U.S.A. 86:3554-3558(1989).
                                                                                                                                                                                                                                                               28
                                  SITE (POTENTIAL).
REPEATS OF G-G-A-V-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li J.L., Fairweather N.F., Novotny P., Dougan G., Charles I.G., "Cloning, nucleotide sequence and heterologous expression of the protective outer-membrane protein P.68 pertactin from Bordetella
 ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                          1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA
                                                                                                                                                                                                           9
                                                                                                                                                                         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                        01-7AN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
Pertactin precursor (Outer membrane protein P.69) (P.93).
PRIN OR OMD69A.
                                                                                                                                                                                                           Indels
                                                                                                   80 3 (APPROXIMATE).
01 7 X 3 AA REPEATS OF P-Q-P.
93995 MW; 3078DF6EC2D987A1 CRC64;
                                                                                                                                                                     Score 284; DB 1; L4
Pred. No. 9.2e-11;
0; Mismatches 0;
                              ELL ATTACHMENT
X 5 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                 910 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Microbiol. 138:1697-1705(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                   LINES)
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92407514; PubMed=1527510;
                                                                                                                                                                     84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 264 AND 332.
                                                                                                                                                                                                           52; Conservative
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                703
275
270
275
280
                                                                                                                      601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis.
                                                                                                                                   911 AA;
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONCENTRATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bronchiseptica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CN2992
                                                                                                                                                                                                                                                                                                                                                             PERT_BORPE
P14283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella.
                                                                                                                                       SEQUENCE
                                                                                                                                                                         Query Match
                                                                                                                                                                                             Best Local
                                                                                    REPEAT
                                                                                                    REPEAT
                                                                                                                      DOMAIN
                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                               PERT_BORPE
                                                                                                                                                                                                         Matches
SHEHELES
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EMBL; J04560; AAA22980.1; ALT_SEQ.

PRO-RICH.

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1,32
4,28
449 AA;
  228
260
485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
                                              Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                      MATURATION.
                                                                                                                                                                                          APG OR CEX
                                                                                                                                     APG_BRANA
P40603;
            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 G 52
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                                      Query Match
  DOMAIN
                                               Best Loca
Matches
                                                                                                                    RESULT 5
APG_BRANA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               28
                                                                                                                                   X 5 AA TANDEM REPEATS OF G-A-V-P
                                                                                                                                                                                                                                                                                                                                                                     Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                         CELL ATTACHMENT SITE (INVOLVED IN ADHESION TO VARIOUS EUKARYOTIC CELL
                                                                                                                                                                                                                                                     1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQRPQPPAGRELSAA
                                                                                                                                                                                                                                     16;
                                                                                                                                                                               (APPROXIMATE).
X 3 AA TANDEM REPEATS OF P-Q-P.
A169871E20A2E7DB CRC64;
                                                                                                                                                                                                                   Length 910;
                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                 Score 209; DB 1;
Pred. No. 2.3e-06;
0; Mismatches 1;
                                                                                       PERTACTIN (P.69).
                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Sulfated surface glycoprotein 185 (SSG 185).
                                                                                                                                                                      (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update
                                                                                                                                                                                                                                                                                                                   485 AA
                                                              Outer membrane; Signal; Virulence; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A33647; A33647.
Glycoprotein; Sulfation; Hydroxylation.
                                                                                                  POTENTIAL
        InterPro; IPR004899; Pertact_sup.
InterPro; IPR003992; pertactin.
InterPro; IPR003991; pertactin_vir.
Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                   PRT;
                                           PRINTS; PR01482; PERTACTIN.
PRINTS; PR01484; PRTACTNFAMLY.
                                                                                                                                                                                                93452 MW;
                                                                                                                                                                                                                  62.48;
70.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51616; CAA35953.1; -
                                                                                                                                                                                                                                   41; Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                            276
281
286
579
910 AA;
                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                 SSGP_VOLCA
P21997;
                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                  Query Match
                                                                                      CHAIN
PROPEP
SITE
                                                                     SIGNAL
                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                              REPEAT
                                                                                                                                                     REPEAT
                                                                                                                                                             REPEAT
                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                RESULT 4
SSGP_VOLCA
                                                                                CHAIN
                                                                                                                                                                                                                                   Matches
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(See http://www.isb-sib.ch/announce/
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MEDLINE-94004980; PubMed-8401599;
MEDLINE-94004980; PubMed-8401599;
MCDEDELINE-STOCK R.;
Draper, J., Scott R.;
Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Gametophytic and sporophytic expression of an anther-specific Arabidopsis thaliana gene.";
Plant J. 3:111-120(1993).
--- TISSUE SFECIFICITY: FOUND IN ANTHER, ONLY IN MALE FERTILE PLANTS.
--- DEVELOPMENTAL STAGE: EXPRESSED IN MALE GAMETOGENESIS, DURING MICROSPORE MITOSIS WITH A DRAMATIC DECLINE DURING POLLEN
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sperimatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KAPPAPKPAPQPGPQPGPQPPQPPQP------PQPPQPPQPPQRQPEAPAPQPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Anter-specific proline-rich protein APG (Protein CEX) (Fragment).
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                                                                                        Length 485;
                                                                                                                                              Indels
                                                                                                                                                                                                                                          5 РРАРКРАРОРСРОРСРОРРОРРОРРОРРОРРОРРОРОВЕЛРАРОРР 50
                         50436 MW; A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
9EFB6A3AB28EEA15 CRC64;
                                                                                  49.6%; Score 166; DB 1; L. 56.5%; Pred. No. 0.00048; Live 2; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 165.5; DB 1
llarity 47.5%; Pred. No. 0.00049;
Conservative 4; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                        449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
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POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01098; LIPASE GDSL SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S16748; S16748.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60376; CAA42924.1; -.
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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487 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
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ACRO_RABIT
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Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Haffull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen J.I., Wang F., Kieff E.; "Spatein Parr virus nuclear protein 2 mutations define essential domains for transformation and transactivation."; J. Virol. 65.2545-2554(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                             MEDLINE-901147. PubMed=2105723;
MEDLINE-90116t J., Planells R., Thouveny Y., Fontes M.;

**Presence in invertebrate genomes of sequences characterized by the repetition of the triplet CCPurine.";

**Plane Blophys**

**Plan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90266473; Pubmed-2161150;
Pett1 L., Sample C., Kieff E.;
Subbuclear localization and phosphorylation of Epstein-Barr virus
latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                           Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 161; DB 1; Length 141;
Pred. No. 0.00039;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epetein barr virus (strain 895-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA; 15745 MW; B294E884D152BDB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-T-H MOTIF (POTENTIAL).
                                         YPRO_OWEFU STANDARD; PRT; 141 AA. P21266; P21261; 16. Seated) Ol-MAY-1991 (Rel. 18, Last sequence update) 01-MAY-1995 (Rel. 18, Last sequence update) 01-NOY-1995 (Rel. 32, Last annotation update) Hypothetical proline-rich protein (Fragment). Owenia fusiformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91202599; PubMed-1850028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 310:207-211(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EBNA-2 nuclear protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10377;
                                                                                                                                                                                                                                                       NCBI_TaxID=6347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBN2_EBV
P12978;
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DOMAIN
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Matches
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SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-New Zealaid white; TISSUE-Testis;
MEDLINE-94168861; PubMed-8086468;
MEDLINE-94168861; PubMed-8086468;
MEDLINE-94168861; PubMed-8086468;
MICHAGON R.T., O'RAND M.G.;
Cloning and sequencing of CONAS for rabbit preproacrosin and a novel preproacrosin-related CDNA.";
Blochin. Blophys. Acta 1219:115-218(1994).
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           franscription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQR-----QPEAPAPQPPAGREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 X 2 AA TANDEM REPEATS OF 
DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152.5; DB Pred. No. 0.003; 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; V01555; CAA24877.1; ALT_INIT.
TRANSFAC; T01618; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33, Created)
33, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U05204; AAA61630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 48.2 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Repeat.
DOMAIN 59 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                              - PTM: PHOSPHORYLATED.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                          259
259
299
455
455
4453
4453
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Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=164623;
                                                                                                                                                                                                                       Glycoprotein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOG6_NPVOP
                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y066_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ancoding cell wall hydroxyproline rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-i- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
Pfam; PF00089; trypsin; 1.

PRINTS; PR0722; CHYMOTRYPSIN.

BARRT; SM0020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_LES; 1.

PROSITE; PS00135; TRYPSIN_LES; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
                                                                                                                                                                             ACROSIN LIGHT CHAIN (BY SIMILARITY).
ACROSIN HEAVY CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Bukaryota; Viidiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonaceae; Chlamydomonas.
NCBL_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILNB-21159092; Pubmed-11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPI_CHLRE STANDARD, PRT, 555 AA.

O9FPO6, 003927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91017504; PubMed-1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AKAPPAPKPAPQPGPQP-GPQPP----QPPQPPQPPQPPQPPQRQPEAPAPQPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1C015A4E0BC0C668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                   PRO-RICH.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: Associates with GP2 and GP3.-1- PIM: N-glycosylated and O-glycosylated.
                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                               SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46422 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA;
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29; Conserv
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ACT_SITE
ACT_SITE
SEQUENCE
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Matches 2
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PROPEP
DOMAIN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear nollyhadrogialvirus genome".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95343549; PubMed-7618274;
Ahrens C.H., Carlson C., Rohrmann G.F.;
"Identification, sequence, and transcriptional analysis of lef-3,
gene essential for Orgyia pseudotsugata baculovirus DNA
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
VEGETATIVE CELL WALL PROTEIN GP1.
49 x 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ahrens C.H., Rohrmann G.F.; "The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            083949; 065364; 010233; 01-0023; 01-00-1997 (Rel. 35, Created)
01-00v-1997 (Rel. 35, Last sequence update)
01-00v-1997 (Rel. 35, Last annotation update)
Hypothetical 98.6 kDa protein (ORF71).
Orgyla pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.2%; Score 148; DB 1; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 APPAPKPAPQPGPQPPQPPQPPQPPQP---PQPPQPPQRQPEAPAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 210 372-382(1995).
-1- SIMILARIȚY: TO CORRESPONDING ORF IN ACMNPV AND LDMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.00
2; Mismatches
                                                                                                                                                         EMBL; M58496; AA69706.1; ALT_SEQ. GlycoSulteDB; Q9FPQ6; InterPro; IPR002965; P_itch_extensn. InterPro; IPR003882; Pistil_extensin. PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Virol. 77:825-837(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54219 MW;
                                                                                                                             EMBL; AF309494; AAG45420.1; -
                                                                                                                                                                                                                                                                                                                                                              Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyhedrosis virus genome."
Virology 229:381-399(1997).
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us-09-855-754b-19.rsp

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                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          5 PPAPKPA-----PQPGPQPGPQPPQPP-----QPPQPPQPPQRQPEAPAPQ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Complete viria type 1.";
herpes simplex viria type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBW BPLE1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 X 2 AA TANDEM REPEATS OF P-Q.
                                                                                                                                                                    Score 148; DB 1; Length 875; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC5D31FF4F9FE3F4 CRC64;
                                                                                                                    DOMAIN 86 91 POLY-PRO.
SEQUENCE 875 AA; 98603 MW; F03DB1B430D33C42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3164 AA.
                                                                                                                                                                    Query Match 44.2%; Score 148; DB Best Local Similarity 47.5%; Pred. No. 0.008 Matches 29; Conservative 3; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TK; 130065; WMBEH6.
nterPro; IPR005210; Herpes_UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3164 AA; 335857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14112; CAA32311.1; -. PIR; I30085; WMBEH6.
                              EMBL, 075930; AAC59070.1; -. EMBL, U39145, AAB04047.1; -. EMBL, D45397; BAA08236.1; -. HSSP; P01100; IFOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                  Hypothetical protein.
DOMAIN 86 9
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                TEGU_HSV11
                                                                                                                                                                                                                                                                                                                                              146 P 146
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                      between the Swiss Institute of Bioinformatics and the EMBL outstation—
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grusby-Jackson L., Kuo A., Leder P.;
"A variant limb deformity transcript expressed in the embryonic mouse
                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PPAPK---PAPQPGPQPGPQPPQPPQPPQPPQPPQRQP----EAPAPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
MISSING (IN REF. 2).
L -> V (IN REF. 2).
05FF0A093DIABD9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MNY_2000 (Rel. 39, Last annotation update)
FMN OR LD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 141; DB 1
Pred. No. 0.013;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1206 AA.
                                                                                                                                                                                                                                                                                                                                                             CYS/PRO-RICH.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                              MGD; MGI:95653; Gapds.
InterPro: IPR000173; GAP_dhdrogenase.
Pfam: PF00044; gpdh; 1.
Pfam: PF02800; gpdh_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Embryo;
MEDLINE-92112033; PubMed=1339380;
                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; NAD
                                                                                                                                                                                                                                                                              Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47657 MW;
                                                                                                                                                          EMBL; M60978; AAA53033.1; -.
EMBL; U09964; AAA80276.1; -.
HSSP; P56649; IDSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.18;
illarity 54.78;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
43
440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
                                                                                                                                                                                                                                                                                                                                          Glycolysis;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FM14_MOUSE
Q05859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FM14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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- FOUCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING THE SWITCH
BETWEEN DIFFERENT PATHWAYS FOR ENERGY PRODUCTION DURING
SPERMIOGENESIS AND IN THE SPERMATOZOON.
- CATALYTIT OF TYVETALGEHYGE 3-Phosphate + phosphate +
NADL+) = 3-phospho-D-glyceroyl phosphate + NADH.
-- PATHWAY: Second phase of 91ycolysis; first step.
-- SUBDINIT HOMOTETRAKER (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT DAY 20 IN POST-MEIOTIC
GERM CELLS. LEYELS INCREASE UNTIL DAY 24 AND THEN REMAIN CONSTANT
                                                                                                                ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. BY SIMILARITY. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  3 KAPPAPKPAPQPGPQPGPQ-----PPQPPQP-PQPPQPPQPPQPPQRPPAP----- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STASUE-Testis;
MEDLINE-95254745; PubMed-7736666;
Welch J.E., Brown P.R., O'Brien D.A., Eddy E.M.;
"Genomic organization of a mouse glyceraldehyde 3-phosphate dehydrogenase gene (Gapd-s) expressed in post-meiotic spermatogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CD-1; TISSUE-Testis;
MEDLINE-92273722; PubMed-1775514;
Welch J.E., Schatte E.C., O'Brien D.A., Eddy E.M.;
Expression of a glyceraldehyde 3-phosphate dehydrogenase gene specific to mouse specimatogenic cells.";
Biol. Reprod. 46:869-878(1992).
                                                                                                                                                                                                                                                                              Score 141.5; DB 1; Length 534; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            064467; 060650;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                                                                                                            S -> P (IN REF. 1).
E -> A (IN REF. 1).
E -> H (IN REF. 1).
BA851DG3CF7429DB CRC64;
                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                   POTENTIAL
                                     Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
PIR; S21961; S21961.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                               141 E
325 E
58007 MW;
                                                                                                                                                                                                                                                                            sh 42.2%;
| Similarity 43.9%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1.12) (GAPDH).
                                                                                                                                                                                                                                       534 AA;
                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DURING MATURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||
158 PPKPPA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EČ 1.2.1.12) (
GAPDS OR GAPD-S
                                                                                                                                                                                                                                                                                                                                                                                                                                    46 APQPPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G3PT_MOUSE
                                                                                                                    CHAIN
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                 CONFLICT
                                                                                 Signal.
                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                 Matches
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PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.

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Gaps

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SUBFAMILY.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                             locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney, and Testis;
MEDLINE-90363291; PubMed-2392150;
Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.;
"'Formins': proteins deduced from the alternative transcripts of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 APPAPKPAPQPGPQP---GPQPPQPPQPPQP------PQPPQPPQRQPEAPAPQPP 50
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-i- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97224459; PubMed-9119367;
Wang C.C., Chan D.C., Leder P.;
"The mouse formin (Fmn) gene: genomic structure, novel exons, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62379; CAA44244.1; -.
PIR; S24407; S24407.
MGD; MG: 101815; Fmn.
InterPro; IPR003104; FH2.
InterPro; IPR003104; FH2.
Pfam; PF02181; FH2; 1.
PRINTS; PR00828; FORMIN.
SMARY; SM00498; FH2; 1.
Nuclear protein; Developmental protein; Alternative splicing; Phosphorylation; Colled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 140.5; DB 1; Length 1206; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 POLY-SER.
133464 MW; 4DFB38CB52BD8EE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
FH1 (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL). POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last annotation update)
Formin 1 isoforms I/II/III (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 29, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 39:303-311(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       limb deformity gene.";
Nature 346:850-853(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMN1_MOUSE
Q05860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 PG 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMN OR LD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FMN1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                            11. FIGURE 1. Acad. Sci. U.S.A. 90:5554-5558(1993).

12. FUNCTION: IS IMPORTANT FOR THE MORPHOGENESIS OF LIMB AND KIDNEY
AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR MAY BE
INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

12. SIMPORTATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (SHOWN HERE), IB,

11. III AND IV (AC 005889); ARE PRODUCED BY ALTERNATIVE SPLICING.

2. I-ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (SHOWN HERE), IB,

2. II, III AND IV (AC 005889); ARE PRODUCED BY ALTERNATIVE SPLICING.

2. OFFERENT SIZE TRANSCRIPES EXIST WITHIN ANY ONE TISSUE.

2. III, III AND IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND

3. IS SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY. TESTIS,

2. ILIMB, OVARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HANDERIAN

2. IS EXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL

3. SEXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL

3. OCHAPARTENTY PREDOMYMANTY IN THE POSTERROR RESCION TO

3. THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.

3. THE EPITHELIAL COMPARTMENT ON SERINE AND POSSIBLY THRECHINE RESIDUES.

4. STHILARITY: CONTAINS I FORMIN HOMOLOGY 1 (FH1) DOMAIN.

5. STHILARITY: CONTAINS I FORMIN HOMOLOGY 2 (FH2) DOMAIN.

5. STHILARITY: BELONGS TO THE FORMIN HOMOLOGY 2 (FH2) DOMAIN.
                                 Vogt T.F., Jackson-Grusby L., Rush J., Leder P.; "Formins: phosphoprotein isoforms encoded by the mouse limb deformity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 APPAPKPAPQPGPQP----GPQPPQPPQPPQP------PQPPQPPQRQPEAPAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Developmental protein; Alternative splicing; Phosphorylation; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 140.5; DB 1; Length
Pred. No. 0.033;
1; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF2FB1E9CA9DAF43 CRC64;
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MISSING (IN ISOFORM III).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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POLY-PRO.
POLY-SER.
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MEDLINE=93296176; PubMed=8516300;
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MGD; MGI:101815; Fmn.
InterPro; IPR003104; FH2.
InterPro; IPR001265; Formin.
Pfam; PF02181; FH2; 1.
PRINTS; PR00828; FORMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X53599; CAA37668.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00498; FH2; 1.
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OM protein - protein search, using sw model

Run on:

7, 2003, 16:41:02 ; Search time 10.8688 Seconds (without alignments) 513.008 Million cell updates/sec

US-09-855-754B-19 Title: Perfect score: Sequence:

335 1 GAKAPPAPKPAPQPGPGPP......ORQPEAPAPPAGRELSAA

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	pertactin - Bordet	68K outer membrane	outer membrane pro	hypothetical 47.8K	sulfated surface q	proline-rich prote	pherophorin-S - Vo	hypothetical proli	hypothetical prote	w	cysteine-rich exte	acrosin (EC 3.4.21	chitinase (EC 3.2.	hypothetical prote	-	hypothetical prote		proline-rich prote	hypothetical prote	hydroxyproline-ric	hypothetical prote		extensin homolog T	T20H2.9 protein -	qlyceraldehyde-3-p	hypothetical prote	formin isoform IV	formin - mouse	hypothetical prote
SUMMARIES	ID	S15204	A47675	A32560	JC2301	A33647	S16748	T10798	A34043	AE2295	S42442	A48232	S47538	S51939	T48814	B48232	T10340	WMBEH6	T17547	н83619	T07907	B96534	S21961	T06291	A86335	149681	C96623	S24407	S11515	F75518
	DB	7	7	7	7	7	~	7	~	~	7	7	~	7	7	7	~	-	7	7	~	~	a	N	~	~	~	7	N	~
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ď	Query Match	100.0	84.8	62.4	50.3	49.6	49.4	49.3	48.1	46.6	45.5	45.4	44.9	44.8	44.8	44.3	44.2	43.7	43.6	43.1	43.1	43.0	43.0	42.2	42.2	42.1	42.1	41.9	41.9	41.8
	Score	335	284	209	168.5	166	165.5	165	191	156	152.5	152	150.5	150	150	148.5	148	146.5	146	144.5	144.5	144	144	141.5	141.5	141	141	140.5	140.5	140
	Result No.	-	7	ო	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

protein-tyrosine-p	pistil extensin-li	extensin - Volvox	requlatory factor	pistil extensin-li	unknown protein (1	microfilarial shea	acrosin (EC 3.4.21	hypothetical prote	hypothetical prote	ORF2 protein - sai	immediate-early pr	alpha/beta-qliadin	spliceosome-associ	proline-rich prote	proline-rich prote
			•												
T14355	PQ0476	S22697	A35913	J01696	G86441	846965	A34170	A71416	T31611	B34770	EDBEIF	E22364	A47655	C29149	вз906е
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1494	154	464	979	426	1201	228	415	645	1585	102	1460	320	464	227	278
41.2	41.0	40.9	40.7	40.4	40.3	40.1	40.1	40.1	40.1	40.0	40.0	39.7	39.7	39.6	39.4
138	137.5	137	136.5	135.5	135	134.5	134.5	134.5	134.5	134	134	133	133	132.5	132
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
S15204
pertactin - Bordetella parapertussis
N:Alternate names: outer membrane protein P70
C; Species: Bordetalla parapertussis
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999 C:Accesion: 616-204
Rill, LiJ. Dougan, G.: Novotny, P.: Charles, I.G.
Mol. Microbiol. 5, 409-417, 1991
A,Title: P!70 pertactin, an outer-membrane protein from Bordetella parapertussis: clo
A; Reference number: S15204; MUID:91251771; PMID:2041476
A; Accession: S15204
A:Molecule type: DNA
A; Residues: 1-922 < LIL>
A; Cross-references: EMBL: X54547; NID: q39761; PIDN: CAA38419.1; PID: q39762
C; Genetics:
A;Gene: prn
C;Keywords; membrâne protein
Ouerv Match 100.0%: Score 335: DB 2: Length 922:
Best Local Similarity 100.0%; Pred. No. 7.9e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ОУ 1 САКАРРАЙКРАРОРСТРОРРОВРОВРОВРОВРОВРОВРЕВЕВЕРОВЕТСЯВ 58
DD 564 GAKAPPAPKPAPOPGPOPGPOPPOPPOPPOPPOPPOPOROPEAPAPOPPAGRELSAA 621

RESULT 2

.

68K outer membrane protein P.68 pertactin - Bordetella bronchiseptica
C; Species: Bordetella bronchiseptica
C; Date: 19-Decc-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C; Accession: A47675
R; Li, J; Fairweather, N.F; Novotny, P.; Dougan, G; Charles, I.G.
A; Title: Cloning, nucleotide sequence and heterologous expression of the protective of A; Reference number: A47675; MUID:92407514; PMID:1527510

A) Accession: A47675 A) Status: preliminary A; Wolecule type: incleic acid A; Residues: 1-911 <LII> A; Cross-references: GB:X54815; GB:S46416; NID:g39396; PIDN:CAA38584.1; PID:g39397 A; Note: sequence extracted from NCBI backbone (NCBIN:113318, NCBIP:113319)

; 9 Query Match

84.8%; Score 284; DB 2; Length 911;
Best Local Similarity 89.7%; Pred. No. 1.3e-11;
Matches | 52; Conservative 0; Mismatches 0; Indels

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Gaps

1 GAKAPPAKRAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRPPRAPAPQPPAGRELSAA 58

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Length 485;
                                                                                           5 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165; DB 2; Le
Pred. No. 0.00033;
1; Mismatches 20;
Score 166; DB 2;
Pred. No. 0.00024;
2; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00
1; Mismatches
                                               5;
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49.6%;
llarity 56.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 49.4%;
Best Local Similarity 47.5%;
Matches 29; Conservative
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Best Local Similarity 55.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pherophorin-S - Volvox carteri
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                         Similarity
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    Query Match
Best Local S
Matches 26
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                                                                                                                                                                                                      RESULT 6
S16748
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C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Date: 11-Apr-1990 #sequence_revision 13347
A;Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A;Reference number: A33647; MUID:90094551; PMID:2689458
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nilternate names: ORF-3
C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-May-1999
C;Accession: JC2301
R;Wada, M.; Nakamura, Y.
Nam Res. 1, 163-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
                                                                                                       outer membrane protein P.69 precursor - Bordetella pertussis
C; Species: Bordetella pertussis
C; Species: Bordetella pertussis
C; Species: Bordetella pertussis
C; Species: Bordetella pertussis
C; Accession: A32560
R; Charles, I.G.; Dougan, G.; Pickard, D.; Chatfield, S.; Smith, M.; Novotny, P.; Morriss Proc. Natl. Acad. Scl. US.A. 86, 3554-3558, 1989
A; Title: Molecular cloning and characterization of protective outer membrane protein P.6
A; Reference number: A32560; MUID:89264462; PMID:2542937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1; PID:d1007278;
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A;Reaidues: 1-485 <ERT>
A;Cross-references: GBX51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------APAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 15910 <CHA>
A; Cross-references: GB:J04560; NID:g144053; PIDN:AAA22980.1; PID:g144054
A; Note: 1t is uncertain whether Met-1 or Met-3 is the initiator
       GAKAPPAPKPAPQPGPQPG-----PQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAKAPPAPKPAPQPGPQPFQPPQPPQPPQPPQPPQPPQPPQRDPAPQPPAGRELSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                              C:Keywords: membrane protein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-910/Product: outer membrane protein P6.9 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 910;
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Pred. No. 7.5e-07;
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llarity 52.5%; Pred. No. 0.00015;
Conservative 2; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 47.8K protein - Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.4%;
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A; Residues: 1-430 <WAD>
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                                                                                                                                                                                                                                                                                                      A; Accession: A32560
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proline-rich protein - rape (fragment)
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S16748
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J
submitted to the EMBL Data Library, August 1991
A;Reference number: S16748
A;Reference number: S16748
A;Reference number: S16748
A;Reference number: S16748
A;Residues: 1-449 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C)Accession: T10798
K;GGd1, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophori A;Reference number: Z17154; MUID:97162277; PMID:9009264
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A.Experimental source: strain HK 10; sub_specifies Nagaritensis
A.Note: in contrast to the other pherophorins, pherophorin-5 is targeted to the cell-c. Reywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment) C; Species: Owenia fusiformis C; Dates: OY-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000 C; Accession: A34043; B34044 B3 P34045; Planells, R.; Thouveny, Y.; Fontes, M. Biochem. Biophys. Res. Commun. 166, 66-73, 1990
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.00025;
4; Mismatches 17; Indels 11
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C;Superfamily: ac;Osin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;40-283/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                            Query Match
Best Local Simijarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-209 < WUA>
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Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24877.1; PID:91632787
R;Dambaugh, T.; Hennessy, K.; Chamnankit, L.; Kieff, E.
Proc. Natl. Acad. Sci. U.S.A. 81, 7632-7636, 1984
A;Title: U2 region of Epstein-Barr virus DNA may encode Epstein-Barr nuclear antigen 2.
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Proc. Natl. Acad. Sci. U.S.A. 83, 5096-5100, 1986
A;Title: Nucleotide sequences of mRNAs encoding Epstein-Barr virus nuclear proteins: a
A; Reference number: S42440; MUID:86259739; PMID:3460083
A; Accession: S42442
Title: Presence in invertebrate genomes of sequences characterized by the repetition Reference number: A90159; MUID:90147742; PMID:2105723
Accession: A34043
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A;Experimental source: strain PCC 7120
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C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S42442; S32988; S42447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 161; DB 2; Length 14
Pred. No. 0.0002;
0; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00087;
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A; Residues: 1487 <SAM>
R; Farrell, P.J.
R) Parrell, P.J.
R; Farrell, P.J.
R; Farrell, P.J.
R; Farence number: S32973
A; Reference number: S32973
A; Accession: S32988
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Best Local Similarity 55.1%;
Matches 27; Conservative
                                                                        A, Accession: A34043
A, Molecule type: DNA
A, Residues: 1-141 < BAK>
A, Cross references: GB:M32217
A, Accession: B34043
A, Molecule type: DNA
A, Residues: 59-136 < BAZ>
A; Cross-references: GB:M32217
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hes 25; Conservative
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A; Residues: 1-487 <FAR>
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A;Molecule type: DNA
A;Residues: 1-383 <KUR>
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Matches
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cysteine-rich extensin-like protein 1 precursor - common tobacco C; Species: Nicotiana tabacum (common tobacco)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C; Accession: A48332; P00475; S24617
R; Wu. H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
R; Wu. H.; Zoud, S.; May, B.; Gu, Q.; Cheung, A.Y.
A; Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A; Reference number: A4832; MUID:93342083; PMID:8341705
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A;Reference numbe:: PQ0474; MUID:93005740; PMID:1392607
A;Accession: PQ0475
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R;Rtchardson, R.T.; O'Rand, M.G.
Blochim. Biophys. Acta 1219, 215-218, 1994
A;Title: Cloning and sequencing of CDNAs for rabbit preproacrosin and a novel preproa A; Reference number: $47538; MUID: 94368861; PMID: 806468
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 26-Dec-1994 #sequence_revision 10.Nov-1995 #text_change 22-Jun-1999
                                                        A;Molecule | type: jNA
A;Residues: 1-88,'PpP',89-487 <DAM>
A;Cross-references: EMBL:K03333; NID:g330443; PIDN:AAA45903.1; PID:g330444
C;Superfamily: hydroxyproline-rich glycoprotein
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A; Cross reference; EMBb:U05204; NID:9451841; PIDN:AAA61630.1; PID:9451842
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A;Title: Developmental expression of tobacco pistil-specific genes encod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: cell wall; extracellular matrix; fertilization; glycoprotein E;1-19/Domain: signal sequence #status predicted <SIG>
E;20-209/Product; cysteine-rich extensin-like protein 1 #status experimer
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Pred. No. 0.00099;
I; Mismatches 15; Indels
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Petit Havana SR1
A;Reference number: S42447; MUID:85063846; PMID:6209719
A;Accession: S42447
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Pred. No. 0.0018;
4; Mismatches 20;
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A:Residues: 39-209 <GGL>
A:Cross-references: EMBL:Z14020; NID:g19918;
Experimental source: stigma, style; strain
C; Superfamily: glutelin
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54.08;
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Liarity 48.2%;
Conservative 4
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cysteine-rich extensin-like protein 2 precursor
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                                                                                                                                                                                                                                                 chitinase (EC 3.2.1.14) precursor - beet
C;Species: Beta vulgaris (beet)
C;Species: Beta vulgaris (beet)
C;Accession: S51939; S72315; S45025
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.
Plant Mol. Biol. 27, 211-216, 1995
A;Title: A proline-rich chitinase from Beta vulgaris.
A;Reference number: S51939; MoID:95170004; PMID:7865792
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bate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA
A; Residues: 1-439 < BER>
A;Cross-references: EMBL:X79301; NID:g488730, PID:g488731
A;Note: the authors translated the codon TGC for residue 416 as Gly
A;Accession: S72315
               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KAPPAPKPAPQPGPQPGPQPPQPPQP-PQPPQPPQPPQRDEA-PAPQPPAGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 150; DB 2; Length 439;
Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-1952 <SCH>
A; Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A; Experimental source: cosmid contig 15E6; strain 74
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 15E6.220 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQPPA 51
Score 150.5; DB 2;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 150; DB 2; L
Pred. No. 0.0073;
3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: plant chitinase homology
C;Keywords: glycosidase; hydrolase
F;1-25/Domain: signal sequence #status predicted
F;26-439/Product: chitinase #status predicted <AM
F;183-423/Domain: plant chitinase homology <PCH>
                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 44.8%;
1 Similarity 50.0%;
27; Conservative
           44.9%;
nilarity 52.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 51.1%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 191-397 <BER2>
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
Introns: 248/1; 300/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: NCSP:15E6.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: T48814
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S51939
                                                        29;
                                                      Matches
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A.Status: preliminary
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Rolecule type: mRNA
A.Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A.Rolecule number: PQ0474; MUID:93005740; PMID:1392607
C; Species: Nicotiana tabacum (common tobacco)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C; Accession: B48232; PQ0474; S24616
R; Wu H; Zou, J; May, B; Gu, Q; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S. A. 90, 6829-6833, 1993
A; Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma A; Reference number: A48232; MUID:93342083; PMID:8341705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: glutelin
C; Keywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence *status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 *status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.3%; Score 148.5; DB:
50.9%; Pred. No. 0.0016;
tive 5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: mRNA
A, Residues: 'MAG',1-105 <GOL>
A, Cross-references: EMBL:214014
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Best Local Similarity 50.99
                                                                                                                                                                                                                              A; Accession: B48232
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Search completed: May 7, 2003, 16:55:29 Job time: 12.8688 secs

Sequence 47, Appl Sequence 2, Appl Sequence 20, Appl Sequence 20, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 7, Appl Sequence 1002, Ap Sequence 1002, Ap Sequence 1002, Ap Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl Sequence 11345, A Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 60, Appl Sequence 60, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 62, Appl

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Thu May
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Sequence 19, Application US/09855754

Sequence 19, Application US/09855754

Sequence 19, Application US/0020192237A1

GENERAL INFORMATION:

APPLICANT: BOURSAUX-EUDE, CAROLINE

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED

TITLE OF INVENTION: BONDETELLA PARAPERTUSSIS, AND BORDETELLA

TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: UNMBER: US/09/855,754

CURRENT APPLICATION NUMBER: US/09/855,754

CURRENT PILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/206,969

PRIOR APPLICATION NUMBER: 60/206,969

NUMBER OF SEQ 1D NOS: 24

SOFTWARE: PATENTING NOS: 24
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Sequence 6, Application US/09855754

Publication No. US20020192237A1

GENERAL INFORMATION:

APPLICANT: BOURSAUY.

APPLICANT: GUISO-MACLOUF, NICOLE

TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 US-10-023-523-47

US-09-823-240-2

US-09-823-240-2

US-09-91-111-7

US-10-043-487-282

US-10-043-487-282

US-10-020-215-2

US-10-111-384-3

US-09-9770-689A-5

US-09-994-987-7

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-09-925-299-1002

US-10-925-299-1002

US-10-101-873-10

US-10-042-471-3488

US-10-042-471-3488

US-10-042-471-32

US-10-042-471-32

US-10-042-471-32

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US-10-048-44-2

US-10-086-464-2
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Best Local Similarity 100.0%; Pred. No. 2.9e-16;
Matches 58; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-789-054A-10
US-10-077-584-9
US-09-298-523B-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 19
; LENCTH: 58
; TYPE: PRT
; ORGANISM: Bordètella bronchiseptica
US-09-855-754-19
                                                                 US-09-855-754-19
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Sequence 18, Appli
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Sequence 22, Appli
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Sequence 43,
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Sequence 47,
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                                                                                                                                                                                                                                 US-09-855-754B-19
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1 GAKAPPAPKPAPQPGPQPGP.....QRQPEAPAPQPPAGRELSAA
                                                                                                                                                    7, 2003, 16:53:34; Search time 17.3901 Seconds
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                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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US-09-855-754-16
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US-09-855-754-17
US-09-855-754-20
US-09-855-754-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB s
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CURRENT APPLICATION NUMBER: US/09/855,754
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US-09-855-754-4
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LENGTH: 52
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PERTOSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: HANDHOGENIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR PILLING DATE: 2000-05-25
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: AMMINGGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-000000
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TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNCERNIC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 06/2206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 922;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 335; DB 9; Best Local Similarity 100.0%; Pred. No. 2.7e-15; Matches 58; Conservative 0; Mismatches 0;
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94.8%; Pred. No. 3.6e-14;
tive 0; Mismatches 1.
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US-09-855-754-18
                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bordetella parapertussis US-09-855-754-6
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Publication No. US20020192237A1
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APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 55; Conserv
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LENGTH: 922
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US-09-855-754-16
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GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISAUX-EUDE, CAROLINE
APPLICANT: GUISAUX-EUDE, NICOLE
APPLICANT: GUISAUX-EUDE, NICOLE
APPLICANT: GUISAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PRAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENC COMPOSITIONS
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR APPLICATION NUMBER: 2000-05-25
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APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BOADETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BARONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 03459-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
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                                                                                                                                                                                                                                                                                                           Length 59;
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89.7%; Pred. No. 5.9e-13;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                  Score 298.5; DB 9;
Pred. No. 7.3e-14;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 59
                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-16
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; ORGANISM: Bordetella bronchiseptica
US-09-855-754-15
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Best Local Similarity 95.0%;
Matches 57; Conservative
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Matches 52; Conservative
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SOFTWARE: Patentin Ver.
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NUMBER OF SEO ID NOS: 24
SOFTWARE: Patentin Ver. 2
SEQ ID NO 20
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       US-09-855-754-22
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Fublication No. US20020192237A1

GENERAL INFORMATION:
APPLICANT: BOURSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PREPARTUSSIS,
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION WHORER: US/09/855,754
CURRENT PILING DATE: 2001-09-10

PRIOR PRILING DATE: 2000-09-10

PRIOR PRILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 24

SEQ ID NO 9: 24

LENGTH: 52
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Pred. No. 7.7e-12;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                   Score 284; DB 9;
Pred. No. 6e-12;
0; Mismatches 0
                                                                                                        TYPE: PRT ORGANISM: Bordetella bronchiseptica
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US-09-855-754-17
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ORGANISM: Bordetella bronchiseptica
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Best Local Similarity 89.7%;
Matches 52; Conservative
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Best Local Similarity 87.9%;
Matches 51; Conservative
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SOFTWARE: Patentin Ver.
SOFTWARE: Patentin Ver.
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LENGTH: 54
                                  SEQ ID NO 4
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APPLICANT: BOUSSAUX-EUDE, NICOLE
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE REPRENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ. ID NOS: 24
SOFTWARE: PATCHILING PARE: 2010-05-25
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Publication No. 19220020192237A1
GENERAL INFORMATION:
APPLICANT: BOUGSAUX-EUDE, CAROLINE
APPLICANT: BOUGSAUX-EUDE, CAROLINE
APPLICANT: GUISO-MACLOUE, NICOLE
TITLE OF INVENTION: POLYPERTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: BRONGFIELLA PERTUGSIS,
TITLE OF INVENTION: BRONGFIELLA PERTUGSIS, AND BORDETELLA
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
TITLE OF INVENTION: LAMUNGENIC COMPOSITIONS
CURRENT APPLICATION NUMBER: 2001-09-10
CURRENT FILING DATE: 2001-09-10
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   Score 265; DB 9;
Pred. No. 1.1e-11;
0; Mismatches 5;
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PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANIŚM: Bordetella bronchiseptica
US-09-855-754-14
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US-09-855-754-20
                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
      79.18;
84.58;
Query Match
Best Local Similarity 84.59
Matches 49; Conservative
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Gaps

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Indels

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RESULT 14
US-09-855-754-24
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LENGIH: 910
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LENGTH: 39
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Best Local S
Matches 41
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Matches
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APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYEPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: POLYEPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BRONGHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
FILE REPERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: 05/09/855,754
CURRENT APPLICATION NUMBER: 60/206,969
PRIOR PLING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUISO-MACLOUF, NICOLE
TITLE OF INVENTION: POLYPETIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS
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GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQRPQRDFAPAPQPPAGRELSAA
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1 Similarity 70.7%; Pred. No. 4.1e-08;
41; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 03495-0206-0000
CURRENT APPLICATION NUMBER: US/09/655,754
CURRENT FILING DATE: 20001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bordetella bronchiseptica US-09-855-754-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION: APPLICANT: BOURSAUX-EUDE, CAROLINE
                                                                                                                                        Sequence 21, Application US/09855754 Publication No. US20020192237A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 76.4%;
l Similarity 84.5%;
49; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-(NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 3
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Matches 41; Conserva
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Best Local Similarity
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US-09-855-754-23
                                                                                                                             US-09-855-754-21
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
TITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA PRINCEDIA PARAPERTUSSIS, AND BORDETELLA PARAPERTUSSIS, AND IN TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS
                                                                                                                                               REPEATED
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TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATITLE OF INVENTION: REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
FILE REFERENCE: 03495-0206-00000
CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT PILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BORDETELLA PARAPERTUSSIS, AND BORDETELLA TITLE OF INVENTION: BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS CHIEFRICE: 03455-0206-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 209; DB 9;
Pred. No. 4.9e-07;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/855,754
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/206,969
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-855-754-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/09855754
Publication No. US/0020192237A1
GENERAL INFORMATION:
APPLICANT: BOURSAUX EUDE,
                                                                                         CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bordetella pertussis
US-09-855-754-5
Sequence 5, Application US/09859; Publication No. US20020192237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 62.4%;
1 Similarity 70.7%;
41; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                         APPLICANT: BOURSAUX-EUDE,
                                                              GENERAL INFORMATION
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GENERAL INFORMATION:

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Searched: 262574 segs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries
ase : Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 6. Appli	4	. (Н	16,	134	7,	Sequence 11, Appl	8	Sequence 28, Appl	29,	30,	31,	9	Sequence 6, Appli	42,	21,	Sequence 15, Appl	12,	Sequence 12, Appl	2, 2	143	138,	Sequence 143, App	Sequence 138, App
GI GI	US-08-460-269C-6	US-08-460-269C-4	US-08-460-269C-2	5202236-37	5202236-3	US-08-246-982A-16	US-08-453-265-16	US-09-314-268-134	US-09-095-443-2	US-08-237-716-11	US-08-457-273B-8	US-09-041-886-28	US-09-041-886-29	US-09-041-886-30	US-09-041-886-31	US-08-246-982A-6	US-08-453-265-6	US-08-457-273B-42	US-08-556-419-21	US-09-041-886-15	US-08-534-342-12	US-08-675-140-12	US-08-155-888-2	US-08-818-112-143	US-08-818-111-138	US-09-056-556-143	US-09-072-596-138
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% Query Match Length	922	911	910	331	334	3119	3119	106	1274	33	3118	513	530	552	589	3144	3144	3144	3144	3144	9	9	478	174	174	174	174
% Query Match	100.0	84.8	62.4	44.8	43.0	40.1	40.1	38.4	38.1	37.9	37.8	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.6	37.5	37.5	37.5	37.2	37.2	37.2	37.2
Score	335	284	209	150	144	134.5	134.5	128.5	127.5	127	126.5	126	126	126	126	126	126	126	126	126	125.5	125.5	125.5	124.5	124.5	124.5	124.5
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1 GAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSAA

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Sequence 11, Appl Sequence 160, App	, ,	Sequence 2, Appl1 Sequence 32, Appl	Sequence 65, Appl	Sequence 65, Appl	Sequence 65, Appl	Sequence 66, Appl	Sequence 2, Appl1	Sequence 4, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appl1	Sequence 8, Appli	Sequence 66, Appl	Sequence 33, Appl	Sequence 66, Appl
US-08-750-624-11 US-08-961-083-160	US-08-749-391-2	US-09-390-200-2 US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65	US-09-179-558-66	US-08-929-417-2	US-09-080-897-4	US-08-899-595-1	US-09-323-735-4	US-09-109-841-2	US-08-460-269C-8	US-07-609-716-66	US-08-642-255-33	US-08-475-411A-66
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24 641	485	330	408	408	408	311	351	1255	1255	1255	490	23	357	357	357
37.0	36.6	36.0	36.4	36.4	36.4	35.8	35.8	35.5	35.5	35.5	35.1	34.9	34.9	34.9	34.9
124	122.5	122	122	122	122	120	120	119	119	119	117.5	1117	117	117	117
28,	30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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                                                                                                           APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922;
                                                                                                                                                                                               NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Millen, White, Zelano & Branigan, P.C.
STREEF: 2200 Clarendon Blvd., Suite 1400
CITT: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                              MEDȚUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
CEMPATING SYSTEM: PC-DOS/MS-DOS
SOFȚWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 335; DB 4; Best Local Similarity 100.0%; Pred. No. 1.4e-21; Matches 58; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILLING DATE: 02-Jun-1995
ATTORNEY AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
                                        Sequence 6, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                      YEAST
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                     STATE: VA
COUNTRY: US
ZIP: 22201
                       US-08-460-269C-6
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RESULT 1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID M.; STRAUSBERG, ; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID ; TILLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, ; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID ; TILE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 APPAPAFAPAPALAPAPPNPNPPSPPSPPSPPSPPSPPSPPSPPSPPSP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 APPAPKPAPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPAPQPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 150; DB 6;
Pred. No. 2.8e-06;
0; Mismatches 21,
                                                                                                                                                                                                                                                                                                                                                                                    Score 209; DB 4;
Pred. No. 6.7e-11;
0; Mismatches 1
APPLICATION NUMBER: US/08/460,269C
                                                                                                 REFERENCE/DOCKET NUMBER: POPOV-2 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 243-6333
                                                                                                                                                                                                                                       TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
                                                             NAME: Lebovitz, Richard M. REGISTRATION NUMBER: 37,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-WAY-1990
APPLICATION NUMBER: 80,456
FILING DATE: 07-AUG-1987
                                                                                                                                                          TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 933,945 FILING DATE: 24-NOV-1986 APPLICATION NUMBER: 933,945 APPLICATION NUMBER: 550,128 FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.4%;
Best Local Similarity 70.7%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5202236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5202236-37; Patent No.
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5202236-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08460269C
Setent No. 6197548
GENERAL INFORMATION:
CLARE, JEFFREY J.
APPLICANT: CLARE, JEFFREY J.
TILLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN
                                                                                                               APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 284; DB 4;
Pred. No. 2.9e-17;
0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: POPOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-460-269C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                               Sequence 4, Application US/08460269C Patent No. 6197548 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 911 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 24
TELEPAX: (703) 243-
INFORMATION FOR SEQ ID NO: 4:
SECHENCE FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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Matches 52; Conservative
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                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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US-08-460-269C-2
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Query Match

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 134.5; DB 1;
Pred. No. 0.00041;
3; Mismatches 17;
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Pred. No. 6.9e-05;
3; Mismatches 17
                                                                                                                                                     3: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ludvig, Steven R.
RECISTRATION NUMBER: 36,203
REFERENCE/POCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371.2600
TELEPA: (202) 371.2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 134, Application US/09314268 Patent No. 63463,77
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: PatentIn Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.9%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 39.7%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-453-265-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 179
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Hum
US-09-314-268-134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Pat.
SEQ ID NO 134
LENGTH: 106
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                                                                                                                                     Gaps
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                                                                                                                                                                                          4 APPAPKPAPQPG-----PQPGPQ-----PQPGPQ-PQPPQPPQPPQPPQRQPEAPAP 47
                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3119;
                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Gusella, James F.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 QPPPQPPPPPPPPPQPPQQPPPQGQPPPPPPLP-GPAEEPLHRPKKELSA 73
                                                                                                ; DB 6; Length 334;
9.1e-06;
                                                                                                                               18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: May 20, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134.5; DB 1;
Pred. No. 0.00041;
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                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                Score 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 16, Application US/08453265
; Patent No. 5693757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.9%;
Matches 28; Conservative
                                                                                                43.08;
                                                                                                                    44.48;
       ; FILING DATE: 13-SEP-1984; SEQ ID NO:3:
                                                                                           Query Match
Best Local Similarity 44.49
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-246-982A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                             , LENGTH: 334
5202236-3
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STREET: 110
                                                                                                                                                                                                                                                                                                                                        US-08-246-982A-16
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US-08-453-265-16
                                                                                                                                                                                                                                     48 QPP 50
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STATE:
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GENERAL INFORMATION:
APPLICANT: DOORDAR, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLLOMA
TITLE OF INVENTION: VIRUSES
FILE REFERENCE: 3789/80902
CURRENT APPLICATION NUMBER: US/09/314,268
CURRENT FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 PKPAPQPGPQPGP------QPPQ-----PPQPPQPPQPPQPPQRQPEA---PA 46
Length 3119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 106;
                                                                                                                    9 KPAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP--PAGRELSA 57
                                              Indels
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APPLICANT: CHARLES, Ian G
APPLICANT: FAIRWEATHER, Noil F
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREESSE: Nixon ...
STREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUCATION: 1..2
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Region
LOCATION: 4..7
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 10.31
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: Patent7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                          STREET: 1100 NO CITY: Arlington STATE: Virginia
                                                                                                                                                                              STATE: Virginia
COUNTRY: USA
ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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US-08-457-273B-8
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   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 127.5; DB 4; Length 1274; Pred. No. 0.00074; 1; Mismatches 12; Indels 35;
                                                                                                                                                                              Sequence 2, Application US/09095443
; Patent No. 6342593
; GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Poles, Elor
TITLE OF INVENTION: OF ALP RELATED DISORDERS
; VUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,477
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: WATBULEY, RICHARD J.
REGISTRATION NUMBER: 23,327
REFRENCE/DOCKET NUMBER: 23,327
REFRENCE/DOCKET NUMBER: 23,327
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER: IBM COMPATIBLE ...
COMPOTER: IBM COMPATIBLE ...
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASICED for Windows 2.0
CURRENT APPLICATION DATA:
PILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 QAPGLLPPQSPYAPQAPGVLGQPP 649
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 Q-----QPP. QPEAPAP----QPP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.1%;
Best Local Similarity 43.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-09-095-443-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                         98 PPPNGHD 105
                                                          47 POPPAGRE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-237-716-11
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                                                                                                                                                   RESULT 9
US-09-095-443-2
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Sequence 11, Application US/08237716 Patent No. 5589384

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Gaps
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pertussis sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
E: Nixon & Vanderhye, P.C.
1100 No. 5589384th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 37.9%; Score 127; DB 1; L
Best Local Similarity 57.5%; Pred. No. 3.3e-05;
Matches 23; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 PAPQPGPQPGPQPPQPPQPPQPPQPPQRQPEAPAPQP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= LTB sequence
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/237,716
FILING DATE: 02-MAY-1994
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/896,003
FILING DATE: 11-UN-1992
APPLICATION NUMBER: US 07/896,003
APPLICATION NUMBER: US 07/896,003
APPLICATION NUMBER: US 07/896,003
ATORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117-157
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08457273B Patent No. 5849995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WILSON, MAIY J
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PGPEIAPQPGPQPPQPPQP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin, Biaoyang
Nasir, Jamal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                          13 QPGPQPGPQPPQPPQPPQPPQP--PQRQPEAPAPQPPAG------RELSA 57
                                                                                                                                                                                                                                                             Score 126; DB 4; Length 513;
Pred. No. 0.00044;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz TITLE OF INVENTION: Proapoptotic Peptides; Dependenc TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ОРСРОРСРОРРОРРОРРОРРОР--РОКОРЕАРАРОРРАС-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 4;
Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDRER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEO ID NO: 29:
SEQUENCE CHARACTERISTICS:
           P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/041,886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                            TELECOMMUNICATION INFORMATION TELEPHONE: (619) 535-9001
                               TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8001
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amin
                                                                                                                                                                                                                                                             Query Match 37.6%;
Best Local Similarity 47.5%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4370 La Jolla VI
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.5
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                         TOPOLOGY: Inear
MOLECULE TYPE: Peptide
US-09-041-886-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-09-041-886-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-041-886-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3118;
    Mouse Model for Huntington's Disease and Related DNA Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 QPPPQAPPPPPPPPPQPPPQQPPPQQPPPPPLP-GPAEEDLHRPKKELSA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KPAPQPGPQPPGPPQPPQPPQPPQPPQRQPEAPAPQP--PAGRELSA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 126.5; DB 2; Length
Pred. No. 0.002;
3; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proappototic Peptides, Dependenc
TITLE OF INVENTION: Proappototic Peptides of Use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE S: 6
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477-85A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                             STREET: PO bon CITY: Raleigh STATE: No. 5849995th Carolina
                                                                                    E: Virginia Bennett
PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NITORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.8%;
Best Local Similarity 52.9%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Diego
California
Y: United States
TITLE OF INVENTION: MOUSTITLE OF INVENTION: Rela
TOTHE OF SEQUENCES: 42
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Virginia Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                     800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-457-273B-8
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Sequence 30, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizach, Sharroz
TITLE OF INVENTION: Polypeptides and Methods of Use
TITLE OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependenc
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                     2IP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ОРGРОРСРОРРОРРОРРОРРОРРОР--РОКОРЕАРАРОРРАС-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 4;
Pred. No. 0.00047;
1; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-LJ 2626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELERAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 30: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 37.6%;
Best Local Similarity 47.5%;
Matches 28; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 43/C. CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 552 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
COUNTRY: United States
2IP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-041-886-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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| CLASSIFICATION:
| ATTORNEY/AGENT INFORMATION:
| NAME: Campbell, Cathryn A. |
| REGISTRATION NUMBER: 31,815 |
| REFERENCE/DOCKET NUMBER: 11,815 |
| TELECOMMUNICATION INFORMATION: |
| TELEPHONE: (619) 535-9001 |
| TYPE: amino acids |
```

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